2022台灣昆蟲學會第45屆年會

電馭蟲客

數位科技下的昆蟲學脈動

時間：10月19-20日

地點：國立臺灣大學社會科學院

福來朗
HUKUROU

全民都能享受無蟲害的健康環境

All People Share a Healthy Environment Without Pest.

第四十五屆台灣昆蟲學會年會

The 45th Annual Meeting of Taiwan Entomological Society

2024 年 10 月 19 - 20 日

台灣 | 台北 | 國立台灣大學

Oct. 19 - 20, 2024

National Taiwan University

協辦單位: 農業部、國立台灣大學昆蟲學系

各位昆蟲學界的朋友、前輩先進們，大家好：

隨著秋意漸濃，我們再度迎來了一年一度的昆蟲學年會。剛參加完八月底在日本京都舉辦的 ICE2024 國際昆蟲學大會，相信許多人都深刻感受到台灣昆蟲研究的蓬勃發展。透過國際交流，再回顧台灣昆蟲學會的發展歷程，我們更加確信：過去數十年來，昆蟲年會所守護的優良傳統，與時俱進的創新精神，已為學術界、產業界與政府機構搭建了一個良好的交流平台，並持續為未來累積動能。

今年年會的主題為「電馭蟲客：數位科技下的昆蟲學脈動」。即使對 Cyberpunk 文化不甚了解，光是這個主題的視覺意象便能引發對科技與現實之間張力的聯想。近年來，昆蟲學年會的主題緊貼時代脈動和重大議題，今年更是聚焦於科技發展與人工智慧的影響。在科技與 AI 快速演進的當下，我們一方面對未來充滿期待，另一方面也抱有一些疑慮。然而，昆蟲學與各種跨領域技術的緊密結合，正在為這個領域的未來開創新篇章。

在今年的年會中，將透過專題演講與工作坊的形式，深入探討昆蟲學如何與智慧農業整合、AI 世代下的昆蟲學發展趨勢與其應用案例、以及昆蟲 3D 影像技術在昆蟲學研究與科教上的應用，為與會者帶來昆蟲科學的知識饗宴。我們很榮幸邀請到四位專家進行專題演講，包括江昭皚教授（臺大生物機電工程學系）、羅中泉教授（清華大學生命科學系）、林達德教授（臺大生物機電工程學系）和蕭崇德教授（中原大學生物科技學系）。此外，還特別邀請到美國德州農工大學都市暨結構昆蟲學捐贈講座教授 Dr. Edward Vargo，講述台灣家白蟻如何席捲美國，回顧其入侵生物學史；以及中國科學院昆明動物研究所進化生態與多維組學研究員兼學科組負責人呂雪梅博士，她將談論如何透過各層次基因體演化分析技術，來探索蜻蜓和豆娘複眼功能演化的原動力。由曾惠芸副教授主持

的「3D 影像於昆蟲教育及研究的應用工作坊」則是以工作坊的形式，和與會者分享 3D 影像數位化技術如何革新昆蟲科學教育的內容和拓展昆蟲學研究的維度。

今年，我們感謝中西化學工業股份有限公司的贊助，設立了「台灣昆蟲學會中西化學永續獎」，持續鼓勵全國科展以昆蟲為材料的優秀團隊。本次我們也邀請到獲獎團隊之一的高雄市明華國中師生參與年會，懇請大家不吝給予鼓勵。

在我擔任理事長的這四年間，承蒙眾多廠商與合作夥伴的支持，我深感榮幸。無論是提供經費或資源，大家對於學會和活動的支持，都是我們順利運作的關鍵；學會工作團隊在繁忙的研究與生活之餘，依然竭力推動會務；會員朋友們的熱情響應與參與，則是學會蓬勃發展的最大動力。再次感謝各位，也懇請大家繼續陪伴學會，一同為台灣昆蟲的學術社群與產業服務，邁向更光明的未來。

理事長

蕭旭峰

敬上

2024 年 10 月 18 日

第 45 屆昆蟲學會幹部

理事長	蕭旭峰	國立台灣大學昆蟲學系
President	Shiuh-Feng Shiao	Department of Entomology, NTU
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	蔡偉皇	農業部科技司
	Wei-Huang Tsai	Department of Science and Technology, Ministry of Agriculture
	謝佳宏	中國文化大學森林暨自然保育學系
	Chia-Hung Hsieh	Department of Forestry and Nature Conservation, CCU
執行秘書	羅意瑜	台灣昆蟲學會
Executive secretary	Yi-Yu Luo	Taiwan Entomological Society
學術暨國際組	曾書萍	國立台灣大學昆蟲學系
Academic and international section	Shu-Ping Tseng	Department of Entomology, NTU
	林宗翰	國立台灣大學昆蟲學系
	Tzong-Han Lin	Department of Entomology, NTU
	蕭昀	國立台灣大學生態學與演化生物學研究所
	Yun Hsiao	Institute of Ecology and Evolutionary Biology, NTU
活動組	林柏安	國立台灣大學昆蟲學系
Activities section	Po-An Lin	Department of Entomology, NTU
公關組	邱名鍾	國立台灣大學昆蟲學系
Public relations section	Ming-Chung Chiu	Department of Entomology, NTU
	林韋宏	艾爾生態有限公司
	Peter Lin	A.I.R Ecological Education
企劃組	呂曉鈴	國立虎尾科技大學生物科技系
Project planning section	Hsiao-Ling Lu	Department of Biotechnology, NFU
資訊組	吳士緯	國立台灣博物館
Information section	Shipher Wu	National Taiwan Museum
會計組	黎瑞鈴	國立台灣大學昆蟲學系
Accounting section	Jui-Ling Lee	Department of Entomology, NTU
總務組	王詩儀	國立台灣大學昆蟲學系
General affair section	Shih-Yi Wang	Department of Entomology, NTU
台灣昆蟲期刊主編	路光暉	國立中興大學昆蟲學系
Formosan Entomologist editor in chief	Kuang-Hui Lu	Department of Entomology, NCHU
台灣昆蟲副總編輯	吳明城	國立中興大學昆蟲學系
Formosan Entomologist deputy editor in chief	Ming-Cheng Wu	Department of Entomology, NCHU
海外昆蟲學者召集人	蕭昀	國立台灣大學生態學與演化生物學研究所
International academic convenor	Yun Hsiao	Institute of Ecology and Evolutionary Biology, NTU

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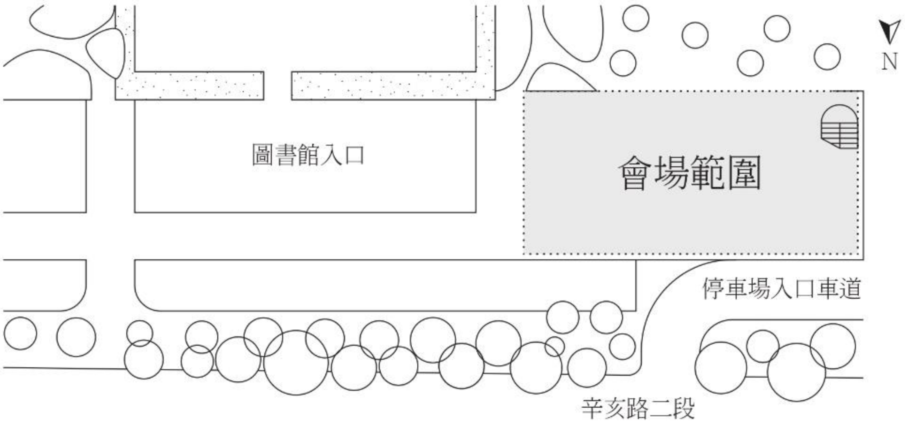
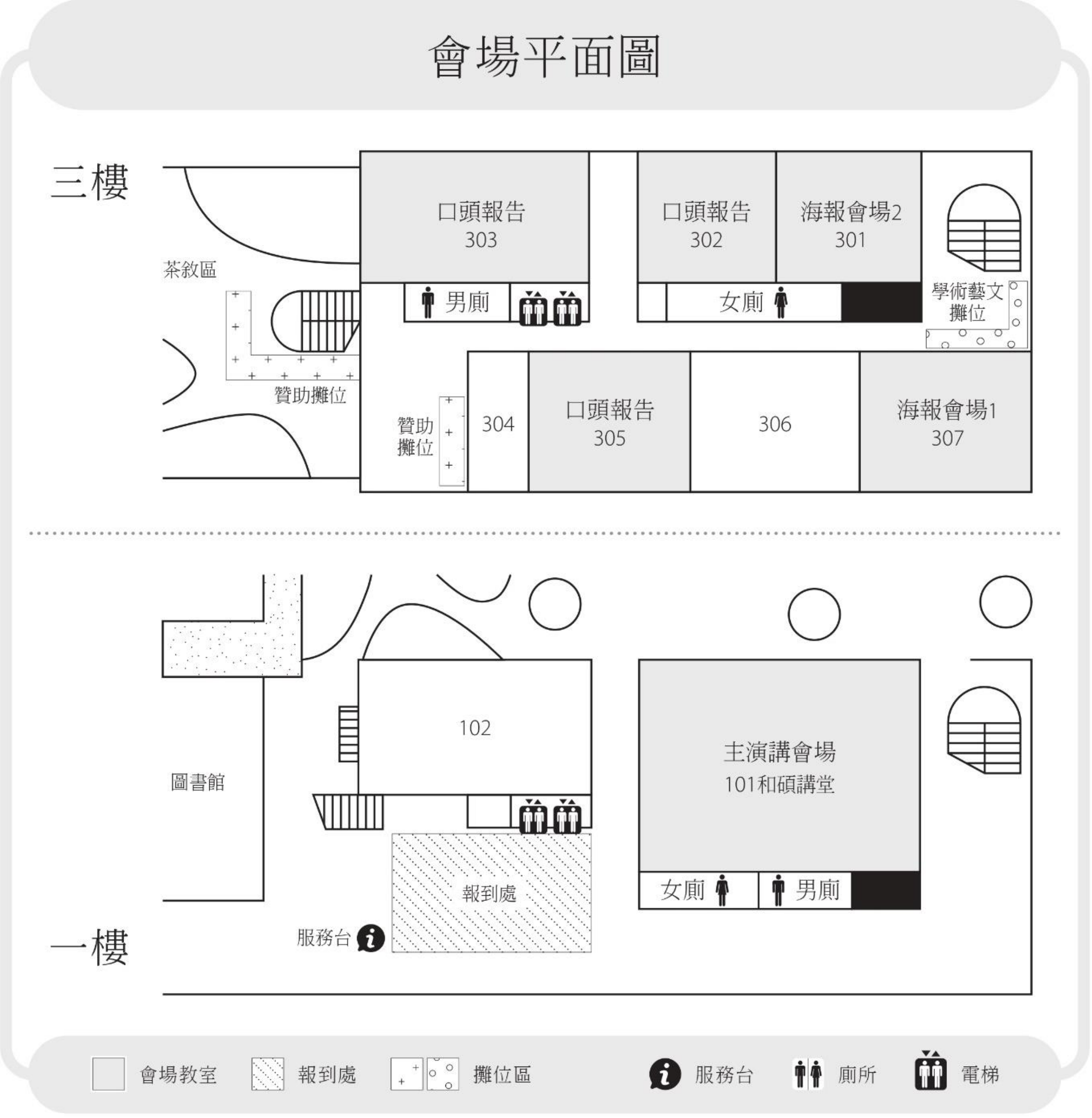
會場平面圖 Floor Plan

台灣昆蟲學會
第45屆年會

交通位置





大會資訊 Meeting Information

大會地點 Meeting Venue

本屆大會於國立台灣大學社會科學院（台北市大安區羅斯福路四段 1 號）舉行。主要場地包括和碩講堂(101 教室)、303 階梯教室、301、302、305 和 307 教室。

The conference will be held at College of Social Sciences Building, NTU (No. 1, Sec. 4, Roosevelt Rd., Da'an Dist., Taipei City). The venue includes Room 101, 303, 301, 302, 305 and 307.

論文宣讀者注意事項 Guidelines for Oral Presenters

所有場地皆備有電腦及投影機，所有講者務必於 10 月 19 日前將檔案上傳至雲端。每位講者有 15 分鐘，包括演講時間 12 分鐘，討論、回答提問與換場時間 3 分鐘。

PCs with Windows systems and projectors are available in all meeting rooms. All presenters must upload their presentation files to the provided link by Oct. 19. Each speaker has 15 minutes: 12 minutes for the oral presentation and 3 minutes for Q&A.

海報宣讀者注意事項 Guidelines for Poster Presenters

請自行準備您的海報，並於第一天 10 月 19 日中午時段至 301、307 教室依編號張貼。現場備有黏貼工具，務必於海報時間之前張貼完畢。請宣讀者於海報時間在海報旁介紹研究內容並回答問題，海報評分時段為 10 月 19 日 14 點 45 分至 15 點 30 分。並務必於 10 月 20 日 15:30 前自行將海報撤下。

Participants are required to prepare their posters in advance and mount it in Room 301 or 307 during the noon session on the initial day of the conference, October 19th. Necessary mounting supplies will be available at the venue. Presenters must be present at their respective posters throughout the session to elucidate their research findings and engage in discussions. The assessment of posters will occur between 14:45 and 15:30 on October 19th. Please ensure that all posters are dismantled and removed by the presenters by 15:30 on October 20th.

大會專題演講 Keynote Speech

江昭皚 博士

國立臺灣大學生物機電工程學系 特聘教授

Dr. Joe-Air Jiang

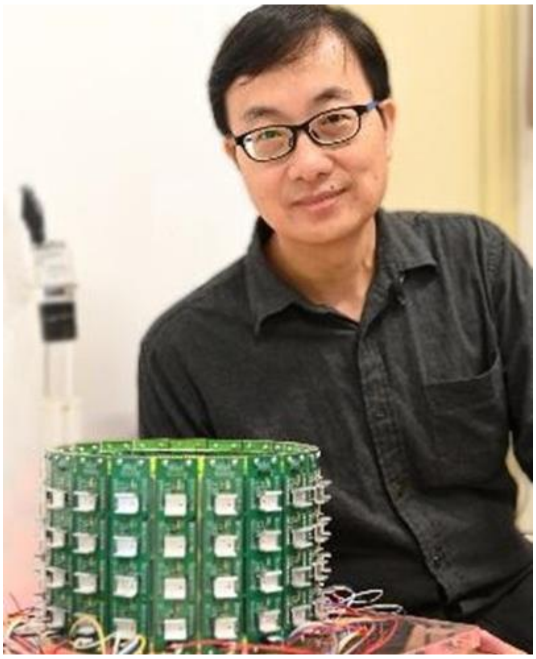
融合物聯網與人工智慧邁入生物防治新時代—臺灣案例研究

Incorporating IoT and AI into the new era of biological control — Case studies in Taiwan

時間(Time): 2024. 10. 19 (Sat.) 09:50 - 10:50

地點(Venue): 和碩講堂 Room 101

大會專題演講 Keynote Speech



羅中泉 博士

國立清華大學系統神經科學研究所 教授

兼系統神經科學研究所 所長

Dr. Chung-Chuan Lo

昆蟲的智慧：微小的大腦如何帶領我們走向下世代的仿神經運算

Insect Intelligence: How tiny brains are leading us to next-generation neuromorphic computing

時間(Time): 2024. 10. 19 (Sat.) 10:50 - 11:50

地點(Venue): 和碩講堂 Room 101

大會專題演講 Keynote Speech

Dr. Edward Vargo

美國德州農工大學都市暨結構昆蟲學

捐贈講座教授

Endowed Chair in Urban and Structural

Entomology at Texas A&M

剖析臺灣家白蟻在美國的入侵生物學史

Deciphering the invasion history of the Formosan subterranean termite in the U.S.

時間(Time): 2024. 10. 20 (Sun.) 09:30 - 10:10

地點(Venue): 和碩講堂 Room 101

大會專題演講 Keynote Speech

呂雪梅 博士

中國科學院昆明動物研究所進化生態與

多維組學動態學科組 研究員兼負責人

Dr. Xue-Mei Lu

蜻蜓目及其視覺能力的基因組進化研究

The evolution of dragonflies and their superior visual ability

時間(Time): 2024. 10. 20 (Sat.) 10:10 - 10:50

地點(Venue): 和碩講堂 Room 101

大會專題演講 Keynote Speech

蕭崇德 博士

中原大學生物科技系 特聘教授

Dr. Chung-Der Hsiao

利用 AI 助力昆蟲行為的研究?

How to Utilize AI to Assist in the Study of Insect Behavior

時間(Time): 2024. 10. 20 (Sat.) 10:50 - 11:50

地點(Venue): 和碩講堂 Room 101

大會專題演講 Keynote Speech

林達德 博士

國立臺灣大學生物機電工程學系 特聘教授

Dr. Ta-Te Lin

智慧蜂箱的數位軌跡

Digital Trajectories of Smart Beehives

時間(Time): 2024. 10. 20 (Sun.) 14:45 - 15:45

地點(Venue): 和碩講堂 Room 101

議程大綱

10 月 19 日 (六)

時間/地點	和碩講堂前			
08:30 - 09:30	報到			
時間/地點	和碩講堂			
09:30 – 09:50	開幕致詞、合照			
09:50 – 10:50	大會主題演講 江昭皚博士 將物聯網與人工智慧融入生物防治新時代—台灣案例研究			
10:50 – 11:50	大會主題演講 羅中泉博士 昆蟲的智慧：微小的大腦如何帶領我們走向下世代的仿神經運算			
11:50 – 13:15	休息用餐 / 12:00 – 13:15 理監事會 (404 教室)			
時間/地點	和碩講堂	303 階梯教室	302 教室	305 教室
13:15 – 14:45	生物多樣性、族群與群聚生態學 OB01-OB05	農業昆蟲學 OA01-OA06	系統分類、族群遺傳、演化 OS01-OS05	行為、生理、個體生物學 OE01-OE06
14:45 – 15:30	茶敘 / 海報時間 (301、307 教室)			
15:30 – 16:45	工作坊 3D 影像於昆蟲教育及研究的應用	農業昆蟲學 OA07-OA10	都市昆蟲/ 醫學昆蟲 OU01/OM01-OM02	行為、生理、個體生物學 OE07-OE10

議程大綱

10 月 20 日(日)

時間/地點	和碩講堂前			
09:00 - 09:30	報到			
時間/地點	和碩講堂			
09:30 – 10:10	專題演講 Edward Vargo 博士 剖析台灣家白蟻在美國的入侵生物學史			
10:10 – 10:50	專題演講 呂雪梅博士 蜻蜓目及其視覺能力的基因組進化研究			
10:50 – 11:50	大會主題演講 蕭崇德博士 如何利用 AI 助力昆蟲行為的研究			
11:50 – 13:00	休息用餐(會員大會 12:00 - 13:00)			
時間/地點	和碩講堂	303 階梯教室	302 教室	305 教室
13:00 – 14:00	生物多樣性、族群與群聚生態學 OB06-OB09	農業昆蟲學 OA11-OA14	都市昆蟲/醫學昆蟲 OU02/OM03-OM04	
14:00 – 14:45	茶敘 / 海報時間 (301、307 教室)			
時間/地點	和碩講堂			
14:45 – 15:45	大會主題演講 林達德博士 智慧蜂箱的數位軌跡			
15:45 – 16:20	閉幕暨頒獎典禮 / 抽獎			

Program at a Glance

Oct. 19, 2024 (Sat.)

Time/Place	Gate of College of Social Sciences Building			
08:30 - 09:30	Registration			
Time/Place	Room 101			
09:30 – 09:50	Opening Welcome/Group Photo			
09:50 – 10:50	Keynote Speech: Dr. Joe-Air Jiang Incorporating IoT and AI into the new era of biological control — Case studies in Taiwan			
10:50 – 11:50	Keynote Speech: Dr. Chung-Chuan Lo Insect intelligence: How tiny brains are leading us to next-generation neuromorphic computing			
11:50 – 13:15	Lunch Break / 12:00 – 13:15 Board of Directors Meeting (Room 404)			
Time/Place	Room 101	Room 303	Room 302	Room 305
13:15 – 14:45	Biodiversity, Population and Community Ecology OB01-OB05	Agricultural Entomology OA01-OA06	Systematics, Population Genetics and Evolution OS01-OS05	Ethology, Physiology and Organismic Biology OE01-OE06
14:45 – 15:30	Tea Break / Poster Time (Room 301, 307)			
15:30 – 16:45	Workshop: 3D Imagination in Entomological Education and Research	Agricultural Entomology OA07-OA10	Urban Entomology/ Medical Entomology OU01/OM01-OM02	Ethology, Physiology and Organismic Biology OE07-OE10

Program at a Glance

Oct. 20, 2024 (Sun.)

Time/Place	Gate of College of Social Sciences Building
09:00 - 09:30	Registration

Time/Place	Room 101
09:30 – 10:10	Keynote Speech: Dr. Edward Vargo Deciphering the invasion history of the Formosan subterranean termite in the U.S.
10:10 – 10:50	Keynote Speech: Dr. Xue-Mei Lu The evolution of dragon flies and their superior visual ability
10:50 – 11:50	Keynote Speech: Dr. Chung-Der Hsiao How to use AI to aid the study of insect behavior?
11:50 – 13:00	Lunch Break / Annual General Meeting (12:00 - 13:00)

Time/Place	Room 101	Room 303	Room 302	Room 305
13:00 – 14:00	Biodiversity, Population and Community Ecology OB06-OB09	Agricultural Entomology OA11-OA14	Urban Entomology/ Medical Entomology OU02/OM03-OM04	
14:00 – 14:45	Tea Break / Poster Time (Room 301, 307)			

Time/Place	Room 101
14:45 – 15:45	Keynote Speech: Dr. Ta-Te Lin Digital Trajectories of Smart Beehives
15:45 – 16:20	Award Ceremony & Farewell / Raffle

編碼對照表

List of Abbreviations

K	大會專題演講 Keynote speech
OA	論文宣讀: 農業昆蟲學 Oral Session: Agricultural Entomology
OB	論文宣讀: 生物多樣性、族群與群聚生態學 Oral Session: Biodiversity, Population and Community Ecology
OE	論文宣讀: 行為、生理、個體生物學 Oral Session: Ethology, Physiology and Organismic Biology
OM	論文宣讀: 醫學昆蟲學 Oral Session: Medical Entomology
OS	論文宣讀: 系統分類、族群遺傳、演化 Oral Session: Systematics, Population Genetics and Evolution
OU	論文宣讀: 都市昆蟲學 Oral Session: Urban Entomology
PA	壁報展示: 農業昆蟲學 Posters: Agricultural Entomology
PB	壁報展示:生物多樣性、族群與群聚生態學 Posters: Biodiversity, Population and Community Ecology
PE	壁報展示:行為、生理、個體生物學 Posters: Ethology, Physiology and Organismic Biology
PM	壁報展示:醫學昆蟲學 Posters: Medical Entomology
PS	壁報展示:系統分類、族群遺傳、演化 Posters: Systematics, Population Genetics and Evolution
PU	壁報展示:都市昆蟲學 Posters: Urban Entomology

論文宣讀總表

*底線為論文宣讀者，粗體為參加競賽

10 月 19 日 (六)

時間/地點	和碩講堂前
08:30 - 09:30	報到
時間/地點	和碩講堂
09:30 – 09:50	開幕致詞、合照
09:50 – 10:50	大會主題演講 江昭皚博士 將物聯網與人工智慧融入生物防治新時代—台灣案例研究 【主持人: 楊恩誠博士】
10:50 – 11:50	大會主題演講 羅中泉博士 昆蟲的智慧：微小的大腦如何帶領我們走向下世代的仿神經運算 【主持人: 麥德倫博士】
11:50 – 13:15	休息用餐 / 12:00 – 13:15 理監事會 (404 教室)

時間/地點	和碩講堂	303 階梯教室	302 教室	305 教室
主題	生物多樣性、族群與群聚生態學 【主持人: 郭祺筠博士、許峰銓博士】	農業昆蟲學 【主持人: 吳怡慧博士、宋一鑫博士】	系統分類、族群遺傳、演化 【主持人: 鄭任鈞博士、李奇峯博士】	行為、生理、個體生物學 【主持人: 何熙誠博士、孫烜駿博士】
13:15 - 13:30	**OB01** **透過生態聲學技術揭開都市綠地之直翅目昆蟲鳴叫多樣性** **洪嘉謙、廖鎮磐、曾惠芸**	**OA01** **分析不同咖啡因劑量對蚜蟲生殖與胚胎發育的影響** **區嘉曦、賴峻偉、張俊哲**	**OS01** **臺灣產寡毛實蠅亞科 (雙翅目：果實蠅科) 分類學研究與雄蟲生殖器形態描述** **黃千育、蕭旭峰**	**OE01** **脫共生對孤雌胎生蚜蟲的繁殖力影響：研究平台建立與卵巢結構解析** **張致榕、賴峻偉、區嘉曦、張俊哲**

13:30 - 13:45	**OB02** **蟬鳴聲的人工智慧自動分類** **王壯平、黃紹毅**	**OA02** **自動化監測系統應用於果實蠅的番茄非疫生產點評估** **葉紹翔、洪傳捷、林劭霖、劉嘉聞、林晁毅、江昭皚、周明儀**	OS02 台灣產水黽(半翅目: 水黽科)分類學初探 劉興哲、馬承漢、三田村敏正	**OE02** **馬尼拉小繭蜂共生病毒透過 miRNA 調控寄主胰島素信號路徑** **蘇榆娟、林鈺淳、吳岳隆**
13:45 – 14:00	**OB03** **Experimental warming disrupts reproductive performance but not parental care in the burying beetle, *Nicrophorus nepalensis*** **Tanzil Gaffar Malik, Benjamin J.M. Jarrett, Syuan-Jyun Sun**	**OA03** **優化 MaxEnt 模型預測氣候變遷對秋行軍蟲 *Spodoptera frugiperda* 於臺灣分佈的影響** **李之鏵、戴正、吳立心**	OS03 透過古生物學剖析偽瓢蟲科多樣性演化動態 蕭昀、維奧莉塔·托馬舍夫斯卡	**OE03** **空間混疊對蜜蜂著陸行為的影響** **謝祥文、楊恩誠**
14:00 - 14:15	**OB04** **The impact of forest fires on termite diversity and food resources** **Hsiang-Chun Liu, Hou-Feng Li**	**OA04** **生物刺激素在增強番茄植株對抗菸草粉蝨與番茄黃化捲葉泰國病毒的潛力** **林晉玨、蔡志偉**	OS04 一種怪螳於台灣的增補(螳螂目: 怪螳科) 王遠騰、葉文斌、邱名鍾	**OE04** **使用 UV 燈防治疣胸琉璃蟻之研究** **李殊智**
14:15 - 14:30	**OB05** **Whole genomic variants unravel the population dynamic and conservation status of endangered butterfly, *Papilio maraho* Shiraki & Sonan, 1934** **Bo-Cheng Wang, Li-Wei Wu**	**OA05** **蟲生真菌防治藍莓之小黃薊馬潛力評估** **林昕佑、陳怡如、乃育昕、陳錦木**	OS05 黃鳳蝶臺灣亞種的"絕滅"是天災還是人禍? 顏聖紘、徐堉峰	**OE05** **不同產卵間隔天數對漿黑卵蜂 *Telenomus remus* 族群性別比以及體內 *Wolbachia* wRem 感染滴度的影響** **吳瑜婷、賴慶庭、吳立心**
14:30 - 14:45		**OA06** **秋行軍蟲核多角體病毒之微生物**		**OE06** **穀蠹後腸水通道蛋白與殺蟲劑感**

		防治引發幼蟲隱性感染和抑制蟲口族群密度的重要性 謝佳芬、李培安、段淑人、唐政綱		**受性之關聯及 RNAi 方法最佳化 王冠文、陳美娥**
14:45 – 15:30	茶敘 / 海報時間 (301、307 教室)			
時間/地點	和碩講堂	303 階梯教室	302 教室	305 教室
主題	工作坊	農業昆蟲學 【主持人: 吳怡慧博士、宋一鑫博士】	都市昆蟲/醫學昆蟲 【主持人: 唐政綱博士、蔡正隆博士】	行為、生理、個體生物學 【主持人: 何熙誠博士、孫烜駿博士】
15:30 – 15:45	3D 影像於昆蟲教育及研究的應用 【主持人: 曾惠芸博士】 與談人: ● 楊恩誠博士 (國立台灣大學昆蟲學系) ● 鄭卜元先生 (Funique VR Studio 董事長) ● 梁維仁博士 (MICRODO 微蟲堂 技術長) ● 扶尚睿先生 (國立台灣大學昆蟲學系)	OA07 分秘夜蛾在三種禾本科作物生長表現之研究 蔡恕仁、許育慈	**OU01 新北市虎頭蜂分布熱點調查 陳琬鎰、丁婕、扶尚睿、謝祥文、楊淑方、葉豐錫、楊恩誠**	**OE07 *Asaia bogorensis* DP3 菌株作為蜜蜂益生菌之潛力及功能性基因分析 馬威鈞、陳竑宇、吳明城**
15:45 – 16:00		OA08 應用深度學習於寄生性天敵昆蟲的計數與性別辨識:以 *Trissolcus sp.* (膜翅目: 緣腹細蜂科) 為例 董巧若、郭彥甫、李世仰、吳怡慧	**OM01 臺北地區犬心絲蟲病媒蚊感染率及其族群動態 黃大綱、蔡志偉**	OE08 無氧代謝協助蜜蜂平衡熱逆境引發之活性氧化物 呂昀恆、劉宸佑、吳岳隆
16:00 – 16:15		OA09 黑水虻於花蓮特色農產之循環農業應用初探 林俊成、林立	**OM02 Effects of emerging contaminants on the development and swimming behavior of dengue vector mosquitoes 林芳伶、蔡坤憲**	OE09 黑翅晦螢的夜間行為與光環境的關係 李佳銘、王子元

16:15 – 16:30		OA10 無人機智慧施放赤眼卵蜂球技術在玉米秋行軍蟲生物防治應用 謝佳宏、張光華、林立、郭東禎、陳昇寬		OE10 Parental care confers offspring developmental plasticity for heat stress tolerance in burying beetles Tanzil Gaffar Malik、蔡沐慈、Benjamin J.M. Jarrett、孫烜駿
16:30 – 16:45				

論文宣讀總表

10 月 20 日(日)

時間/地點	和碩講堂前			
09:00 - 09:30	報到			
時間/地點	和碩講堂			
09:30 – 10:10	專題演講 Dr. Edward Vargo 剖析台灣家白蟻在美國的入侵生物學史 【主持人: 李後鋒博士】			
10:10 – 10:50	專題演講 呂雪梅博士 蜻蜓目及其視覺能力的基因組進化研究 【主持人: 王弘毅博士】			
10:50 – 11:50	大會主題演講 蕭崇德博士 如何利用 AI 助力昆蟲行為的研究 【主持人: 蔡坤憲博士】			
11:50 – 13:00	休息用餐(會員大會 12:00 - 13:00)			
時間/地點	和碩講堂	303 階梯教室	302 教室	305 教室
13:00 – 14:00	生物多樣性、族群與群聚生態學 【主持人: 呂昀恆博士】	農業昆蟲學 【主持人: 蔡志偉博士】	都市昆蟲/醫學昆蟲 【主持人: 郭奇芊博士】	
13:00 – 13:15	OB06 台灣甲蟎分類研究史與研究展望	OA11 不同植物基質來源對麵包蟲(*Tenebrio molitor L.*)生長影響之初	OU02 都市地區臺灣家白蟻巢群分布與餌站系統防治成效評估	

	盧勇仁、王巧萍	探 馮文斌、林柏文、許北辰、董耀仁、段浩文、石憲宗	林玟俊、陳冠豫、賴佑宜、黃建宏、李後鋒	
13:15 – 13:30	OB07 Resolving the paradox of local warning signal diversity: possible mechanisms and a framework for hypothesis testing 郭祺筠	OA12 利用原民作物營造農田促進害蟲調節服務功能 李忠泰、林立、游之穎、鍾雨橋	OM03 土地利用型態改變了海拔梯度上的蚊蟲群聚相 劉鎮、李家儀、蔡坤憲、郭奇芊	
13:30 – 13 :45	OB08 透過貝氏可加性迴歸樹評估台灣農業生態系害蟻之分布及相關因素 林宗翰、許峰銓、方怡婷、曾書萍	OA13 2007–2023 年臺灣進口多肉植物檢出介殼蟲 陳淑佩	OM04 以媒介昆蟲採血法結合兩種納米孔定序策略調查台灣及離島的牛隻病毒 曾皓佑、林春福、丁履紉、廖癸閔、杜武俊	
13:45 - 14:00	OB09 中國蜻蜓多樣性和分類學研究進展 張浩淼	OA14 建立有機栽培甜椒之害蟲綜合管理模式 林鳳琪、徐孟瑜、賴政融、易俞均、王昭月		
14:00 – 14:45	茶敘 / 海報時間 (301、307 教室)			
時間/地點	和碩講堂			
14:45 – 15:45	大會主題演講 林達德博士 智慧蜂箱的數位軌跡 【主持人: 蕭旭峰博士】			

15:45 – 16:20	閉幕暨頒獎典禮 / 抽獎

Conference Agenda

＊Underline denotes speakers, Bold denotes competition

Oct 19 (Sat.)

Time/Place	Entrance of Room 101			
08:30 - 09:30	Registration			
Time/Place	Room 101			
09:30 – 09:50	Opening Welcome/ Group Photo			
09:50 – 10:50	Keynote Speech: Dr. Joe-Air Jiang Incorporating IoT and AI into the new era of biological control — Case studies in Taiwan 【Host: Dr. En-Cheng Yang】			
10:50 – 11:50	Keynote Speech: Dr. Chung-Chuan Lo Insect Intelligence: How tiny brains are leading us to next-generation neuromorphic computing 【Host: Dr. Te-Lun Mai】			
11:50 – 13:15	Lunch Break / 12:00 – 13:15 Board of Directors Meeting (Room 404)			
Time/Place	Room 101	Room 303	Room 302	Room 305
主題	Biodiversity, Population and Community Ecology 【Host: Dr. Chi-Yun Kuo, Dr. Hsu Feng-Chuan】	Agricultural Entomology 【Host: Dr. Yi-Hui Wu, Dr. I-Hsin, Sung】	Systematics, Population Genetics and Evolution 【Host: Dr. Ren-Chung Cheng, Dr. Chi-Feng Lee】	Ethology, Physiology and Organismic Biology 【Host: Dr. Hsi-Cheng Ho, Dr. Syuan-Jyun Sun】
13:15 - 13:30	**OB01** **Unveiling the Orthoptera calling diversity across**	**OA01** **An analysis of the impacts of varying caffeine dosages**	**OS01** **A taxonomic study of Dacinae fruit flies (Diptera:**	**OE01** **Exploring the impact of aposymbiosis on the**

	urban green spacesthrough ecoacoustics method **Chia-Chien Hung, Chen-Pan Liao, Hui-Yun Tseng**	**on aphid reproduction and development** **Simon Au, Chun-wei Lai, Chun-Che Chang**	**Tephritidae) of Taiwan with description of male genitalia** **Chien-Yu Huang, Shiuh-Feng Shiao**	**reproductive capacity of parthenogenetic and viviparous aphids: establishment of research platforms and analysis of ovarian structures** **Chih-jung Chang, Chun-wei Lai, Simon Au, Chun-che Chang**
13:30 - 13:45	**OB02** **Artificial intelligence automated classification of cicada sounds** **Jhuang Ping Wang, Shaw Yhi Hwang**	**OA02** **The evaluation of the automated monitoring system applied to tephritid pest free production sites for tomatoes** **Shao-Hsiang Yeh, Chuan-Jie Hong, Shao-Lin Lin, Chia-Wen Liu, Chao-Yi Lin, Joe-Air Jiang, Ming-Yi Chou**	OS02 Preliminary study on the taxonomy of the water striders (Hemiptera: Gerridae) in Taiwan Hsing-Che Liu, Chen-Han Ma, Toshimasa Mitamura	**OE02** ***Snellenius manila* barcovirus regulate insulin signaling pathway in *Spodoptera litura* though miRNA** **Yu-Juan Su, Yu-Chun Lin, Yueh-Lung Wu**
13:45 – 14:00	**OB03** **Experimental warming disrupts reproductive performance but not parental care in the burying beetle, *Nicrophorus nepalensis*** **Tanzil Gaffar Malik,**	**OA03** **Model optimization: predicting the impact of climate change on the distribution of *Spodoptera frugiperda* in Taiwan using MaxEnt** **Zhi-Hua Li, Jheng Dai, Li-**	OS03 Paleontology provides new insights into diversity dynamics of handsome fungus beetles (Coleoptera: Endomychidae) Yun Hsiao, Wioletta Tomaszewska	**OE03** **Effects of spatial aliasing on honey bee landing behavior** **Hsiang-Wen Hsieh, En-Cheng Yang**

	Benjamin J.M. Jarrett, Syuan-Jyun Sun	**Hsin Wu**		
14:00 - 14:15	**OB04** **The impact of forest fires on termite diversity and food resources** **Hsiang-Chun Liu, Hou-Feng Li**	**OA04** **The potential of biostimulants in enhancing tomato resistance to *Bemisia tabaci* and tomato yellow leaf curl Thailand virus** **Jin-Chueh Lin and Chi-Wei Tsai**	OS04 A supplement to an *Amorphoscelis* species (Mantodea: Amorphoscelididae) in Taiwan Yuan-Teng Wang, Wen-Bin Yeh, Ming-Chung Chiu	**OE04** **Using UV light to prevent and control *Dolichoderus thoracicus*** **Shu-Jhih Li**
14:15 - 14:30	**OB05** **Whole genomic variants unravel the population dynamic and conservation status of endangered butterfly, *Papilio maraho* Shiraki & Sonan, 1934** **Bo-Cheng Wang, Li-Wei Wu**	**OA05** **The potential evaluation of entomopathogenic fungi for controlling yellow tea thrips (*Scirtothrips dorsalis* Hood) of blueberry** **Hsin-Yu Lin, Yee-Ru Chen, Yu-Shin Nai and Chin-Mu Chen**	OS05 Is the extinction of *Papilio machaon sylvina* caused by natural hazards or humans? Shen-Horn Yen, Yu-Feng Hsu	**OE05** **Effects of different egg-laying rest days on the sex ratio and *Wolbachia* titer in the *Wolbachia* wRem-infected population of *Telenomus remus*** **Yu-Ting Wu, Ching-Ting Lai, Li-Hsin Wu**
14:30 - 14:45		**OA06** **The microbiological pest management of SfMNPV plays a crucial role in covert infection to constantly suppressed the population of *Spodoptera frugiperda*** **Jia-Fen Xie, Pei-An Lee,**		**OE06** **Association between hindgut aquaporins and pesticide susceptibility in *Rhyzopertha dominica* (F.) and optimization of RNAi methods** **Guan-Wen Wang, Mei-Er**

		Shu-Jen Tuan, and Cheng-Kang Tang		**Chen**
14:45 – 15:30	Tea Break / Poster Time (Room 301, 307)			
Time/Place	Room 101	Room 303	Room 302	Room 305
主題	Workshop	Agricultural Entomology 【Host: Dr. Yi-Hui Wu, Dr. I-Hsin, Sung】	Urban Entomology/ Medical Entomology 【Host: Dr. Cheng-Kang Tang, Dr. Cheng-Lung Tsai】	Ethology, Physiology and Organismic Biology 【Host: Dr. Hsi-Cheng Ho, Dr. Syuan-Jyun Sun】
15:30 – 15:45	3D Imagination in Entomological Education and Research 【Host: Dr. Hui-Yun Tseng】 Panelists: ● Dr. En-Cheng Yang (Department of Entomology, National Taiwan University) ● Pu-Yuan Cheng (Founder of Funique VR Studio) ● Dr. Wei-Ren Liang (Chief echnology officer of MICRODO) ● Shang-Jui Fu (Department of Entomology, National Taiwan University)	OA07 Study on the growth performance of *Mythimna separata* (Walker) (Lepidoptera: Noctuidae) feeding on three Poaceae crops Shu-Jen Tsai, Yu-Tzu Hsu	**OU01** **Investigation of hornet distribution hotspots in New Taipei City** **Wan-Yi Chen, Chieh Ting, Shang-Jui Fu, Hsiang-Wen Hsieh, Shu-Fang Yang, Feng-Shi Yeh, En-Cheng Yang**	**OE07** **Evaluation of the probiotic potential for honey bees (*Apis mellifera*) and functional gene analysis of *Asaia bogorensis* DP3** **Wei-Juin Ma, Hung-Yu Chen, Ming-Cheng Wu**
15:45 – 16:00		OA08 Application of deep learning in counting and gender identification of parasitoid wasps: a case study of *Trissolcus* sp. (Hymenoptera: Scelionidae) Chiao-Jo Tung, Yan-Fu Kuo, Shih-Yang Lee, Yi-Hui Wu	**OM01** **Infection rate and population dynamics of *Dirofilaria immitis* vector mosquitoes in Taipei** **Da-Gang Huang, Chi-Wei Tsai**	OE08 Temperature-Driven metabolic shifts in honey bees for balancing reactive oxygen species Yun-Heng Lu, Chen-Yu Liu, Yueh-Lung Wu

16:00 – 16:15		OA09 A preliminary study on the application of black soldier flies in circular agriculture of agricultural products in Hualien Jyun-Cheng Lin, Li Lin	**OM02** **Effects of emerging contaminants on the development and swimming behavior of dengue vector mosquitoes** **Fang-Ling Lin, Kun-Hsien Tsai**	OE09 Nocturnal behavior of *Abscondita cerata* related to their photic environment Chia-Ming Lee, Tzi-Yuan Wang
16:15 – 16:30		OA10 Application of smart drone technology for releasing *Trichogramma* wasp balls in the biological control of fall Armyworm in corn Chia-Hung Hsie, Kuang-Hua Chang, Li Lin, Dong-Jhen Guo, Sheng-Kuan Chen		OE10 Parental care confers offspring developmental plasticity for heat stress tolerance in burying beetles Tanzil Gaffar Malik, Mu-Tzu Tsai, Benjamin J.M. Jarrett, Syuan-Jyun Sun
16:30 – 16:45				

Conference Agenda

＊Underline denotes speakers, Bold denotes competition

Oct 20 (Sun.)

Time/Place	Entrance of Room 101			
09:00 - 09:30	Registration			
Time/Place	Room 101			
09:30 – 10:10	Keynote Speech: Dr. Edward Vargo Deciphering the invasion history of the Formosan subterranean termite in the U.S.【Host: Dr. Hou-Feng Li】			
10:10 – 10:50	Keynote Speech: Dr. Xue-Mei Lu The evolution of dragonflies and their superior visual ability 【Host: Dr. Hurng-Yi Wang】			
10:50 – 11:50	Keynote Speech: Dr. Chung-Der Hsiao How to use AI to aid the study of insect behavior? 【Host: Dr. Kun-Hsien Tsai】			
11:50 – 13:00	Lunch Break / Annual General Meeting (12:00 - 13:00)			
Time/Place	Room 101	Room 303	Room 302	Room 305
13:00 – 14:00	Biodiversity, Population and Community Ecology 【Host: Dr. Yun-Heng Lu】	Agricultural Entomology 【Host: Dr. Chi-Wei Tsai】	Medical Entomology/ Urban Entomology 【Host: Dr. Chi-Chien Kuo】	
13:00 – 13:15	OB06 The history and research	OA11 Preliminary study on the effects	OU02 Colony Distribution of	

	prospects of oribatida mites Taxonomy in Taiwan Yung-Jen Lu, Chiao-Ping Wang	of different plant-based substrates on the growth of yellow mealworm (*Tenebrio molitor* L.) Wen-Bin Feng, Bo-Wen Lin, Hao-Wen Duan, Pei-Chen Hsu, Yaw-Jen Dong, Hsien-Tzung Shih	*Coptotermes formosanus* and Evaluation of the Effectiveness of Bait Station Systems in Urban Areas Wen-Jun Lin, Guan-Yu Chen, Yu-Yi Lai, Chien-Hung Huang, Hou-Feng Li	
13:15 – 13:30	OB07 Resolving the paradox of local warning signal diversity: possible mechanisms and a framework for hypothesis testing Chi-Yun Kuo	OA12 Using indigenous crops to build farmland to promote pest regulation service functions Zhong-Tai Li, Lily Lin, Chih-Ying Yu, Yu-Chiao Chung	OM03 Land use alters mosquito communities along altitudinal gradients in Taiwan Jhen Liu, Jia-Yi Li, Kun-Hsien Tsai, Chi-Chien Kuo	
13:30 – 13 :45	OB08 Distribution and associated factors of pest ants in agroecosystem from Taiwan evaluated by Bayesian additive regression trees Tzong-Han Lin, Feng-Chuan Hsu, Yi-Ting Fang, Shu-Ping Tseng	OA13 Scale insects (Hemiptera: Coccoidea) intercepted from imported succulent plants in Taiwan during 2007–2023 Shu-Pei Chen	OM04 Vector-based approach with two nanopore sequencing strategies to survey bovine viruses in Taiwan and offshore islands Hau-You Tzeng, Chuen-Fu Lin, Lu-Jen Ting, Kuei-Min Liao, Wu-Chun Tu	
13:45 - 14:00	OB09 Biodiversity and taxonomy of dragonflies and damselflies from China	OA14 Establishing an integrated pest management program for organic bell pepper cultivation		

	Haomiao Zhang	Feng-Chyi Lin, Meng-Yu Hsu, Cheng-Jung Lai, Yu-Chun Yi, Jau-Yueh Wang		
14:00 – 14:45	Tea Break (20 minutes) / Poster Time (Room 301, 307)			
Time/Place	Room 101			
14:45 – 15:45	Keynote Speech: Dr. Ta-Te Lin Digital Trajectories of Smart Beehives 【Host: Dr. Shiuh-Feng Shiao】			
15:45 – 16:20	Award Ceremony & Farewell / Raffle			

壁報展示總表 Poster List

農業昆蟲學
Agricultural Entomology

【評審: 曾慶慈博士、吳立心博士】
【Judges: Dr. Ching-Tzu Tseng, Dr. Li-Hsin Wu】

編碼 Code	論文標題 Title	作者 Authors
PA01	**針對小樣本影像發展番茄潛旋蛾成蟲 AI 辨識模型** **Development of an AI recognition model for the adults of *Phthorimaea* (*Tuta*) *absoluta* (Lepidoptera: Gelichiidae) based on a small set of images**	**吳承澤，洪傳捷，王壯平，林晁毅，蔡鴻旭，周明儀** **Cheng-Tse Wu, Chuan-Jie Hong, Jhuang-Ping Wang, Chao-Yi Lin, Hung-Hsu Tsai, Ming-Yi Chou**
PA02	**新竹縣白蘭部落與苗栗縣百壽部落蜂花粉來源植物分析** **Analysis of pollen sources for honeybees in R'uyan Tribe of Hsinchu County and Sawi Tribe of Miaoli County**	**孫千雅、陳本翰、趙家慧、徐培修** **Chien-Ya Sun, Pan-Hen Chen, Chia-Hui Chao, Pei-Shou Hsu**
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生物多樣性、族群與群聚生態學
Biodiversity, Population and Community Ecology

【評審: 蔡經甫博士、譚景文博士】
【Judges: Dr. Jing-Fu Tsai, Dr. Ching-Wen Tan】

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PB09	塑膠微粒與底棲大型無脊椎動物的生物多樣性：以台灣中部大甲溪為例 Microplastics and biodiversity of benthic macroinvertebrates: A case study in the Dajia River in central Taiwan	郭美華、陳昭汝、陳柏凱、吳友誠 Mei-Hwa Kuo, Zhao-Ru Chen, Bo-Kai Chen, Yu-Cheng Wu

PB10	雪霸國家公園溪流中微塑膠的垂直通量和底棲大型無脊椎動物的生物多樣性 Vertical flux of microplastics and biodiversity of benthic macroinvertebrate from streams in the Shei-Pa National Park	陳昭汝、丘明智、郭美華 Zhao-Ru Chen, Ming-Chih Chiu, Mei-Hwa Kuo
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行為、生理、個體生物學 【評審：呂曉玲博士、吳立偉博士】
Ethology, Physiology and Organismic Biology 【Judges: Dr. Hsiao-Ling Lu, Dr. Li-Wei Wu】

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系統分類、族群遺傳、演化
Systematics, Population Genetics and Evolution

【評審: 蔡經甫博士、譚景文博士】
【Judges: Dr. Jing-Fu Tsai, Dr. Ching-Wen Tan】

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PS03	臺灣的長毛跗蟎屬蜂蟎 Bee mites of genus *Sennertia* from Taiwan	趙家慧、陸聲山、宋一鑫 Chia-Hui Chao, Sheng-Shan Lu, I-Hsin Sung
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都市昆蟲學/醫學昆蟲學 【評審: 曾書萍博士、李後鋒博士】
Urban Entomology/Medical Entomology 【Judges: Dr. Shu-Ping Tseng, Dr. Hou-Feng Li】

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大會專題演講

Keynote Speech

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融合物聯網與人工智慧邁入生物防治新時代—台灣案例研究

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使用化學農藥是慣行農業中常用的害蟲防治方法。然而，大規模灑佈農藥不僅會造成環境破壞，害蟲也會發展出抗藥性，產生惡性循環，導致防治效力下降。以生物防治技術之天敵昆蟲來進行農業害蟲的防治，不僅可以降低化學農藥的使用，亦能有效地減少害蟲數量。目前，天敵昆蟲的生產方式仍多仰賴密集的人力與細微的操作工作，商用量產工作仍屬空談，難以廣泛使用。融合物聯網與人工智慧技術，將可取代過去天敵昆蟲飼養需要大量仰賴人力作業的生產流程，大幅降低生產成本與人力需求，促進天敵昆蟲的生產邁入智慧化量產的新紀元。本次演講將介紹基徵草蛉與瓢蟲的智慧化量產系統的個案研究成果。

關鍵字：生物防治、天敵昆蟲、物聯網、人工智慧

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昆蟲的智慧：微小的大腦如何帶領我們走向下世代的仿神經運算
Insect Intelligence: How Tiny Brains Are Leading Us to Next-Generation Neuromorphic Computing

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Insects are evolutionary marvels, renowned for their ability to survive and adapt to a wide range of environments. These remarkable capabilities are powered by their compact brains, which contain the secrets of efficient neural computation within small, highly specialized neural circuits. By unraveling the workings of insect neural circuits, we gain insights applicable to designing artificial intelligence systems with constrained computational resources. Recent advances in connectomic databases of fruit fly brains have opened up unprecedented opportunities to study the neural mechanisms underlying insect behavior in exquisite detail. In this presentation, I will review recent progress in understanding the neural circuit mechanisms that underlie spatial computation in fruit fly brains. Additionally, I will discuss related research conducted in my lab, including the investigation into the wiring diagrams of the fruit fly central complex and how these tiny insects maintain orientation memory, make decisions about movement direction, and perform sensorimotor control. Finally, I will demonstrate how insights gained from studying insect nervous systems can be applied to neuromorphic engineering, aiding in the design of navigation and obstacle avoidance systems for drones and robots.

Keywords: Neural circuits, central complex, vision, navigation, neuromorphic engineering

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Deciphering the invasion history of the Formosan subterranean termite in the U.S.

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Native to eastern Asia, the Formosan subterranean termite *Coptotermes formosanus* is one of the most destructive invasive pests in the world, with established populations in Japan, Hawaii and the southeastern US. Using a panel of single nucleotide polymorphisms (SNPs), we retraced the invasion history of this species through approximate Bayesian computation. We found a complex invasion history, with initial introductions to Hawaii which then served as the source for an introduction to the southeastern US. A separate introduction event from southcentral China subsequently occurred in Florida. We also examined the breeding structure of colonies in various native and introduced populations. We found population varied in the proportions of colonies forming simple families (a single queen and king present) and those headed by extended families (multiple inbreeding queens and kings), but no consistent difference between native and invasive populations. Overall, these findings reinforce the pivotal role of bridgeheads in the spread of invasive species and illustrate that the global distribution of *C. formosanus* has been shaped by multiple introductions out of China, which may have prevented and possibly reversed the loss of genetic diversity within its invasive range, and that changes in colony breeding structure cannot account for the invasion success of this species.

Keywords: Invasion biology, invasive species, *Coptotermes formosanus*, population genetics, breeding system

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蜻蜓目及其視覺能力的基因組進化研究

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蜻蜓目是昆蟲綱中物種極其豐富的類群，牠與古翅下綱的蜉蝣目以及新翅下綱三者之間的系統發育關係一直存在爭議，也缺乏全基因組水平的有力證據。蜻蜓在飛行昆蟲中是獵食成功率極高的類群，這與蜻蜓卓越的視覺能力動態追蹤定位獵物有關。基因重覆被認為是具有新基因進化的重要驅動力，基因重覆過程中新拷貝的亞功能化和新功能化對物種表型的功能演化提供原材料。我們對蜻蜓二十個科的物種全基因組系統發育分析結果發現，蜻蜓目和新翅下綱組成姐妹群，蜉蝣目是兩者的外群；蜻蜓和豆娘的祖先大約在 241.9 My 出現分歧。基因家族擴張收縮分析發現，視紫紅質基因家族分別在差翅亞目祖先和蜻蜓目祖先發生了顯著的基因家族擴張。對 26 個組織的轉錄組測序後，發現視紫紅質基因家族的多個拷貝在複眼組織中特異高表達。單細胞轉錄組結果表明蝴蝶裂唇蜓複眼共有 16 種細胞類型，其中視紫紅質基因家族擴張拷貝在光感受器細胞類型中特異高表達。本研究首次結合了三代長讀長全基因組，多器官組織以及單細胞轉錄組等組學手段，系統地解析了蜻蜓目系統發育和複眼表型進化，發現基因重覆可能是蜻蜓複眼功能進化的重要驅動力。

關鍵字：蜻蜓目、昆蟲視覺、基因組（體）學、進化（演化）生物學

如何利用 AI 助力昆蟲行為的研究 ？
How to Utilize AI to Assist in the Study of Insect Behavior

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Artificial Intelligence (AI) has revolutionized the study of animal social behavior by offering new methodologies to collect, analyze, and interpret complex high dimensional data. AI-powered tools, such as machine learning algorithms and computer vision systems, enable researchers to track and monitor individual animals within groups, automatically identifying and analyzing their interactions in natural and controlled environments. This allows for the real-time monitoring of social networks, dominance hierarchies, and cooperative behaviors with unprecedented precision and scalability. AI-driven data analytics can uncover patterns and correlations that might be overlooked by human observation, leading to new insights into the evolutionary and ecological drivers of social behaviors. Advanced simulation models, powered by AI, also facilitate the exploration of theoretical scenarios, providing a deeper understanding of the mechanisms underlying social structures. The research in my lab is focusing on animal behavior tracking and quantitative measurement by using deep learning technology. In our previous works, we have established several important techniques for object counting, recognition, locomotion tracking as well social interaction have been established for protozoa (1), bird (2), fish (3) and crayfish (4) studies. In this presentation, I would like to share our updated findings on insect image recognition (spiderID_APP) (5), locomotion tracking (insect larvae) and fighting (stag beetle) studies.

Keywords: Artificial Intelligence (AI), Deep Learning, Computer Vision, Fighting Behavior

智慧蜂箱的數位軌跡
Digital Trajectories of Smart Beehives

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The presentation explores how modern technology is transforming the way we monitor and understand honeybee behavior. It begins by discussing traditional observation methods, such as the waggle dance, which bees use to share information about food sources. As technology has evolved, so have the tools for tracking bees. The presentation highlights the progression from basic camera-based imaging systems to sophisticated multi-sensing systems that monitor various aspects of honey bee behaviors. These advanced systems use tools like weight scales, temperature and humidity sensors, audio monitors, and cameras to gather detailed insights about what happens inside and outside the hive. One notable finding from the presentation is the daily in-and-out behavior of bees. It was observed that bees are most active in leaving the hive before midday, and more than half of their flights last only about three minutes. These observations help researchers better understand bee foraging patterns. Additionally, the presentation highlights six major weight variation patterns observed in beehives. Each pattern corresponds to specific bee activities and environmental conditions, offering deeper insights into hive dynamics. The weight variation patterns were also analyzed alongside other sensor data from the multi-sensing system, including temperature, humidity, acoustics, and bee traffic. This comparison provides a more complete understanding of hive health and activity. The presentation also discusses the practical applications of these technologies, such as monitoring the effects of pesticides on bees. It concludes with a discussion on the future prospects of smart beehives, highlighting the growth of smart beehive companies and the innovative products they offer, which assist beekeepers in more effectively managing their hives. In summary, the presentation underscores how these advancements are simplifying the tracking and understanding of bee behavior, ultimately enhancing hive management and supporting the health and survival of bee populations.

Keywords: smart beehives, honeybee monitoring, machine vision, multi-sensing system, hive health prediction

論文宣讀: 農業昆蟲學

Oral Session: Agricultural Entomology

OA01

分析不同咖啡因劑量對蚜蟲生殖與胚胎發育的影響
An Analysis of the Impacts of Varying Caffeine Dosages on Aphid Reproduction and Development

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背景/研究問題/材料方法
咖啡因是植物天然的殺蟲劑，自上世紀八十年代以來，已有大量研究探討其對各種害蟲的防治效果。然而，有關咖啡因在防治蚜蟲方面的研究相對匱乏。蚜蟲具有孤雌胎生的繁殖能力，使其族群數量能迅速增加，成為農業中的主要害蟲之一。本研究旨在探討咖啡因對孤雌胎生豌豆蚜發育及生殖能力的影響。通過在人工飼料中添加咖啡因，餵食並飼養豌豆蚜，分析咖啡因對其成蟲率、體重、體長及發育時間的影響。此外，通過解剖成蟲卵巢，測量微卵管的長度、統計蛋腔數量、胚胎發育階段與結構、生殖細胞表現等，進一步探討咖啡因對豌豆蚜生殖能力的影響。

結果/結論/應用啟示
在發育方面，咖啡因顯著降低豌豆蚜成蟲率，延長發育時間，並減輕體重及縮短體長。在生殖能力方面，成蟲產下的若蟲數量明顯減少。咖啡因阻礙了蚜蟲卵巢的正常發育，導致卵巢體積因微卵管長度顯著縮短而變小。微卵管縮短的原因在於胚胎發育階段嚴重延遲。隨著咖啡因濃度的增加，豌豆蚜出現不孕現象（即成蟲在未產下子代時即自然死亡），以及生殖細胞缺失的畸形胚胎。本研究總結了咖啡因對豌豆蚜生理和生殖的影響，提供了重要的數據基礎，為新型生物農藥的開發提供了理論支持。

關鍵詞（Keywords）：豌豆蚜（*Acyrthosiphon pisum*）、人工飼料（Artificial Diets）、咖啡因（Caffeine）、生殖能力（Fecundity）、胚胎發育（Embryogenesis）

OA02

自動化監測系統應用於果實蠅的番茄非疫生產點評估
The evaluation of the automated monitoring system applied to tephritid pest free production sites for tomatoes

葉紹翔 [1]、洪傳捷 [2]、林劭霖 [1]、劉嘉聞 [3]、林晁毅 [2]、江昭皚 [1]、周明儀 [2,3]
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背景/研究問題/材料方法

東方果實蠅（*Bactrocera dorsalis*）與瓜實蠅（*Zeugodacus cucurbitae*）都是危害番茄的果實蠅害蟲，影響台灣農產品的出口。依據國際檢疫標準，疫區國可以透過建立非疫生產點，搭配監測作業確保害物未入侵到溫室內。本研究自 2021-2023 年於台灣南部的 2 間番茄溫室進行自動化計數蟲桶與傳統人工計數監測，並使用黃色黏板圖像建立果實蠅的影像辨識模型，探討自動化監測系統應用於非疫生產點的可能。

結果/結論/應用啟示

在監測的 3 年期間，溫室內維持零害蟲入侵的紀錄。自動化計數蟲桶於實驗室內的準確度測試為 98.4 ± 0.8 %。果實蠅的影像辨識模型為另外收集黏板圖像進行作業，共準備 320 張影像依比例 7 : 2 : 1 拆分為訓練集、驗證集及測試集。結果回報的 Precision 為 0.959、Recall 為 0.977，顯示模型的辨識性能良好。實際應用於田間，自動化計數蟲桶在溫室內的平均準確率達 93-100%，溫室周圍則可提供適當的防治建議。當溫室外部的害蟲密度 ＞1 隻/日，便會進行蟲害管理。第 1 間溫室周圍共進行 67 次的監測調查，其中發生 8 次偽陽性、1 次偽陰性的防治建議。第 2 間溫室進行 66 次監測調查，累積 2 次偽陽性、3 次偽陰性的防治建議。防治建議準確度分別為 72.1 ± 9.3 %與 81.7 ± 6.8 %，接受度則是 98.7 ± 1.3 %與 95.3 ± 0.6 %。綜合以上，自動化監測系統於果實蠅的非疫生產點計畫中具有應用的潛力。

關鍵詞（Keywords）：果實蠅（Tephritid）、自動化監測系統（Automatic Monitoring System）、非疫生產點（Pest Free Production Site）、害蟲監測（Pest Monitoring）、影像辨識（Image Recognition）

OA03

優化 MaxEnt 模型預測氣候變遷對秋行軍蟲 *Spodoptera frugiperda* 於臺灣分佈的影響

Model optimization: Predicting the impact of climate change on the distribution of *Spodoptera frugiperda* in Taiwan using MaxEnt

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背景/研究問題/材料方法

秋行軍蟲 *Spodoptera frugiperda* 為嚴重的農業害蟲，主要危害玉米，其次包括小麥、高粱及蔬菜等 80 餘種作物。其發育期隨氣溫提升縮減，考慮全球溫室效應加劇 *S. frugiperda* 世代數增加，為提供更有效、快速全球暖化下分佈的改變，許多研究已用 MaxEnt 模組利用氣溫、濕度及降雨等多因素模擬環境變化，預測未來分佈改變。當前模組仍存在即時預測解析度不足及點位資料不足時易造成預測效能下降等問題。本研究結合 R Studio 及 ArcGIS，以 MaxEnt 為主要預測模組，減緩過度擬合後，探討 *S. frugiperda* 於即時預測中之準確性。

結果/結論/應用啟示

本研究以共享社會經濟路徑 (Shared Socioeconomic Pathways, SSPs) 為預設情境，預測圖與原始點位高度重合，模型穩定 (AUC ≒ 0.8)。*S. frugiperda* 於氣候變遷情境中之預測適宜區域主要分布於臺灣西南部，以雲林、嘉義及台南最甚；而在即時預測中，模型表現出與未來氣候變遷情境相近結果，AUC 值達 0.78 以上。兩種預測結果皆顯示 MaxEnt 模組之高效能，同時即時預測與平均預測並無顯著差異，卻能將預測細分至不同月份，具備即時預測效果。透過預測時間的解析度增加，MaxEnt 可與更多時間模型整合，追蹤農業害蟲分布有望朝即時甚至提早掌握的方向努力。

關鍵詞（Keywords）：物種分布模型（Species Distribution Model）、共享社會經濟路徑（Shared Socioeconomic Pathways）、即時預測（Real-time prediction）

OA04

生物刺激素在增強番茄植株對抗菸草粉蝨與番茄黃化捲葉泰國病毒的潛力

The potential of biostimulants in enhancing tomato resistance to *Bemisia tabaci* and tomato yellow leaf curl Thailand virus

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背景/研究問題/材料方法

菸草粉蝨 (*Bemisia tabaci*) 傳播的番茄黃化捲葉泰國病毒 (tomato yellow leaf curl Thailand virus) 是嚴重危害番茄的病害之一。生物刺激素 (biostimulant) 被定義為能以低劑量刺激植物生長的物質，與農藥或傳統肥料不同，生物刺激素在促進植物生長、增加產量及抗逆境機制中發揮了關鍵作用。近期的研究證實了幾丁寡醣 (oligochitosan) 和卡拉膠 (carrageenan) 等生物刺激素有增強植物對抗病毒感染和昆蟲侵擾的效果。本研究選用 3 種番茄品種並每週對植株葉片施用不同濃度的幾丁寡醣和卡拉膠，然後紀錄植株葉片上的粉蝨數量。抗病毒方面，每週對感染病毒的植株葉片施用不同濃度的幾丁寡醣與卡拉膠，然後紀錄番茄的生長狀況及植株的病徵，並以即時聚合酶連鎖反應 (real-time PCR) 檢測植株內的病毒量。

結果/結論/應用啟示

幾丁寡醣與卡拉膠對聖女番茄的生長沒有影響，也無法有效減輕病徵與植株內的病毒量。1%幾丁寡醣會促進桃太郎番茄的生長，1%幾丁寡醣與 1%卡拉膠會減輕病徵與植物內的病毒量，而 0.1%與 1%幾丁寡醣會抑制植株上粉蝨數量。1%幾丁寡醣與 1%卡拉膠會促進黑柿番茄的生長，只有 1%幾丁寡醣會減輕病徵，而兩種濃度的幾丁寡醣與卡拉膠皆會抑制植株上粉蝨數量。這些結果顯示 1%幾丁寡醣可以增強番茄植株對抗菸草粉蝨與番茄黃化捲葉泰國病毒，效果依番茄品種而有所差異。研究結果提供了幾丁寡醣與卡拉膠應用於番茄病蟲害防治方面的潛力評估。

關鍵詞（Keywords）：菸草粉蝨（*Bemisia tabaci*）、生物刺激素（biostimulant）、植物病毒（plant virus）、植物抗性（resistance）

OA05

蟲生真菌防治藍莓之小黃薊馬潛力評估
The potential evaluation of entomopathogenic fungi for controlling yellow tea thrips (*Scirtothrips dorsalis* Hood) of blueberry

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背景/研究問題/材料方法

In recent years, the value of blueberry imports has grown annually, and the market prices remains high, attracting domestic farmers start trying to cultivate blueberries. Blueberry shoots, petals, and young fruits are easily damaged by the yellow tea thrips (*Scirtothrips dorsalis*), also known as chilli thrips. However, using oil sprays during the flowering and fruiting periods can affect pollination and damage the bloom of the fruit, affecting its appearance. Therefore, other alternative control strategies, such as biological control, are needed. In this study, the life table of yellow tea thrips on blueberry and the field surveillance of yellow tea thrips were conducted. In addition, entomopathogenic fungi which show pathogenesis against yellow tea thrips were selected for evaluating the potential to control this pest.

結果/結論/應用啟示

At 24℃, the durations of each immature stage of yellow tea thrips on blueberry leaves are as follows: egg, first instar, second instar, prepupa, and pupa stages are 7.0, 2.1, 2.4, 0.9, and 1.6 days, respectively, with a total duration of 14.0 days. According to field stick paper monitoring showed the population of yellow tea thrips in March to April starts to increase, reaches its peak in July, and decreased after pruning in August. The above information can serve as a reference for future field control. Entomopathogenic fungi screening results showed that on the seventh day, the mortality rates of *Cordyceps* fungal strains NCHU-213 and NCHU-298 had the highest mortality rates at 93% and 69%, respectively, followed by *Beauveria bassiana* NCHU-157 (49%), *Metarhizium anisopliae* NCHU-69, and *Metarhizium pinghaense* NCHU-125 (37% and 41%), with *B. bassiana* NCHU-153 having the lowest mortality rate. Therefore, in the future, the dose-dependent effect, the efficacy of *Cordyceps cateniannulata* NCHU-213 against different instar larvae, along with greenhouse trial will be tested to evaluate the potential of NCHU-213 on controlling yellow tea thrips.

關鍵詞（Keywords）：藍莓（Blueberry）、小黃薊馬（yellow tea thrips）、蟲生真菌（Entomopathogenic fungi）、生物防治（Biological control）、田間監測（field monitoring）

OA06

秋行軍蟲核多角體病毒之微生物防治引發幼蟲隱性感染和抑制蟲口族群密度的重要性
The microbiological pest management of SfMNPV plays a crucial role in covert infection to constantly suppressed the population of *Spodoptera frugiperda*

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背景/研究問題/材料方法

Integrated pest management (IPM) has been valued in recent years, it utilizes a more diverse and comprehensive approach to control pests. Microbiological control of nucleopolyhedrovirus (NPV) has high host specificity and does not harm non-targeted organisms. To promote sustainable agriculture, an eco-friendly strategy and non-pesticide materials are quite necessary to be developed. We performed the biological activity of *Spodoptera frugiperda* multiple nucleopolyhedrovirus (SfMNPV) to examine the mortality of *S. frugiperda*. With real-time qPCR, we had detected the immune response of SfMNPV-infected *S. frugiperda*. Based on the age-stage two-sex life table, we also found the covert infection in *S. frugiperda* population

結果/結論/應用啟示

The biological activity of SfMNPV showed an absolute pathogenicity to *S. frugiperda* first and second instar larvae. The median lethal concentration of SfMNPV to third instars larvae was 1.46×10^6 OBs/ml for 14 days post-inoculation at 25℃. Besides, we analyzed the effects of SfMNPV on the third instars at the concentration of 10^6 OBs/ml. The population projection showed that SfMNPV could effectively decrease the population size of *S. frugiperda*. Through this study, we explore the effectiveness of SfMNPV application on agricultural pests under the trend of microbiological pest management. The SfNMPV's pathogenicity not only caused individual death but also inherited covert infection among the whole population. These executions show greater performance on insecticidal efficacy, and may become the promising approach to control agricultural pests in future.

關鍵詞（Keywords）： Nuclear polyhedrosis virus, *Spodoptera frugiperda*, microbiological control, synergistic effects, population projection

OA07

分秘夜蛾在三種禾本科作物生長表現之研究
Study on the growth performance of *Mythimna separata* (Walker) (Lepidoptera: Noctuidae) feeding on three Poaceae crops

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背景/研究問題/材料方法

分秘夜蛾（*Mythimna separata* (Walker)）廣泛分布於潮溼的熱帶至溫帶地區，寄主作物範圍廣，以玉米、高粱、水稻、小米等禾本科作物受害較嚴重。近年關山鎮及池上鄉水稻第 2 期作於 10 月中下旬發生分秘夜蛾幼蟲成群為害，嚴重時葉片僅剩主脈、穗部遭啃蝕掉落一地。由於國內缺乏其生活史之基本資訊，爰以三種常見禾木科作物—水稻、玉米及小米，分別飼育分秘夜蛾，記錄其生活史、成蟲產卵量等生長表現資料，做為未來擬定防治策略之參考。

結果/結論/應用啟示

分秘夜蛾 1、2 齡幼蟲在 3 種不同作物上表現的死亡率均高，其中以取食小米的死亡率最高，取食玉米的死亡率最低。取食玉米之幼蟲期僅需 22.57 日，存活率和化蛹率顯著優於其他作物；產卵試驗結果顯示，以取食玉米者具有較高的生殖潛能，產卵數量多且待產天數短，族群擴增潛力大。性比接近 1，但取者水稻和小米者雌性比例略低。各寄主植物上的平均生命週期為：玉米 53.22 日、水稻 56.69 日、小米 58.08 日及牧草 63.12 日。為降低分秘夜蛾的危害，建議農民在插秧前清除田區周圍的禾本科植物，減少幼蟲棲息地，特別是第 2 期作建議進行育苗箱或種子處理藥劑，以降低被害風險。插秧後應定期巡田，並適時使用藥劑防治，這些措施有助於減少害蟲對作物產量的影響。

關鍵詞（Keywords）：分秘夜蛾（*Mythimna separata*）、玉米（maize）、水稻（rice ）、小米（foxtail millet）

OA08

應用深度學習於寄生性天敵昆蟲的計數與性別辨識:以 *Trissolcus* sp. (膜翅目：緣腹細蜂科) 為例
Application of deep learning in counting and gender identification of parasitoid wasps: a case study of *Trissolcus* sp. (Hymenoptera: Scelionidae)

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背景/研究問題/材料方法

以天敵昆蟲進行害蟲防治為友善農業中重要之策略，而其中寄生性天敵昆蟲因體型小，且以雌蜂具寄生能力，因此於建立寄生性天敵昆蟲的量產技術和商品品質時，進行性別識別和計數為必要之流程。本研究以危害柑橘類的角肩椿象(*Rhynchocoris humeralis*) 卵寄生蜂 *Trissolcus* sp.為例，此屬寄生蜂需於顯微鏡下依觸角粗細進行雌雄蜂之辨識，而此過程需有專人且耗時。本計畫開發一套二階段深度學習影像系統，以平板式掃描器取得 *Trissolcus* sp.的高解析度 (6400dpi) 圖片，並後續以 YOLOv7 與 ResNet18 進行模型的建立與優化。

結果/結論/應用啟示

本研究第一階段為物體檢測，首先將影像解析度降低以加速 YOLOv7 的計算速度，並使用 YOLOv7 模型偵測影像中寄生蜂的位置，在此階段中訓練的 YOLOv7 模型達到 98.907%的 mAP@0.5，顯示模型高精度的物體檢測能力。第二階段為雌雄蜂之辨識，利用 YOLO v7 模型在降低解析度影像中偵測到寄生蜂的邊界框 (bounding box)，再從原始影像中剪裁出這些區域，獲得高解析度的個別寄生蜂影像，並輸入至 ResNet18 模型進行性別分類，目前 ResNet18 模型的總體驗證準確率達到 90.8%。本團隊將持續測試不同的分類模型，以改善性別分類之準確性，預計建立一個半自動化的應用系統，僅需將影像上傳後，系統可自動處理並提供數量統計和性別辨識結果，未來應用於生物防治上，可加速量產技術之研究。

關鍵詞（Keywords）：深度學習（deep learing）、生物防治（biological control）、寄生蜂（parasitoid wasp）

OA09

黑水虻於花蓮特色農產之循環農業應用初探

A preliminary study on the application of black soldier flies in circular agriculture of agricultural products in Hualien

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背景/研究問題/材料方法

本研究旨在探討黑水虻於花蓮特色農產循環農業中的應用潛力。因地理環境孤立，花蓮以其獨特農產聞名，但同時也面臨農業副產物清運去化的挑戰。本研究針對文旦與黃豆副產物調製之飼養基質，比較黑水虻幼蟲於不同發酵前處理條件的飼養基質中，分解效率與蟲體增重率之差異，以評估利用黑水虻進行農業副產物的處理與再利用之效果。

結果/結論/應用啟示

經取食文旦果皮與黃豆粕調製之飼養基質 3 日後，黑水虻可減少所有處理組 58~62%之基質乾物質，基質經厭氧發酵處理後幼蟲增重率可達 130%，為未發酵組之 2.2 倍。其蟲體可供禽畜水產養殖、油品與有機防治資材製作等後續用途，蟲糞則可用做堆肥，實現農業資源的循環利用。初步評估黑水虻在花蓮特色農產的循環上具應用潛力，能有效解決農業副產物處理問題，促進永續農業發展。厭氧發酵可作一貯放選項，以處理採收期較短但產量大的作物副產物，同時增進飼養基質之營養效能。

關鍵詞（Keywords）：黑水虻（Black soldier fly, *Hermetia illucens*）、文旦柚（Pomelo）、豆粕（Soybean meal）、厭氧發酵（Anaerobic Fermentation）

OA10

無人機智慧施放赤眼卵蜂球技術在玉米秋行軍蟲生物防治應用

Application of smart drone technology for releasing *Trichogramma* wasp balls in the biological control of fall armyworm in corn

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背景/研究問題/材料方法

自從秋行軍蟲（*Spodoptera frugiperda*）入侵臺灣後，已經成為玉米產業主要害蟲，導致經濟損失。赤眼卵蜂（*Trichogramma* wasps）已被證實可應用於秋行軍蟲生物防治，並助於減少化學農藥的使用。目前赤眼卵蜂施放，透過人力釘放赤眼卵蜂片或投擲蜂球，僅適用於小面積防治，無法滿足大面積作物的需求。本研究開發無人機智慧化施放蜂球技術，可根據田區面積自動運算並精確規劃投放蜂球數量及位置，改善操作便利性與效率。本技術應用範疇可支援大面積玉米田，包括食用玉米及硬質玉米，透過田間防治試驗評估防治效力，提防治策略擬定。

結果/結論/應用啟示

無人機智慧施放天敵技術由「GPS 定位投放裝置」、「投放機構」及「網頁操作平台」構成，可同時執行飛行監測與自動規劃投放點位。整合跨領域之資通訊技術及物聯網等前瞻技術，操作時僅需設定田區範圍，使用規劃飛行模式，即時快速精準投放。每公頃只需 5-10 分鐘即可快速精準地完成蜂球投放，相較於傳統手釘蜂片效率提高 6-10 倍，助於大面積防治。食用玉米田間防治試驗，採用農藥減量結合無人機施放蜂球防治，試驗結果可降低秋行軍蟲受害率，減少農藥施用量 25-50%。硬質玉米田試驗結果，慣行組增加施放蜂球防治，收成產量相對高於慣行組。無人機智慧施放蜂球技術，助於大規模生物防治應用，自動化及智慧化的功能減輕人力負擔，生物防治減少農藥施用，助於友善環境經營及永續農業發展。

關鍵詞（Keywords）：生物防治（Biological control）、天敵（Natural enemy）、蟲害綜合管理（Integrated Pest Management）、人工智慧（Artificial Intelligence）、無人機（Drone）

OA11

不同植物基質來源對麵包蟲(*Tenebrio molitor* L.)生長影響之初探

Preliminary study on the effects of different plant-based substrates on the growth of yellow mealworm (*Tenebrio molitor* L.)

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背景/研究問題/材料方法

昆蟲被全球視為重要的替代蛋白質來源之一，用於取代傳統動物性蛋白質，減少因禽畜飼養造成的溫室氣體排放、土地與用水需求，符合聯合國於 2016 年推動的可持續性發展目標(sustainable development goals, SDGs)。其中麵包蟲(*Tenebrio molitor* L.) 已被廣泛飼養應用於動物或寵物食品，然其飼養過程多以麥麩作為碳水化合物來源、紅蘿蔔或馬鈴薯作為水分來源，導致飼養過程會產生與人類競爭糧食的疑慮或受到進口糧食限制。為解決此問題，尋找適合取代傳統飼料配方之植物基質為全球重要的研究課題之一。本研究以 5 週齡麵包蟲幼蟲作為試驗材料，以粉頭、玉米粉及米糠取代碳水化合物來源-麥麩及浮萍、滿江紅及洋菜塊取代水分來源-紅蘿蔔，將幼蟲飼養至 8 週齡，並收集 8 週齡幼蟲之總重量、平均個體重及食物轉換率等數據，評估不同植物基質對麵包蟲生長之影響，初步探討植物基質取代傳統飼養基質量產麵包蟲之可能性。

結果/結論/應用啟示

碳水化合物替代試驗結果顯示，以玉米粉及米糠飼養之麵包蟲幼蟲於 8 週齡族群重量分別為麥麩飼養的 53.8%及 59.3%，而粉頭飼養之麵包蟲族群重量則為麥麩飼養的 78.7%，但仍以麥麩飼養之麵包蟲族群重量最重，顯示麥麩依然是最適合飼養麵包蟲之碳水化合物基質。水分替代試驗結果顯示，以洋菜塊飼養之麵包蟲於 8 週齡族群重量為紅蘿蔔飼養的 90.4%，而浮萍、滿江紅飼養之麵包蟲族群重量分別為紅蘿蔔飼養的 80.2%及 83.5%。本試驗顯示以植物基質全部取代麥麩飼養麵包蟲仍具挑戰，而以植物基質全部取代紅蘿蔔可行性較高，未來將結合飼養成本及產質，綜合分析植物基質部分或全部取代傳統飼養基質之可行性，以降低未來台灣量產飼料昆蟲所需之成本。

關鍵詞（Keywords）：麵包蟲（*Tenebrio molitor* L.）、動物飼料（animal feed）、植物基質（plant-based substrates）、循環農業（circular agriculture）

OA12

利用原民作物營造農田促進害蟲調節服務功能
Using indigenous crops to build farmland to promote pest regulation service functions

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背景/研究問題/材料方法

花蓮縣織羅部落與屋拉力部落座落於中央山脈及海岸山脈之間，農業耕地鄰近淺山森林，擁有豐富的生態相，部落的農業活動形式在生態系統保護中扮演不可或缺的重要角色。本研究主要探討在有機水稻田與文旦園以原民作物進行地景營造，是否能吸引農田中天敵駐足，增強害蟲調節服務功能。挑選穗花木藍、三/五葉埔姜、馬蘭、仙草、魚腥草等原民會利用的開花植物種植於水稻田埂、邊坡、畸零地與文旦園樹冠下，分析營造前後之關鍵害蟲與天敵的變化，並以天敵數量除以害蟲與天敵數量總和，評估害蟲調節服務。

結果/結論/應用啟示

在織羅部落水稻方面，以穗花木藍、馬蘭、仙草、三葉埔姜、五葉埔姜進行田埂、邊坡、畸零地種植營造後，約三個月植被生長茂密。營造前非禾本科植物覆蓋率原本平均為 23%，營造後則提升至 90%，這些植物提供舞虻及橙瓢蟲棲息空間，以及花粉花蜜提供碳水化合物及胺基酸營養來源，使天敵族群提升為營造前的 3.7 倍，天敵的調節服務功能提升 2 倍；在屋拉力部落文旦園的部分，以特定原民植物進行向陽處及遮陰處種植營造，待植被生長茂密後可吸引關鍵天敵花椿科棲息其中，並取食這些特定植物的花粉花蜜以延長壽命、增加捕食害蟲薊馬的能力以及繁殖後代能力。營造前非禾本科植物覆蓋率原本平均為 8%，營造後則提升至 85%，營造後植被相的改變同樣會間接提升害蟲調節服務功能，花椿象科昆蟲密度即使在沒有害蟲薊馬的情況下，仍能維持數量，且營造的園區果皮被薊馬危害程度平均 19.8%，相較於無植被營造的對照組薊馬危害程度 46.8%減少許多。本研究藉由增加地被植物的多樣性，提供豐富的棲地與食物來源，吸引更多的有益捕食者與寄生者駐足，發揮害蟲調節功能，並減少農藥使用，同時賦予原民植物更多元的利用價值。並朝向與生態給付政策接軌，鼓勵農民一起對生態農業作出正面實踐，以達到生態農業永續經營與傳承原住民文化的雙贏局面。

關鍵詞（Keywords）：生態農業（Ecoagriculture）、棲地營造（Habitat manipulation）、水稻（Rice paddy）、文旦（Pomelo）、天敵（Nature enemy）

OA13

2007–2023年臺灣進口多肉植物檢出介殼蟲

Scale insects (Hemiptera: Coccoidea) intercepted from imported succulent plants in Taiwan during 2007–2023

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背景/研究問題/材料方法

近年來兼具觀賞及減壓的多肉植物(succulent plants)，越來越受到國內外消費者的青睞。隨著國際間大量快速貿易交流，外來有害生物入侵的風險增加，其中介殼蟲(Hemiptera: Coccoidea) 即為經常檢出之重要害蟲。本文整理 2007–2023年間，農業部動植物防疫檢疫署各分署，現場檢疫人員後送進口多肉植物檢出之2,754筆介殼蟲總科樣品。

結果/結論/應用啟示

經由農業試驗所經製成玻片後利用光學顯微鏡加以鑑定，其中盾介殼蟲科為25筆，分屬於6屬8種，其中杉刺圓盾介殼蟲 [*Oceanaspidiotus spinosus* (Comstock, 1883)] 為臺灣未記錄種；粉介殼蟲科為檢出次數最多的科別，共計2,728筆檢出記錄，分屬10屬11種，其中在 *Chorizococcus*、*Rhizoecus* 及 *Vryburgia* 3屬中檢出臺灣3未記錄種；絨介殼科1屬1種。檢出種類均製成玻片標本並存放於農業試驗所應用動物組昆蟲標本館，作為國外進口農產品檢出害蟲之存證標本並建置相關資料。除鑑定外，亦可作為日後供線上快速查詢其害蟲及評估潛在農業外來種害蟲風險之依據。

關鍵詞（Keywords）：多肉植物（succulent plants）、介殼蟲（Coccoidea）、害蟲（pest）

OA14

建立有機栽培甜椒之害蟲綜合管理模式

Establishing an Integrated Pest Management Program for Organic Bell Pepper Cultivation

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背景/研究問題/材料方法

甜椒為連續採收作物，栽培過程中因受多種害蟲嚴重危害影響產量與品質，尤其是有機栽培受限於防治資材要達到生產目標更為困難。為建立適合有機栽培應用的甜椒害蟲綜合管理技術提供有機栽培者應用，本研究透過以黃色黏紙及直接檢視，監測關鍵害蟲的發生密度，並適時導入有效的生物天敵或環境友善之植物保護資材等防治害蟲，自 2021 年起於嘉義縣六腳鄉一處有機栽培設施進行驗證試驗，並分析其防治效果與經濟效益。

結果/結論/應用啟示

根據調查結果顯示，甜椒栽培期間發生的關鍵害蟲為薊馬、粉介殼蟲、蚜蟲、粉蝨及蟎類。經測試應用或保育本土昆蟲天敵，包括南方小黑花椿象（*Orius strigicollis*)、東方蚜小蜂（*Eretmorceus orientalis*)、瓢蟲、草蛉等搭配其他防治技術，均可有效防治關鍵害蟲，較一般慣行栽培延長採收期 6 週，經效益分析，獲利率達 70%以上。合理可行的有機、友善栽培耕作的害蟲管理策略，係善用本土天敵對環境適應之優勢，搭配其他友善防治資材，可發揮截長補短的效果，達到安全生產兼顧品質、產量，並維護環境生態之目標。

關鍵詞（Keywords）：害蟲綜合管理（Integrated pest management）、甜椒（Bell pepper）、南方小黑花椿象（*Orius strigicollis*）、東方蚜小蜂 （*Eretmorceus orientalis*）、有機栽培（Organic Cultivation）

論文宣讀: 生物多樣性、族群與群聚生態學

Oral Session: Biodiversity, Population and Community Ecology

OB01

透過生態聲學技術揭開都市綠地之直翅目昆蟲鳴叫多樣性
Unveiling the Orthoptera calling diversity across urban green spacesthrough ecoacoustics method

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背景/研究問題/材料方法

「生態聲學」(ecoacoustics)意指利用生物發出之聲音訊號進行研究，以瞭解聲音與環境間的關係。此方法可以非侵入性的方式探索一區域之生物多樣性。然而，相對於會鳴叫的直翅目昆蟲，過去之相關研究多專注於脊椎動物，而利用直翅目昆蟲之聲音多樣性作為環境指標仍缺乏研究。此外，於都市化程度上升的今日，都市綠地與其生物多樣性的保育也逐漸受到重視。本研究為了瞭解直翅目聲景於都市環境之狀況，選擇八個都市公園與校園綠地作為樣點架設錄音機(16bit，44.1khz)，以每月三天，每小時五分鐘之排程進行錄音。錄音之檔案被鑑定為不同的聲音種(vocal species)以計算鳴叫發生(occurrence)次數，並分析樣點周圍之地景組成與陸地衛星(landsat)因子，評估直翅目聲音和環境的關聯性，進而瞭解環境因子組成與公園營造對直翅目昆蟲多樣性之影響。

結果/結論/應用啟示

研究結果顯示，大範圍之地景因子對於群落的鳴叫發生(occurrence)與鳴叫多樣性(richness)並無顯著影響，然而，部分物種與特定地景因子則有相關，如褐翅鉦蟋與樹冠覆蓋面積有正相關。此外，鳴叫發生次數也與當月氣溫有關聯，顯示生態聲學資訊亦具反映環境與天氣狀態之潛力。未來將分析鳴叫多樣性與微環境因子的關聯性，期望本研究之成果能在未來為都市綠地規劃提供更環境友善且保留生物多樣性的建議。

關鍵詞（Keywords）：都市化（urbanization）、聲景（soundscape）、陸地衛星（landsat）、鳴叫（chirping）、都市生態學（urban ecology）

OB02

蟬鳴聲的人工智慧自動分類
Artificial Intelligence Automated Classification of Cicada Sounds

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背景/研究問題/材料方法

生物多樣性與人類的生存高度相關，因此正逐漸受到重視，其中昆蟲對生態環境的影響至關重要，然而昆蟲多樣性調查卻十分困難。因此吾人急需一套快速且經濟有效的昆蟲調查方法。得利於資訊科技的發展，以被動式聲學監測結合人工智慧分析的調查方法已多有成功案例。本研究選用季節性明顯、音量巨大且鳴音具有物種專一性的鳴蟬作為實驗材料，於中台灣地區錄製蟬的鳴音，後以短時傅立葉變換繪製成時頻圖後匯入 MobileNet-v3、VGG16、Densenet 121、ResNet 18、ResNet 50 等五種模型進行分類測試，並同步比較目視與蟲網法、燈光誘集法、鳴聲調查法三者的調查有效性。

結果/結論/應用啟示

實驗結果在 Accuracy 方面各模型的成績為 MobileNet-v3 0.92、VGG16 0.25、Densenet 121 0.72、ResNet 18 0.98、ResNet 50 0.99，顯示 ResNet 系列模型最佳；若考量到消耗時間，則以 ResNet 18 較佳，約可達 68.55 倍速。調查方法比較方面，各方法可調查到的物種數量為目視與蟲網法 10、燈光誘集法 6、鳴聲調查法 14，顯示鳴聲調查法最為有效。本研究證實了聲音調查在昆蟲方面的有效性，且具有調查友善、經濟效益高、分析速度快等優點，有望提供更多資訊用於保育生物多樣性以及環境評估等方面之應用。本研究也同步保存鳴蟬標本和有標籤錄音資料，可供後續研究分析與應用。

關鍵詞（Keywords）：鳴蟲（Singing Insects）、生態（Ecology）、監測（Monitoring）、聲學（Acoustics）、機器學習（Machine Learning）

OB03

Experimental warming disrupts reproductive performance but not parental care in the burying beetle, *Nicrophorus nepalensis*

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背景/研究問題/材料方法

Rising temperatures can negatively impact parental care behaviors and reproduction across various taxa. It is crucial to understand how temperature influences different aspects of parental care and their interactions. To address this, we investigated the effects of temperature on parental care and reproductive success in the burying beetle, *Nicrophorus nepalensis*, known for its complex parental behaviors, including pre-hatching (e.g., carcass preparation) and post-hatching care (e.g., offspring provisioning). We exposed breeding pairs of *N. nepalensis* to three temperature regimes (18°C, 20°C, and 22°C) that were in accordance with the projected global warming scenarios, and assessed changes in parental care as well as the development and growth of their offspring.

結果/結論/應用啟示

Our results show that at 22°C, parental care was disrupted, leading to failures in carcass nest building and no successful egg hatching, as well as smaller clutches. A moderate increase to 20°C did not affect egg-hatching rates but resulted in smaller broods and lighter offspring, indicating reduced post-hatching care quality. These findings indicate that while warming has only a minor impact on parental care behaviors, it substantially hinders reproductive performance and the development of offspring. This underscores the need to examine how ambient temperature affects a variety of traits and life-history stages to better understand species' vulnerability under climate change.

關鍵詞（Keywords）： climate change, reproductive success, life history traits, nest construction, warming

OB04

The impact of forest fires on termite diversity and food resources

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背景/研究問題/材料方法

In forest ecosystems, termites and fires play important roles in the carbon cycle. Fires not only remove combustible material but also create new woody material by deteriorating tree health. Fires have influenced the food resources consumed by termites, including litter and wood. A forest fire occurred in May 2021 in Huisun Forest Area, Nantou County, Taiwan, providing an opportunity to study the impact of fires on termite diversity and termites’ food resources. This study aims to determine whether the quantity of litter and wood provided by the forest increased after the fires and whether the diversity of termite species remained unchanged. The burned and unburned stands were investigated to assess the impact of fire. The line intersect method and the plot-based method were applied to quantify wood and litter. The survey for termites was conducted in soil and near the ground.

結果/結論/應用啟示

The abundance of fallen wood was significantly higher in the burned stand than in the unburned stand. The biomass of dead standing trees was significantly greater in the burned stand than in the unburned stand (74.08±42.17 Mg/ha and 18.81±26.68 Mg/ha). The biomass of litter was significantly greater in the unburned stand than in the burned stand (6.48±1.21 Mg/ha and 2.69±1.19 Mg/ha), due to the presence of living trees contributing to litter in the unburned stand. In the unburned stand, *Pericapritermes nitobei*,*Nasutitermes parvonasutus*, *Odontotermes formosanus*, *Reticuiltermes* spp., and *Neotermes* spp. were collected. However, in the burned stand, only *Na. parvonasutus, O. formosanus,*and *Reticuiltermes* spp. were found. According to the termite survey, the abundance of termites in the burned stand was significantly higher than in the unburned stand. The increase in food resources post-fire led to an increase in termite abundance, while the fire disturbance impacted on the survival of soil-feeding termites and Kalotermitidae species.

關鍵詞（Keywords）： Coarse wood debris, Termite diversity, Fires

OB05

Whole genomic variants unravel the population dynamic and conservation status of endangered butterfly, *Papilio maraho* Shiraki & Sonan, 1934

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背景/研究問題/材料方法

Papilio maraho, known as the broad-tailed swallowtail, is famous for its unique wing marking and historical biogeography. Because of its special evolutionary status, this butterfly becomes an icon of species conservation in Taiwan. Due to the commercial collecting and limited larval hostplant, *Papilio maraho* is listed as an endangered species in Taiwan. Nevertheless, the conservation genomics of its population remains largely unknown. In this study, we use NGS resequencing method to obtain genome-wide single nucleotide polymorphism (SNP) data for estimating its historical demography, inbreeding and mutation load via comparing individuals of *Papilio maraho* (N=9) and *Papilio elwesi* (N=24).

結果/結論/應用啟示

Our results showed that *Papilio maraho* has smaller effective population size, lower genetic diversity and higher level of inbreeding than the sister *Papilio elwesi*. However, the mutation load of these two species is near identical. In addition, our findings suggest that the lower genetic diversities and higher level of inbreeding of *Papilio maraho* does not significantly accumulate deleterious mutation and decrease the fitness of *Papilio maraho*.

關鍵詞（Keywords）： next-generation sequencing, population genetics, genetic load

OB06

台灣甲蟎分類研究史與研究展望
The history and research prospects of oribatida mites Taxonomy in Taiwan

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背景/研究問題/材料方法

甲蟎為落葉層及土壤常見小型節肢動物，分類位階為蛛形綱(Arachnida)、蜱蟎亞綱(Acari)、疥蟎目(Sarcoptiformes)、甲蟎亞目(Oribatida)的成員。甲蟎廣泛分布於全世界的陸域棲地，多數類群棲息於腐植質豐富的森林地區，部分類群甚可分布於潮間帶。由於體型微小且土壤的不透明性，使得食性不易觀察。普遍認為甲蟎的功能群屬分解者，可能係分解落葉之碎食性或為腐食性。但近期研究使用穩定同位素進行食性分析發現其食性廣泛且橫跨不同功能群。故值得進一步進行分類鑑定，以利後續土壤生態相關之研究。盤點台灣過去的甲蟎分類研究約從 1980 年代開始，曾義雄先生分別於 1982、1984 年發表共 28 科 56 屬 76 種。其後，日本土壤動物分類學者青木淳一博士以及大久保憲秀陸續發表了採自盧山、北大武山、南湖大山及福山之甲蟎。1997 年，朱耀沂博士與青木淳一博士共同發表福山植物園調查到之甲蟎名錄，共計 37 科 66 屬 75 種。之後 10 年甲蟎分類研究停擺，至 2008 及 2009 才有零星研究報告。2017 年起，廖治榮博士與俄國學者合作陸續發表數個新種。時至今日，台灣總計記錄到 72 科 165 屬 301 種。

結果/結論/應用啟示

然而，過去研究多於中高海拔進行，低海拔之原始林、近郊之次生林及中海拔森林樹皮、苔蘚或樹冠層等不同棲地尚待探索。未來除持續進行甲蟎採集與分類研究，增加台灣甲蟎多樣性資料外，期望能結合形態分類及土壤化學性質等，探討土壤動物類群組成與土壤營養間關係。

關鍵詞（Keywords）：甲蟎（Oribatida mites）、穩定同位素（stable isotopes）、土壤化學性質（soil chemical properties）

OB07

Resolving the paradox of local warning signal diversity: possible mechanisms and a framework for hypothesis testing

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背景/研究問題/材料方法

Müllerian mimicry is a classic example of convergent evolution driven by positive frequency-dependent selection that preserves only the most common warning signal. However, warning signal diversity at local scales is commonly observed in nature and has long stood as a paradox. There are three potential explanations for this puzzling phenomenon. First, predation is extremely relaxed such that selection for convergence in signal appearance is practically nonexistent. Second, the presence of rarer warning signals within a community is the result of local extinction and immigration instead of long-term persistence. Third, local warning signal diversity can be maintained by “unforgetful” predators that can retain learned avoidance for long enough (the Unforgetful Predator Hypothesis).

結果/結論/應用啟示

To test these hypotheses requires two types of experiments. (1) Field learning experiments that present both profitable and unprofitable prey to the entire predator assemblage. These experiments detect trivial prey mortality, as well as measure predator avoidance and forgetting rate. (2) Population genomic analyses that quantify the extent and direction of dispersal between the focal and neighboring populations. Extensive dispersal into the focal population, particularly for species displaying rarer warning signals, would suggest that the presence of these rarer signals is the result of continuous immigration following local extinction instead of true persistence. Appropriate levels of predator avoidance and forgetting rate, plus the absence of immigration, will support the Unforgetful Predator Hypothesis.

關鍵詞（Keywords）： aposematism, convergent evolution, Müllerian mimicry, predator learning, positive frequency-dependent selection

OB08

透過貝氏可加性迴歸樹評估台灣農業生態系害蟻之分布及相關因素

Distribution and associated factors of pest ants in agroecosystem from Taiwan evaluated by Bayesian additive regression trees

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背景/研究問題/材料方法

Pest ants are major challenges in agroecosystem management, threatening crop production and biodiversity. Predicting their distribution is crucial for preventing agricultural damage, mitigating conservation risks, and ensuring ecosystem sustainability. Accurate predictions of pest distribution can help prioritize areas for intervention, leading to more efficient pest management strategies. Several species distribution modeling have been proposed, including the novel application of Bayesian additive trees (BART). However, the comparative performance of different models in agroecosystem contexts has not been thoroughly evaluated. In this study, we applied three tree-based approaches, RandomForest (RF), Boosted regression trees (BRT), and BART, to predict the distribution of major pest ants in Taiwan. We then assessed model performance using statistical metrics to determine their suitability and compared the predicted distribution.

結果/結論/應用啟示

We presented the potentially influenced farm area for three pest ant species and the associated factors of their distribution. Across the focal taxa, we found no distinct differences in model statistics and simulated projections across focal taxa, with only slight discordance in selected variables. This suggests that the choice of algorithm in species distribution modeling pose little impact of the results, whereas parameter tuning should be prioritized. We recommend further model refinement and validation through extensive field surveys and collaboration with local farmers to verify whether the selected factors accurately explain pest ant habitat suitability.

關鍵詞（Keywords）： Agroecosystem, Formicidae, Pest ants, Spatial modeling, Species distribution model

OB09

中國蜻蜓多樣性和分類學研究進展

Biodiversity and taxonomy of dragonflies and damselflies from China

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背景/研究問題/材料方法

蜻蜓目是迄今最古老的飛行昆蟲之一，蜻蜓目是昆蟲綱中較小的一個目，全世界目前已發現了 6500 余種。中國是世界上蜻蜓物種最豐富的國家，前期已經記錄了超過 900 種，然而隨著調查的深入更多的新紀錄和新物種陸續被發現。

結果/結論/應用啟示

經過研究團隊最近幾年的考察，中國蜻蜓的總數已經超過 1000 種，成為全球最受關注的蜻蜓熱點區域。物種組成上包括古北界和東洋界系兩大區系成分，但東洋界物種豐富占主要，其中西南地區和華南地區的物種最豐富，僅雲南省就記錄蜻蜓接近 450 種。本次報告將重點介紹研究團隊在昔蜓科、蜓科和裂唇蜓科等重要類群上的重要發現和分類學研究現狀，以及研究在蜻蜓進化領域取得的研究進展。

關鍵詞（Keywords）：蜻蜓目（Odonata）、多樣性（Biodiversity）、分類學（Taxonomy）、進化（Evolution）

論文宣讀: 行為、生理、個體生物學

Oral Session: Ethology, Physiology and Organismic Biology

OE01

脫共生對孤雌胎生蚜蟲的繁殖力影響：研究平台建立與卵巢結構解析

Exploring the Impact of Aposymbiosis on the Reproductive Capacity of Parthenogenetic and Viviparous Aphids: Establishment of Research Platforms and Analysis of Ovarian Structures

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背景/研究問題/材料方法

蚜蟲具備孤雌生殖和胎生繁殖的特性，無需交配即可透過母體直接產下發育完全的後代，這使得它們能夠快速擴張族群，成為農業上的重要害蟲。本研究旨在探討去除初級內共生菌 *Buchnera aphidicola* 對豌豆蚜蟲生殖能力的影響，特別是脫共生（aposymbiotic）蚜蟲的生育能力是否能在重新培養於正常植株或人工飼料上後恢復。我們透過解剖成蟲的卵巢結構，計算每條微卵管中的平均蛋腔數量，並測量最成熟蛋腔的長度，藉此探討脫共生蚜蟲生殖能力下降的原因。這些分析方法為了解脫共生蚜蟲生殖障礙提供了詳細的結構性依據。

結果/結論/應用啟示

研究結果顯示，脫共生豌豆蚜的生殖能力完全喪失，無論是卵巢結構、蛋腔數量，還是最成熟蛋腔的長度，與未經抗生素處理的對照組蚜蟲相比，都存在顯著差異。這些發現印證了過去研究的結果，並揭示了脫共生蚜蟲生殖能力喪失的原因。由於蚜蟲的孤雌生殖和胎生繁殖特性是其迅速繁殖的關鍵，脫共生後的生殖受阻現象將有助於深入理解相關的分子機制。本研究未來將結合 *in vitro* 和 *in vivo* 的基因表現分析，期望透過生殖發育基因的解析，解開脫共生蚜蟲不孕的分子機制，為害蟲控制提供新的應用方向。

關鍵詞（Keywords）：豌豆蚜（*Acyrthosiphon pisum*）、內共生菌（endosymbionts）、人工飼料（artificial diet）、微卵管（ovariole）、昆蟲發育（insect development）

OE02

馬尼拉小繭蜂共生病毒透過 miRNA 調控寄主胰島素信號路徑

Snellenius manila barcovirus regulate insulin signaling pathway in *Spodoptera litura*though miRNA

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背景/研究問題/材料方法

寄生蜂會透過寄生因子毒液、畸形細胞、以及寄生蜂共生病毒（PDV）調控寄主的生理，以利寄生蜂子代得以在寄主體內存活發育。前人研究發現 PDV 可以抑制寄主免疫反應、調控生長代謝。本研究欲探討馬尼拉小繭蜂（*Snellenius manilae*）是否會透過小繭蜂共生病毒（SmBV）來調控寄主斜紋夜蛾（*Spodoptera litura*）的胰島素信號路徑。我們以次世代定序分析注入 SmBV 的寄主，發現寄主體內會表現小片段 RNA（miRNA），並分析 miRNAs 對寄主脂肪代謝的影響。

結果/結論/應用啟示

研究發現 SmBV 會抑制寄主體內三酸甘油脂含量，並透過在寄主體內表現 miRNA 潛在抑制宿主胰島素信號路徑基因 PI3K 和 TOR，進而下調脂肪代謝路徑基因表現、影響宿主體內脂肪生合成。本研究調查 miRNA 如何抑制寄主體內脂肪含量來促進寄生蜂子代在寄主體內發育。未來有潛力開發基因農藥於生物防治，抑制農業害蟲族群擴散。

關鍵詞（Keywords）：小繭蜂共生病毒（Bracovirus）、胰島素信號路徑（Insulin signaling pathway）、斜紋夜蛾（*Spodoptera litura*）、小片段 RNA（miRNA）、馬尼拉小繭蜂（*Snellenius manila*）

OE03

空間混疊對蜜蜂著陸行為的影響

Effects of spatial aliasing on honey bee landing behavior

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背景/研究問題/材料方法

當飛行昆蟲的前方背景中出現許多重複性的圖案時，若單個重複圖案產生的視角小於兩倍昆蟲兩個小眼間的夾角，就會使昆蟲產生視覺的空間混疊 (spatial aliasing)。為了探討空間混疊是否會對昆蟲的著陸行為產生影響，我們利用 3D 軌跡追蹤系統，記錄蜜蜂在 8 種不同寬度的黑白條紋圖樣上著陸的整個過程。

結果/結論/應用啟示

透過分析蜜蜂在著陸過程與著陸處正下方條紋圖案之間的視角，證實 0.95 公分寬的黑白條紋圖案所產生視角，在整個蜜蜂著陸軌跡中會有 43.3%產生視覺空間混疊的情況，並顯著地增加蜜蜂尋找糖水的時間，且造成 75%的蜜蜂無法在記憶的位址著陸；而更細的 0.475 和 0.23 公分寬的黑白條紋圖案產生的視角，更讓蜜蜂產生空間混疊的比率提高至 72.1%與 88%，且著陸失敗的比率接近 90%，同時來回飛行穿過記憶位址上方的次數也皆有顯著的增加。因此，透過本實驗結果得知圖案造成的空間混疊確實會讓蜜蜂在著陸時更加的困難甚至導致著陸失敗。

關鍵詞（Keywords）：蜜蜂（honey bee）、著陸行為（landing behavior）、空間混疊（spatial aliasing）、3D 軌跡追蹤系統（3D trajectory tracking system）

OE04

使用 UV 燈防治疣胸琉璃蟻之研究
Using UV light to prevent and control *Dolichoderus thoracicus*

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背景/研究問題/材料方法

臺灣受疣胸琉璃蟻嚴重侵擾，儼然成為國家安全問題。由於疣胸琉璃蟻喜歡在人造密閉空間內築窩，我想了解如何解決此問題。我組裝二十四個白鐵小配電箱，裡面裝有燈管支架、日光燈管或 UV 燈管、電閘、溫濕度計，實驗有三個操作組別，分別是：亮 UV 燈管、亮日光燈管和不亮燈管，配電箱安裝在埔里鎮有很多疣胸琉璃蟻出沒的田園，藉以觀察燈光預防疣胸琉璃蟻入侵的效果。另外拍照記錄已經有大量疣胸琉璃蟻築窩的六個配電箱，在其中安裝亮 UV 燈管、亮日光燈管和不亮燈管，隔週記錄螞蟻數量，研究燈光驅趕疣胸琉璃蟻的效果。

結果/結論/應用啟示

燈光能有效防蟻：燈光可以事前預防性防治和事後驅趕疣胸琉璃蟻。UV 燈效果比日光燈更好：日光燈和 UV 燈都能防治疣胸琉璃蟻，然而 UV 燈的防治效果比日光燈還要來的好，但還需注意 UV 燈可能對皮膚和眼睛造成傷害，並加快材料老化和變色，日光燈則須注意陰影會影響防治效果。使用 UV 燈徹底驅趕已經入侵電器設備的疣胸琉璃蟻、在重要的設備裡面預先架設燈光、在電力公司地下電纜涵洞與陰暗密閉空間預先架設燈光，是很好的永續、環保方法，只要明確警示疣胸琉璃蟻不要過來侵擾人類生活領域，那麼牠就不是危害了，懇切地拜託大家幫忙推廣使用燈光防蟻。

關鍵詞（Keywords）：疣胸琉璃蟻（*Dolichoderus thoracicus*）、防治（Prevent and control）、燈光（light）、環保（Environmental friendly）、永續（Sustainable）

OE05

不同產卵間隔天數對漿黑卵蜂 *Telenomus remus* 族群性別比以及體內 *Wolbachia w*Rem 感染滴度的影響

Effects of different egg-laying rest days on the sex ratio and *Wolbachia* titer in the *Wolbachia w*Rem-infected population of *Telenomus remus*

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背景/研究問題/材料方法

漿黑卵蜂 (*Telenomus remus*) 是一種繁殖率高且對秋行軍蟲效果佳的生物防治資源，在世界各地已被廣泛使用。前人研究發現漿黑卵蜂感染 PI-*Wolbachia* (parthenogenesis-inducing (PI) *Wolbachia*) 後，生殖模式會從未受精產雄生殖 (androtoky) 轉變為未受精產雌 (thelytoky)，且雌性比接近 100%。然而實驗室內感染 PI-*Wolbachia w*Rem 品系之漿黑卵蜂族群在持續且密集的繼代環境下，產出 50%的雄性子代；而繼代頻率重新放緩時，雌性比便會回升。文獻曾指出連續產卵可能降低親代體內 *Wolbachia* 的滴度，因此本試驗設計漿黑卵蜂不同的產卵間隔對 1) 子代雌性比、2) 子代總數及 3) 親代 *w*Rem 滴度的影響。

結果/結論/應用啟示

感染 *w*Rem 之漿黑卵蜂產下的後代雌蟲率，受到開始寄生時間的影響，若是在羽化後 6 小時內給予卵寄生，雌性比會下降。*w*Rem 可能需要時間轉移至子代；*w*Rem 品系的漿黑卵蜂在產卵後體內的 *w*Rem 滴度較剛羽化時高，表示 *w*Rem 在漿黑卵蜂體內持續擴增。若累代進行且無休息繼代處理，PI 的效果會持續降低；親代及子代體內 *w*Rem 滴度也會隨累代而降低。未來將延續上述結果，針對產卵休息、*w*Rem 滴度的變動及持續累代的影響─三個方向進行，試圖歸納實驗室內取得大量漿黑卵蜂雌蟲的最佳飼養模式，減少取得雌蟲所需的時間及資源成本。

關鍵詞（Keywords）：生物防治（Biological Control）、wRem 共生菌（wRem symbiotic bacteria）、子代雌性比（Female offspring ratio）

OE06

穀蠹後腸水通道蛋白與殺蟲劑感受性之關聯及 RNAi 方法最佳化

Association between hindgut aquaporins and pesticide susceptibility in *Rhyzopertha dominica* (F.) and optimization of RNAi methods

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背景/研究問題/材料方法

穀蠹（*Rhyzopertha dominica*）是廣布全球的重要積穀害蟲，具多種藥劑之抗藥性，有鑑於穀倉環境乾燥，水通道蛋白在水動態平衡的調控相當關鍵，其中 *Pyrocoelia rufa* integral protein (Prip) 水通道蛋白在後腸具顯著高的表現量，而於賜諾殺抗性品系表現量則顯著低於感性，以此推論水分再吸收與賜諾殺感受性具相關性。本研究旨在探討後腸水分再吸收與殺蟲劑感受性的關係，並最佳化 RNAi 條件以利基因功能探討。我們以基因表現量判斷與後腸水分再吸收相關的水通道蛋白，餵食 dsRNA 後以殺蟲劑處理，觀察死亡率。在 RNAi 最佳化實驗，我們測試餵食濃度、時間、施用方法與保存性，探討 dsRNA 默化效果之效率與持續時間。

結果/結論/應用啟示

穀蠹水通道蛋白中，Prip 與 *Drosophila* integral protein (Drip) 於後腸表現最顯著，同時默化兩基因後對第滅寧與賜諾殺的感受性皆顯著下降。RNAi 最佳化實驗以滴加 dsRNA 濃度 25、50、100、175 mg/kg 之麥片餵食穀蠹三天皆能顯著默化目標基因。以最低濃度 25 mg/kg 之麥片餵食 1 天、2 天與 3 天皆能顯著默化目標基因；且餵食 1 天的 RNAi 條件下，顯著默化效果可持續至少 15 天。於 -20 ℃ 保存 20 天與 272 天之 dsRNA 默化效果相似。改以滑石粉為媒介將 dsRNA 混拌於麥片表面，其默化效果與滴加方法相似。本研究發現默化後腸水通道蛋白會使穀蠹對殺蟲劑感受性下降，亦最佳化 dsRNA 餵食條件，為穀蠹生理與蟲害管理提供新的參考資訊。

關鍵詞（Keywords）：穀蠹（*Rhyzopertha dominica*）、水通道蛋白（aquaporin）、後腸（hindgut）、殺蟲劑感受性（pesticide susceptibility）、RNA 干擾效率（RNAi efficiency）

OE07

Asaia bogorensis DP3 菌株作為蜜蜂益生菌之潛力及功能性基因分析

Evaluation of the Probiotic Potential for honey bees (*Apis mellifera*) and Functional Gene Analysis of *Asaia bogorensis* DP3

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背景/研究問題/材料方法

Extreme climate and the shortage of forage plants have led to honey bee colony collapse. To address the honey bees' survival challenges, recent studies have focused on identifying potential probiotics from the bee gut and the surrounding environment of bee hives. In this study, we isolated a strain named DP3 from the bee pollen of *Bidens pilosa*. This strain was identified as *Asaia bogorensis* by full-length 16S rDNA. The species is known to inhabit the guts of mosquitoes and other insects as symbiotics, enhancing the expression of hosts' immune and nutritional genes and extending lifespan. However, no studies have yet explored the effects of this bacteria in honey bees. In this study, we test DP3 strain by designing the high sugar osmotic pressure and acidic in vitro culture environment similar to the honeybee gut. Subsequently, we fed the DP3 strain to newly emerged bees to confirm the effects of this strain on the physiological gene expression of the bees and the changes in their gut microbiota. Finally, we use third-generation sequencing to assemble genome of DP3 strain and completed the functional gene analysis, evaluating how this strain may help bees on metabolism and synthesis.

結果/結論/應用啟示

Our study observed that *Asaia bogorensis* DP3 exhibits high tolerance to both high sucrose concentrations and acidic environments. This suggests that DP3 can likely survive in sucrose solutions consumed by honeybees and within the acidic conditions of the bee gut. Additionally, when fed to bees, this strain could temporarily persist in the gut and show neither signs of mortality nor significantly changing in hosts' gut microbiota. In whole genome sequencing of the *Asaia bogorensis* DP3 strain, we identified biosynthetic pathways for compounds such as carotenoids and terpenoids. Further studies will explore whether these biosynthetic products benefit bee gut health and assess its probiotic potential for bees.

關鍵詞（Keywords）： *Apis mellifera*, *Asaia bogorensis*, Functional gene, Probiotics, Gut microbiota

OE08

無氧代謝協助蜜蜂平衡熱逆境引發之活性氧化物
Temperature-Driven Metabolic Shifts in Honey Bees for Balancing Reactive Oxygen Species

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背景/研究問題/材料方法

氣候變遷下，極端高溫在各地愈發頻繁，威脅生態平衡與經濟發展。然而，各地均溫與對於高溫的耐受性不同，找尋該地穩定的「生物指標」作為正在受極端高溫威脅的警示，在近年顯得格外重要。前人研究指出，熱逆境下授粉昆蟲的授粉效率將會降低，將對生態與農業造成衝擊。本研究選用最廣泛飼養與分佈的授粉昆蟲-西方蜂作為模式，探討熱逆境下外勤蜂的生理與行為變化，評估其作為生物指標的可能性。北台灣夏季氣溫近年開始出現 40℃的事件，以此作為極端高溫的模擬，與北台灣夏季平均最低溫約 26℃做比較，以基因表現、代謝產物與換氣效率等指標，找出極端高溫下的生理與行為特徵。

結果/結論/應用啟示

結果顯示，蜜蜂在極端高溫的環境下四個小時，血淋巴之乳酸含量顯著增加，且氧氣消耗與換氣效率下降，顯示無氧代謝途徑增強，而有氧代謝需求減低。血淋巴中的活性氧化物產量與其代謝酵素基因表現量皆顯著增加，單純注射活性氧化物 H_2O_2 至蜜蜂體內，亦使外勤蜂之換氣效率降低，顯示外勤蜂為了平衡體內的活性氧化物而有代謝與行為的適應。若將 ERK 訊號傳遞阻斷，發現此適應的效果消失，造成蜜蜂生存的負面影響，顯示此適應的重要性。此發現將可以成為極端熱逆境下的生物指標，協助當地評估生態與農業將受到的衝擊。

關鍵詞（Keywords）：西方蜂（Western honey bee (*Apis mellifera*)）、熱逆境（heat stress）、無氧代謝（Anaerobic metabolism）、活性氧化物（Reactive oxygen species (ROS)）

OE09

黑翅晦螢的夜間行為與光環境的關係
Nocturnal behavior of *Abscondita cerata* related to their photic environment

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背景/研究問題/材料方法

Fireflies utilize unique flash signals and different light wavelength for mating communication. However, whether their nocturnal behaviors would be interfered by artificial light sources (e.g. street light, flashlight) remains obscure. In this study, we investigated the influences of natural light and artificial light-emitting diode (LED) light to the locomotion behaviors of *Abscondita cerata* (Lampyridae).

結果/結論/應用啟示

This study revealed 70.4% males and 3.6% females were usually in flight while 17.8% males and 8.2% females were maintaining on perch in field during the nocturnal activity time. Their nocturnal activity time could remain for 3 days in laboratory condition. This study further revealed the intensity of environmental green wavelength remained 0.6 – 1.94 μW/cm2 during the flashing time, which closed to the bioluminescent light intensity of males. When they began to fly out from the groves or bushes, the intensity of envrionmental green wavelength reduced to 59 – 462 nW/cm2, which is overlapped with the average intensity of males and females. A short exposure of different wavelengths of LEDs, especially white and blue light, could significantly affect the movements of adult males. Higher intensity of red light could still slightly influence their activity. Moreover, high intensity of green light was found to be able to attract adult males approaching to the light source. These light preferences may explain the locomotion behavior of the fireflies and assist to create an eco-friendly habitat for them.

關鍵詞（Keywords）：螢火蟲（firefly）、螢科（Lampyridae）、晦螢屬（Abscondita）、運動行為（locomotion behavior）、光害（light pollution）

OE10

Parental care confers offspring developmental plasticity for heat stress tolerance in burying beetles

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背景/研究問題/材料方法

Elevated temperature associated with global climate change pose a major challenge for biodiversity and ecosystem health. Behavioural responses, such as parental care, may provide insects with a means of adjusting rapidly to adverse environments. However, recent studies have found contrasting results, possibly because of the multifaceted effects that temperature elevation have on parents, offspring, and/or the parental care delivered to the offspring. In this study, we investigated the effects of elevated temperatures on the reproductive behaviour and offspring performance in the burying beetle *Nicrophorus nepalensis* when they breed under control (17.8°C) and heat stress (21.8°C). We tested whether heat stress (1) reduces clutch size, (2) makes carcass preparation more energetically costly, and (3) disrupts carcass preparation process. In a reciprocal transplant experiment in which we transferred carcass prepared under either control or heat stress conditions to beetles during breeding under both control and heat stress conditions.

結果/結論/應用啟示

We found that heatwaves strongly disrupted parental investment, resulting in lowered clutch size and poor pre-hatching care behaviour. However, our carcass reciprocal transplant experiment revealed that both pre- and post-hatching cares are crucial for buffering offspring against heatwaves. Our study demonstrates the key role of parental care in mitigating the effects of heat stress on offspring in *N. nepelensis*. Pre-hatching care such as carcass preparation and maintenance, along with post-hatching care, provide essential buffering against adverse thermal environments. Nonetheless, parental care also has its limitations, particularly under prolonged heat stress, highlighting the need for further research investigating the adaptive responses and potential long-term consequences of climate change.

關鍵詞（Keywords）： burying beetle, climate change, developmental plasticity, heat stress, reciprocal transplant

論文宣讀: 醫學昆蟲學

Oral Session: Medical Entomology

OM01

臺北地區犬心絲蟲病媒蚊感染率及其族群動態

Infection rate and population dynamics of *Dirofilaria immitis*vector mosquitoes in Taipei

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背景/研究問題/材料方法

犬心絲蟲症 (dirofilariasis) 是由犬心絲蟲 (*Dirofilaria immitis*) 感染寄生所引起，屬於一種蚊媒性人畜共通傳染病，廣泛流行於世界各地。主要宿主為犬隻，成蟲棲息於犬隻的右心室和肺動脈，臨床症狀包括呼吸困難、貧血，甚至死亡。犬心絲蟲也可以感染貓、狼、郊狼和其他動物。本研究的主要目標在持續監測 2023 至 2024 年臺北地區蚊子感染犬心絲蟲的情形。本研究於臺北市內湖區與木柵區使用以乾冰為誘餌的 CDC 捕蚊燈採集蚊子，每兩週採集一個晚上。蚊子鑒定和分池 (pool) 之後，以巢式聚合酶連鎖反應 (nested PCR) 分析可能參與犬心絲蟲傳播的蚊子種類及其族群動態。

結果/結論/應用啟示

本研究共收集 842 隻，包含 7 屬 23 種蚊子。以 nested PCR 檢測犬心絲蟲感染，得到 98 池陽性，共計 20 種蚊子感染犬心絲蟲。全年均有感染，感染高峰為 6 月與 9 月，臺北市蚊子感染率的最大似然估計 (MLE) 為 13.2 (95% 信賴區間: 11.7-15.3)。此外，本研究也首次發現 *Anopheles* 屬、 *Armigeres* 屬、*Culex* 屬、M*ansonia* 屬、*Uranotaenia* 屬共 16 種蚊蟲可以被犬心絲蟲感染。本研究所建立之犬心絲蟲病媒蚊族群動態資料將有助於了解犬心絲蟲在臺北地區流行之情形及與病媒蚊之間的交互作用，可提供病媒防治、獸醫及公共衛生領域防疫政策之重要資訊。

關鍵詞（Keywords）：犬心絲蟲（*Dirofilaria immitis*）、犬心絲蟲症（Dirofilariasis）、蚊子（Mosquito）、巢式聚合酶連鎖反應（Nested PCR）、族群動態（Population dynamic）

OM02

Effects of emerging contaminants on the development and swimming behavior of dengue vector mosquitoes

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背景/研究問題/材料方法

Dengue fever is an important issue in public health in tropical and sub-tropical region, and it is transmitted by two major vectors, *Aedes aegypti* and *Ae. albopictus*. The common breeding sources of *Aedes* mosquitoes are artificial containers, and those emerging contaminants (ECs) may leach from plastic bucket or tire. In addition, those ECs belonging to endocrine-disrupting chemicals, which can mimic mammalian hormones. The ECs may have similar physiological effects on the mosquito's growth and development once larvae exposed to ECs. Furthermore, it may affect the density and size of adult populations in a short time, and also influence the vector competence of *Aedes* mosquitoes to transmit dengue virus. Therefore, the aim of this study is to explore and evaluate the risk of ECs on aquatic organisms based on bioassays in *Aedes* mosquitoes.

結果/結論/應用啟示

First instar larvae of *Ae. aegypti* and *Ae. albopictus* are exposed to different concentrations of PAEs and 6PPD-quinone. The growth durations of each instar and pupae are recorded, and the swimming behavior was also evaluated by light-dark locomotion assay and vibrational startle response assay. In results, it showed that exposed to 1 ppb of 6PPD-quinone prolonged the growth duration from 1st larvae to male of *Ae. albopictus* by about 26.45 hours significantly. 100 ppb of 6PPD-Q significantly accelerated the growth duration from 1st instar larvae to pupation of *Ae. aegypti* by 59.09 hrs. However, there was no significant effects by PAEs. The size of *Ae. albopictus* male whose larvae exposed to 10 ppb of 6PPD-Q was significantly larger than control group. Even though the growth duration of larvae was not significantly affected by PAEs, the adult size of *Ae. albopictus* was significantly increased by 10 ppb of PAEs, but decreased by 100 ppb of PAEs. In swimming behavior, it showed that 100 ppb of PAEs significantly decreased the activity of 4th instar larvae of *Ae. albopictus* during both light and dark cycle, but 10 and 100 ppb of PAEs increased the swimming distance after vibration stimulus. In conclusion, 6PPD-Q had a greater effect on mosquito growth and development and adult body size, but PAEs mainly affected adult body size, larval swimming behavior and response to stimuli. In the future, the dengue vector competence of *Aedes* mosquitoes exposed to ECs would be evaluated.

關鍵詞（Keywords）： *Aedes mosquito*, emerging contaminants, larval development, swimming behavior

OM03

土地利用型態改變了海拔梯度上的蚊蟲群聚相

Land use alters mosquito communities along altitudinal gradients in Taiwan

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背景/研究問題/材料方法

Abundance and species composition of mosquitoes change with elevation, but can also be affected by land use when abiotic (e.g., temperature, humidity) and biotic (e.g., number of predators) conditions are altered. In a world when a rapid change in land use may lead to the expansion and increase in the abundance of mosquitoes and therefore mosquito-borne diseases, a better understanding of how land use change reshapes mosquito communities along the altitudinal gradient is warranted. However, related studies remain very limited. We surveyed mosquitoes and potential predators of mosquitoes every 50m along an elevational gradient (100m to 1,650m amsl) and covered various habitat types (wetland, urban area, rural village, mosaics of agriculture and secondary forests, and mature forest) in northern Taiwan. In addition, mosquitoes were sampled in three habitats (rural village, mosaics of agriculture and secondary forests, and mature forest) at three altitudes (300m, 600m and 1,200m amsl). We apply taxonomic (TD), phylogenetic (PD), and functional diversity (FD) indices to show the community changing along elevational gradient.

結果/結論/應用啟示

TD indices were highest in wetland, while they were lowest in urban. Furthermore, the pattern of PD and FD indices were opposite across land use types. Mosquito communities changed with altitudes naturally, but were modified by land use. Specifically, mosquito communities were more homogeneous in anthropogenic habitats, including urban area, rural villages, and mosaics of agriculture and secondary forests. Rural village and mosaics of agriculture and secondary forests increased the number of *Aedes albopictus*, which is the main vector of dengue virus in northern Taiwan. Natural enemies of mosquitoes, such as dragonflies (*Lyiothemis flava*) and predatory mosquitoes (*Toxorhynchites* spp. and *Lutzia* spp.) occurred at high-elevation sites and mature forest. Altitude and land use can both affect mosquito communities, but through distinct mechanisms. Diverse thermal niches and blood sources are available to mosquitoes along elevational gradients, whereas human land-use create habitats favored by anthropophilic mosquitoes. Moreover, not only temperature, but also resources and predators could influence abundance and species composition of mosquitoes.

關鍵詞（Keywords）：蚊蟲（mosquito）、土地利用（land use）、海拔（altitude）、蟲媒疾病（vector-borne disease）、臺灣（Taiwan）

OM04

以媒介昆蟲採血法結合兩種納米孔定序策略調查台灣及離島的牛隻病毒
Vector-based approach with two nanopore sequencing strategies to survey bovine viruses in Taiwan and offshore islands

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背景/研究問題/材料方法

The vector-based approach is a surveillance method used to simultaneously detect various pathogens in livestock through vector insects. Our goal is to establish an efficient workflow for virus surveillance. In this study, we collected 14,045 vector insects, including 7,436 *Culicoides* biting midges, 4,700 mosquitoes, and 1,909 flies, from cattle farms and pastures in Taiwan, the Kinmen islands, and the Penghu islands during 2021 and 2022. We applied amplicon and cDNA-direct sequencing using the R10.4 flow cell with the MinION from Oxford Nanopore Technologies platform to detect both arboviruses and non-arboviruses. We then evaluated nine viral metagenomic tools for time efficiency, using BLAST+ as a baseline, to develop an optimized pipeline for virus identification.

結果/結論/應用啟示

Our results provided new insights into the viral communities associated with Taiwanese cattle and beef using a vector-based approach combined with nanopore sequencing. Eighteen arboviruses and five non-arboviruses were sequenced, including seven arboviruses identified for the first time in Taiwan. The tools KrakenUniq and Magic-blast demonstrated superior performance in terms of time efficiency, and the use of custom databases at the family level for target viruses significantly enhanced the effectiveness of viral metagenomic identification.

關鍵詞（Keywords）： 媒介昆蟲採血法（vector-based approach）、蟲媒病毒（arbovirus）、牛（cattle）、庫蠓（*Culicoides* biting midge）、蚊（mosquito）

論文宣讀: 系統分類、族群遺傳、演化

Oral Session: Systematics, Population Genetics and Evolution

OS01

臺灣產寡毛實蠅亞科 (雙翅目：果實蠅科) 分類學研究與雄蟲生殖器形態描述

A Taxonomic Study of Dacinae Fruit Flies (Diptera: Tephritidae) of Taiwan with Description of Male Genitalia

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背景/研究問題/材料方法

The fruit flies of subfamily Dacinae (Ditpera: Tephritidae) are a biologically interesting and economically important group. Dacinae is currently divided into 3 tribes, namely Ceratitidini, Dacini, and Gastrozonini, with the latter 2 tribes occurring predominantly in the tropical and subtropical rain forests of South-East Asia and are found throughout Taiwan. Larvae of Dacini mainly feed on fruits of native rainforest plant species, with certain polyphagous and multivoltine species becoming major agricultural pests. Larvae of Gastrozonini feed on stem of Poaceae species, but knowledge regarding taxonomy and biology of the group is still relatively scarce and limited. Traditional taxonomy of both tribes relies on ambiguous characters, such as subtle variation in body color patterning or wing markings, for defining species. Morphology of male genitalia, although generally utilized in insect taxonomy, are seldom provided in species description of Dacinae. This study aimed to revise the Dacinae species of Taiwan and to provide description of male genitalia.

結果/結論/應用啟示

The checklist of Taiwanese Dacinae has been updated, with 32 Dacini species and 14 Gastrozonini species. The male genitalia of 13 Dacini species and 4 Gastrozonini species have been studied, of which 14 species were described for the first time.

關鍵詞（Keywords）：Tephritidae, Dacinae, taxonomy, male genitalia, Taiwan

OS02

台灣產水黽(半翅目：水黽科)分類學初探

Preliminary Study on the Taxonomy of the Water Striders (Hemiptera: Gerridae) in Taiwan

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背景/研究問題/材料方法

水黽科(Gerridae)屬於半翅目的黽椿象下目(Gerromorpha)，外形與蜘蛛相似，體型細長或短小，翅為無翅到長翅等多種形態；其足部細長，跗節具細微毛，使其漂浮於水面，並以漂浮在水面的動物為食。水黽廣泛分布於各大洲的各式水域，同時也是極少數可棲息於海面的昆蟲(Cheng & Mishra, 2022)。台灣的水黽研究始於江崎悌三(Teiso Esaki)的半翅目系列研究，於 1920 年代發表多篇台灣水黽的分類學報告，包含 4 種源自於台灣的新種(台灣東方水黽(*Amemboa fumi*)、黃斑海黽(*Asclepios apicalis*)、台灣水黽(*Gerris cui*)、高橋氏大澗黽(*Rhyacobates takahashii*)) (Esaki, 1923, 1924, 1925)，並根據台灣全島的半翅目調查結果，在 1926 年發表〈Verzeichnis der Hemiptera-Heteroptera der insel Formosa 〉，文中列出 14 種台灣的水黽(Esaki, 1926)，為台灣首次有系統性的水棲半翅目調查。隨後宮本正一(Syoiti Miyamoto)發表來自台灣本島及蘭嶼的新紀錄的扁腹水黽(*Gerris latiabdominis*)、大褐水黽(*Limnometra femorata*)，以及新種的一色氏水黽(*Gerris issikii*) (Miyamoto, 1958, 1964)。此後，Polhemus & Andersen (1984)從台灣東方水黽的標本中發現另一新種，並命名為江崎氏東方水黽(*Amemboa esakii*)，將台灣的水黽物種數增加至 11 屬 18 種。由於台灣的水黽紀錄散見於各篇文獻，至今僅有約百年前的廣泛調查(Esaki, 1926)，但離島及東部資料仍然不足，許多物種的國內分布狀況尚待釐清，因此本研究旨在統整水黽科文獻與全台灣的調查結果，記錄各物種分布、微棲地、海拔等資訊。本研究材料基於博物館、2018 年至今的全台灣調查的標本，採集方法以目視撈捕法採集。

結果/結論/應用啟示

本研究已對台灣本島、金門群島、澎湖群島、蘭嶼及綠島進行調查。分布於台灣的水黽總計有 11 屬 19 種，其中小澤背水黽(*Limnogonus nitidus*)為台灣新紀錄種。蘭嶼及綠島新增暗條澤背水黽(*Limnogonus fossarum*)的地區新紀錄，而澎湖群島有圓臀大水黽(*Aquarius paludum*)和暗條澤背水黽的地區新紀錄。在物種棲息地方面，靜水或緩流域型物種佔最大比例，共 11 種，占台灣水黽科的 57.9%。其次是溪流型物種，共 5 種，占 26.3%。海岸型物種則有 2 種，占 10.5%。在水平分布方面，所有物種均可在台灣本島發現，分布較為侷限的物種包含一色氏水黽，其分布於台灣東北部高山；大褐水黽僅分布於恆春半島、蘭嶼及綠島；江崎氏東方水黽分布於台灣南部及東部；柯氏縊腹澗黽(*Rhagadotarsus kraepelini*)分布於台灣中部以北。大部分物種的垂直分布(海拔)以低海拔為主，但一色氏水黽、台灣水黽及長翅大水黽(*Aquarius elongatus*)可見於中高海拔地區。基於本研究提供的分類研究、檢索表、分布及棲地資訊，建立台灣的水黽科分類學及生態學報告，可為圖鑑、昆蟲誌等提供基礎。

關鍵詞（Keywords）：水棲昆蟲（aquatic insect）、半水棲椿象（semi-aquatic bugs）、分布資訊（distribution）、新紀錄（new record）、棲息地資訊（habitat）

OS03

透過古生物學剖析偽瓢蟲科多樣性演化動態

Paleontology provides new insights into diversity dynamics of handsome fungus beetles (Coleoptera: Endomychidae)

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背景/研究問題/材料方法

古生物學研究有助於我們了解物種的起源與宏觀演化，透過對化石與現生物種的比較分析，重建生物演化歷程的編年史。偽瓢蟲科（Endomychidae）為一群中等多樣性的中小型甲蟲，全球大約包含 1300 個已描述種，目前的親緣關係研究認為他們主要包含兩個支系，分別為基部的基群偽瓢蟲類（Basal Endomychidae）與冠群的高等偽瓢蟲類（Higher Endomychidae）。牠們大多為菌食性，以真菌孢子和菌絲為食。雖然我們對於其多樣性、形態特徵、系統分類與親緣關係、生態習性、以及化石紀錄已有初步的認識，然而在更進一步探討該類群的宏觀演化上，仍舊較少有專門研究觸及。因此，本研究將焦點鎖定在偽瓢蟲科整體多樣性及其結構隨時間的演變及其可能的成因。

結果/結論/應用啟示

生物多樣性分析的結果顯示，新生代早期的偽瓢蟲科多樣性高於中生代晚期，這說明了偽瓢蟲科在中生代過渡到新生代期間，歷經了一波多樣化進程。在多樣性組成結構上，高等偽瓢蟲類在該科整體多樣性的佔比明顯隨時間上升，逐漸形成當今的優勢地位。多樣化速率估算顯示基群偽瓢蟲類一開始較為平緩，但在始新世早期（約 5100–5300 萬年前左右）時，其淨多樣化速率突然歷經了一次飛躍式上升，顯示牠們可能拓殖到新的生態棲位，這與螞蟻在化石紀錄中大量出現的時間點一致，考慮到喜蟻性偽瓢蟲皆隸屬於基群偽瓢蟲類，我們認為喜蟻性的新棲位可能促使了這一波快速的多樣化。而高等偽瓢蟲類的淨多樣化速率則自白堊紀中期起穩定上升，歸功於滅絕速率的逐步降低，我們推測這可能是由於該類群多樣化的防禦機制，例如警戒色、化學防禦、從足部關節流出血淋巴、大量聚集行為等，促進了其多樣性演化上的成功。

關鍵詞（Keywords）：古昆蟲學（Paleoentomology）、宏觀演化學（Macroevolution）、生物多樣性動態（Biodiversity dynamics）、多樣化（Diversification）、菌食性甲蟲（Mycophagous beetles）

OS04

一種怪螳於台灣的增補(螳螂目：怪螳科)

A Supplement to an *Amorphoscelis* species (Mantodea: Amorphoscelididae) in Taiwan

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背景/研究問題/材料方法

怪螳屬 *Amorphoscelis* Stål, 1871 為 2023 年首次確認於台灣分布之新記錄科、新記錄屬之螳螂，然存證標本僅一筆，對於其分類地位的確認、生物學特性及分布棲所等訊息皆相當有限。經過一年的調查研究及公民科學的參與，獲得更多資料，對於其形態、棲所、分布及生物學資訊，均有更進一步的了解，有助於了解該怪螳是否為新種。

結果/結論/應用啟示

本研究除分類學上的形態研究鑑定外，藉由公民科學的參與，得知怪螳的發生時間不只是先前認知的 7 月，而是 7-11 月，並瞭解到其好發季節應為 7 月。共獲得 6 隻成熟雄性個蟲；分布地點目前得知為新北市，其棲所主為山區之河谷樹林，對於更詳細的環境及棲息植物，尚需更多調查結果才能更明確。文獻顯示，此怪螳物種應為新種，怪螳屬物種的相關鑑定特徵，如複眼後緣、前胸背板、雄蟲尾毛及生殖器等均顯示其為全新物種。此外，此一研究為昆蟲分類及生物多樣性研究上，少數藉由公民科學參與調查獲得相關資訊的案例；顯示公民科學的應用，的確可加速台灣地區螳螂之研究，也顯示團隊參與對於野外調查研究的貢獻。

關鍵詞（Keywords）：螳螂目（Mantoda）、怪螳科（Amorphoscelididae）、公民科學（citizen science）、分布（Distribution）

OS05

黃鳳蝶臺灣亞種的“絕滅”是天災還是人禍?
Is the extinction of *Papilio machaon sylvina* caused by natural hazards or humans?

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背景/研究問題/材料方法

Old World Swallowtail (*Papilio machaon* Linnaeus, 1758) is a well-known butterfly that is widespread in the Palearctic region with numerous subspecies recognized (Nazari et al. 2023). In Taiwan, two subspecies are known to occur: the population in Matsu Islands is closely related to *P. m. schantungensis* Eller, 1936, while the main Island of Taiwan hosted an endemic subspecies, *P. m. sylvina*. *Papilio machaon* “sylvia” was described in 1930 by Japanese Lepidopterists Teiso Esaki and Tadao Kano from mainland Taiwan. The catastrophic earthquake that shook Taiwan on 21 September 1999 resulted in multiple landslides in the habitat of *P. m. sylvina* that permanently altered the landscape in many parts of the Island. Since then, despite exhaustive searches, *P. m. sylvina* has not been seen again, it is thus presumed extinct. Many questions persist about the faith of *sylvina* but also about its taxonomic status, range, and genetic affinity with respect to other conspecific populations across its range. To compare the genetic characteristics of this population, we obtained a COI barcode sequence from a specimen of *P. m. sylvina* reared in 1995. We also compared the life history of this subspecies with those of the adjacent populations. We then used ecological niche modeling to infer the distributions of both *P. m. sylvina* and its hostplant.

結果/結論/應用啟示

For the first time, we obtained a COI DNA barcode from museum specimens of *P. m. sylvina*. We demonstrate that this population was not only phenotypically distinct, but also had a unique mitochondrial haplotype among all other Holarctic populations of *P. machaon*. The life history of *P. m. sylvina* from rearing experiments carried out in the 1990s also show distinct characterists from those of other subspecies. Since the hostplant persists well in the known localities, we rise a hypothesis that commercial harvest for international trade might be responsible for the decrease of viable population size of this subspecies before the earthquake. This inference, however, still requires evidence from trade data and genetic information, which are now difficult to obtain.

關鍵詞（Keywords）： 物種保育（species conservation）、商業採集（commercial harvest）、天災（catastrophe）、物種絕滅（species extinction）、分子系統學（molecular systematics）

論文宣讀: 都市昆蟲學

Oral Session: Urban Entomology

OU01

新北市虎頭蜂分布熱點調查
Investigation of Hornet Distribution Hotspots in New Taipei City

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背景/研究問題/材料方法

近年來，全臺各地受虎頭蜂螫傷甚或致死的事件層出不窮。民眾於新北市山區遭虎頭蜂襲擊之事件愈發頻傳，為避免此類憾事重演，本計畫針對歷年新北市消防局與動保處的通報資料進行彙整分析，建立新北市的虎頭蜂築巢與螫傷熱點地圖，並規劃便民查詢之虎頭蜂熱點與相關科普資訊網站，藉此提醒民眾應避免進入高風險區域外，同時宣導防範蜂螫威脅的正確知識，以達到減少虎頭蜂螫傷事故發生之目的。

結果/結論/應用啟示

分析結果顯示，新北市虎頭蜂案件的通報量逐年增加，且每年 6 至 9 月為通報高峰期。虎頭蜂築巢通報熱點主要集中於住宅區與淺山地區，尤其是新店、淡水與汐止等區域；螫傷熱點則分布在市區及郊山步道景點處。本計畫現已完成歷年虎頭蜂築巢和蜂螫傷亡的熱點地圖，並將熱點成果整合至「新北市虎頭蜂熱點網站」中，便於民眾查詢虎頭蜂築巢及螫傷熱區，從而提升對高風險區域的警覺性，進而減少螫傷事故發生。此外，網站中亦刊載虎頭蜂辨識、防範及螫傷救治等科普資料，幫助民眾提升遭遇虎頭蜂威脅時的應對能力。本研究為虎頭蜂螫傷的預防策略提供了重要基礎，未來將進一步應用熱點地圖資料規劃即時的警訊通知系統，增加民眾對虎頭蜂出沒熱點的警覺性，以切實預防蜂螫致死憾事發生。

關鍵詞（Keywords）：虎頭蜂（Hornet）、虎頭蜂築巢熱點（Hornet Nesting Hotspots）、虎頭蜂螫傷熱點（Hornet Sting Hotspots）

OU02

都市地區臺灣家白蟻巢群分布與餌站系統防治成效評估

Colony Distribution of *Coptotermes formosanus* and Evaluation of the Effectiveness of Bait Station Systems in Urban Areas

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背景/研究問題/材料方法

家白蟻屬（*Coptotermes*）是全球都市地區主要危害的白蟻類群。每年臺灣因白蟻危害所造成的經濟相當龐大。大量的設置白蟻餌站系統進行區域性防治，能有效預防並長期控制當地的白蟻危害風險，而白蟻的巢群分布以及餌站的設置會影響區域性防治投入的成本與防治成效。本研究在台中與新竹的都市地區分別各設置三個樣區，在樣區的綠地內設立木樁監測白蟻取食活動。以微衛星基因確定家白蟻巢群身分及活動範圍，使用 Recruit HD 長效型餌劑防治樣區內的家白蟻巢群。最後根據家白蟻巢群活動範圍，模擬餌站在不同設置間距情況下，如何影響防治成效與成本。

結果/結論/應用啟示

在台中，臺灣家白蟻巢群活動範圍為 97.48 ± 76.51 平方公尺，巢群密度為每公頃 0.78 ± 0.43 巢（n = 5）；在新竹，臺灣家白蟻巢群活動範圍為 905.88 ± 1867.39 平方公尺，巢群密度為每公頃 1.00 ± 0.77 巢（n = 5）。在家白蟻巢群取食餌劑後，平均在 1.82 ± 1.25 個月內死亡，並消耗約 165.29± 69.04 克餌劑（n = 11），試驗結果顯示，少量的長效型餌劑能滅除都市地區的家白蟻巢群。根據模擬餌站設置的結果，餌站設置間距越大，每公頃需裝設的餌站數量會逐漸減少。在臺中，以 5 到 8 公尺為間距設置餌站，預估能有效防治家白蟻，且至少每公頃需要裝設 52.76 到個餌站；在新竹，在 5 到 10 公尺的餌站設置間距下，預估能有效防治家白蟻，餌站佈設數量至少為每公頃 45.32 個餌站。本研究提供都市地區的家白蟻巢群分布狀況，並分析餌站設置的成本與防治成效之關係，為未來制定區域性白蟻防治策略提供參考資訊。

關鍵詞（Keywords）：臺灣家白蟻（*Coptotermes formosanus*）、地下型白蟻（Subterranean termites）、微衛星基因（Microsatellite）、地下型餌站（In-ground station）、白蟻防治（Termite control）

壁報展示: 農業昆蟲學

Posters: Agricultural Entomology

PA01

針對小樣本影像發展番茄潛旋蛾成蟲 AI 辨識模型

Development of an AI recognition model for the adults of *Phthorimaea* (*Tuta*) *absoluta* (Lepidoptera: Gelichiidae) based on a small set of images

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背景/研究問題/材料方法

使用 AI 輔助害蟲的監測作業成為當今農界的熱門研究，目前已成功建立數種鱗翅目昆蟲的辨識模型。其中，番茄潛旋蛾(*Phthorimaea* (*Tuta*) *absoluta*)是危害台灣番茄溫室生產的重要害蟲，目前尚缺乏成蟲的辨識模型。然而，田間作業常會存在許多變因影響模型的訓練，包含目標物受損、圖像樣本過少、非目標物太多等。本研究將 21 張費洛蒙誘引黏板進行分塊裁切與影像擴增技術，擴展為 3 千張以上影像作為 YOLOv7 與 CNN 訓練資料。最後再合併預測結果，開發一套番茄潛旋蛾智慧辨識與計數系統有助於監測作業中的加速進行與降低人力成本。

結果/結論/應用啟示

針對室內標準化拍攝提供黏板影像，兩階段識別模型中第一階段與第二階段最高精準度分別為 0.944 與 0.975。所以最終開發的圖形使用者介面(GUI)選用 8 : 1 : 1 比例將影像拆分為訓練集、驗證集及測試集作為第一階段預測組別，且使用者可以自由決定是否啟用第二階段 CNN 模型組合分類。針對田間回收非標準化拍攝黏板影像，啟用 MobileNet-V2 + Efficientnet-B0 組合測試結果為 Accuracy: 82%、Precision: 74%、Recall: 79% 與 F1 Score: 72%。該系統能夠降低 6.6 ± 1.7 %偽陰性率，且平均推論時間在 6 秒內。相對於傳統人工計數會因為黏板上蟲數多寡而花費 3-60 秒不等計算時間，因此，使用本系統可節省大量人工計數時間成本，並提高人員檢查作業效率。

關鍵詞（Keywords）：番茄潛旋蛾（*Phthorimaea* (*Tuta*) *absoluta*）、影像辨識（Image Recognition）、深度學習（Deep Learning）、影像擴增（Image Augmentation）、害蟲監測（Pest Monitoring）

PA02

新竹縣白蘭部落與苗栗縣百壽部落蜂花粉來源植物分析

Analysis of Pollen Sources for Honeybees in R'uyan Tribe of Hsinchu County and Sawi Tribe of Miaoli County

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背景/研究問題/材料方法

為研究原住民部落的養蜂產業發展方向，我們選擇新竹縣五峰鄉白蘭部落 (R) 與苗栗縣獅潭鄉百壽部落 (S) 兩地作為實驗場域，調查可被蜂群利用的植物資源，R 飼養的蜂種為東方蜂 (*Apis cerana*)，而 S 為西方蜂 (*Apis mellifera*)。實驗期間為 2023 年 4 月至 7 月，我們收集兩地飼養蜂群所產出之蜂花粉，進行花粉型態與分子鑑定，嘗試藉此分析部落周遭的粉源植物種類。因植物的型態分類非常複雜且多樣，且需花費大量時間去蒐集鑑定，曠日廢時，希望藉由蜂花粉來了解整年植物相與開花季節變化，國際間使用基因條碼作為鑑定手段已行之有年，其優點為快速，樣本數需求少，無型態變化限制，實驗使用 Psb-trn 與 rbcL，兩種引子對進行 PCR 擴增，用以交叉比對出植物來源。

結果/結論/應用啟示

從實驗結果來看，R 和 S 全部月分都有鬼針草屬植物，而 R 在 8 月結果出現玉米與 S 在 6、9 月出現稻米與人類種植農作季節基本相符。R 在 4 到 10 月最大宗植物分別為：小葉鼠李、車前草、鬼針草屬、大香葉樹、菊花木、漆樹屬、油芒，S 在 5 到 10 月最大宗植物分別為：相思樹、6 到 9 月鬼針草屬、藿香薊。東方蜂在搜集樣本多樣性上比西方蜂來的高，但礙於海拔與東方蜂囊狀幼蟲病毒（*A. cerana* Sacbrood virus，AcSBV 或 CSBV）引起的囊狀幼蟲病(sacbrood disease)的限制，其作為植物相調查的可能性需再多加研究。

關鍵詞（Keywords）：東方蜂（*Apis cerana*）、西方蜂（*Apis mellifera*）、基因條碼（DNA barcoding）、花粉（Pollen）、植物相（flora）

PA03

台灣的水稻葉蟬相現況調查 (半翅目: 葉蟬科)
Investigation on the current situation of rice leafhoppers in Taiwan (Hemiptera: Cicadellidae)

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背景/研究問題/材料方法

葉蟬 (leafhopper) 是危害水稻的重要害蟲，可作為病毒與植物菌質體等傳播載體，引起水稻黃葉病 (rice transitory yellowing)、水稻黃萎病 (rice yellow dwarf)，以及在南亞和東南亞發生的水稻東格魯病 (rice tungro disease)。台灣的水稻田在實施期作制度下，葉蟬已成為次要害蟲，在近二十多年來該等病害未再普遍，故稻田葉蟬昆蟲相甚少被注目。本研究於 2023 – 2024 年在嘉義、高雄、花蓮及台東等長期生態水稻田區定期調查，並不定期於台中以北、以南及中央山脈以東等平地水稻田區，隨機抽樣調查葉蟬，經由形態與分子技術鑑定水稻葉蟬。

結果/結論/應用啟示

調查發現水稻葉蟬的好發期於水稻抽穗後，且二期作較一期作容易發現。共採集 9 種葉蟬，角頂葉蟬亞科 (Deltocephalinae) 短翅葉蟬族 (Chiasmini) 有偽黑尾葉蟬 (*Nephotettix cincticeps*)、黑條黑尾葉蟬 (*N. nigropictus*)、台灣黑尾葉蟬 (*N. virescens*)；角頂葉蟬族 (Deltocephalini) 電光葉蟬 (*Maiestas dorsalis*) 及 *Maiestas* sp.；二叉葉蟬族 (Macrostelini) *Cicadulina bipunctata*；大葉蟬亞科 (Cicadellinae) 大葉蟬族 (Cicadellini) 有白翅褐脈葉蟬 (*Cofana spectra*)、網翅尖頭葉蟬 (*Xyphon reticulatum*)；小葉蟬亞科 (Typhlocybinae) 斑葉蟬族 (*Erythroneurini*) *Empoascanara* sp.。主要危害水稻的電光葉蟬及三種黑尾葉蟬之田間採集，電光葉蟬之採集難易並未有明顯的區域性差別。在北部 7 處，採獲量以偽黑尾葉蟬居多；南部 9 處則以黑條黑尾葉蟬居多；東部 4 處，台東優勢種以偽黑尾葉蟬偏多，而宜蘭、花蓮則以黑條黑尾葉蟬為主。而台灣黑尾葉蟬，目前僅於南部採集到 1 隻。本研究期望由物種種級鑑定，瞭解水稻葉蟬相與生態消長。未來可應用於害蟲精準診斷、病毒寄主與傳播及用藥管理等植物保護與診療之實務與應用研究。

關鍵詞（Keywords）：水稻田（rice paddy）、葉蟬（leafhopper）、長期生態調查（long-term ecological research）

PA04

二種黑殭菌（*Metarhizium anisopliae*)菌株對水稻瘤野螟（*Cnaphalocrocis medinails*)致病力初步測試

Preliminary Testing of the Pathogenicity of Two Strains of *Metarhizium anisopliae* on the Rice Leaf Roller (*Cnaphalocrocis medinails*)

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背景/研究問題/材料方法

瘤野螟（*Cnaphalocrocis medinalis*）為台灣重要水稻害蟲，經常在二期稻作田區造成嚴重危害，其幼蟲取食水稻葉肉組織形成微白細線狀食痕，二齡幼蟲會吐絲將稻葉縱向捲成縱苞，嚴重影響水稻生長及稻穀稔實率。瘤野螟發生期間大約於水稻孕穗期至抽穗期，與褐飛蝨（*Nilaparvata lugens*）好發時間相近。本研究透過可感染褐飛蝨之黑殭菌（*Metarhizium anisopliae*）菌株進行初步的感染試驗，期望達到應用單一菌株能夠同時防治多種害蟲的效果。在試驗中分別以黑殭菌（*M. anisopliae*) CCC 901 及**MA 624 等二種菌株進行室內接種感染試驗，將 1x10^8 conidia/mL 孢子懸浮液接種於瘤野螟 3-5 齡幼蟲，於 7 日後計算其累積死亡率及換算兩種菌株之防治率。

結果/結論/應用啟示

試驗結果顯示，二種黑殭菌 CCC 901 及**MA 624 菌株對於 3-5 齡瘤野螟幼蟲皆有致病效果。在黑殭菌 CCC 901 菌株處理後，幼蟲於第 2 日之累積死亡率即高達 100%，MA 624 處理後，幼蟲於第四日累積死亡率亦可達到 100%。換算防治率，CCC 901 於第 3 日達到 100%，而 MA 624 第 3 日防治率可達 89.0%。顯示本試驗中二種黑殭菌菌株對於瘤野螟幼蟲均具極佳之感染致死效果。

關鍵詞（Keywords）：瘤野螟（*Cnaphalocrocis medinalis*）、蟲生真菌（entomopathogenic fungus）、黑殭菌（*Metarhizium anisopliae*)

PA05

Interplay of Drought and Herbivore-Induced Volatiles in Enhancing Soybean Defense Against Insect Pests

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背景/研究問題/材料方法

Insects utilize volatile organic compounds (VOCs) for essential ecological functions such as aggregation pheromones in beetles and alarm pheromones in ants, play significant roles in insect ecology, facilitating communication, coordinating group behaviors, and enhancing survival strategies within their environments. Plants, similarly, emit VOCs as a direct defense mechanism against insect herbivores, releasing specific compounds that can repel pests or attract natural enemies. Furthermore, these plant-emitted volatiles can act as signaling agents, not only triggering defensive responses within the emitting plant but also priming nearby plants to bolster their defenses. While much is known about plant VOCs in response to herbivore attacks, the effects of abiotic factors, such as drought, on these emissions, and how these stress-induced volatiles influence insect behavior, remain less explored. This study aims to investigate the volatile emissions from soybean seedlings under combined drought and herbivore attacks, with a focus on key pests like *Spodoptera litura*. By using a volatile collection system and GC-MS analysis, we will identify changes in the volatile profiles of soybean seedlings and assess the potential of these volatiles to prime neighboring plants against insect herbivores.

結果/結論/應用啟示

Preliminary tests identified alpha-farnesene and indole as key volatiles triggered by drought and herbivore attacks, respectively, acting as cues in insect-plant and plant-plant interactions. We will further examine whether these stress-induced volatiles can enhance the defensive abilities of neighboring soybean seedlings under both herbivore and drought stress. Since biogenetic volatile has been shown to have many functions, investigating the unclear role of plant volatiles in plant stress responses and stress preventing responses will be crucial, especially in understanding how plant cope with environmental stresses. This will be an important knowledge for plant protection under current climate change conditions.

關鍵詞（Keywords）：　Drought, Volatile-mediated interactions, Priming, *Spodoptera litura*, Soybean

PA06

木虌果植食性瓢蟲基礎生活史與為害

Life cycle and damage of herbivorous ladybird beetle on gac fruit, *Momordica cochinchinensis* (Lour.) Spreng

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背景/研究問題/材料方法

木虌果（*Momordica cochinchinensis* (Lour.) Spreng.）為葫蘆科苦瓜屬植物，花、嫩梢、葉、青果及熟果均可入菜，成熟果實富含類胡蘿蔔素及茄紅素，是臺東地區極具發展潛力的原生作物。2023-2024 年間臺東縣成功鎮栽培之木虌果上發現植食性瓢蟲，以 DNA 序列比對分析；並將樣本寄農試所李奇峰博士鑑定，為瓜裂臀瓢蟲（*Henosepilachna septima* Dieke）。本蟲首次在木虌果上發現，缺乏基本生態資料。本研究以木虌果葉飼育幼蟲至羽化，記錄各齡期時間，建立生活史；同時調查田間為害情形、天敵發生與種類，做為未來擬定管理策略之參考。

結果/結論/應用啟示

本研究以木虌果葉片飼育瓢蟲，自幼蟲至羽化；成蟲交尾後產下黃色卵堆，平均 40.9 顆卵，卵黃色炮彈形，卵期 4.0 日。孵化後幼蟲體色黃色，橢圓形，背面有分枝的棘狀突起；幼蟲 4 個齡期，各齡期發育日數分別為 2.8 日、3.0 日、1.2 日及 5.7 日。老熟幼蟲直接固著於葉片化蛹，呈黃色，尾端包覆於蛻皮殼內，蛹期 4.6 日，約 23.3 日完成 1 個世代。本蟲成蟲與幼蟲聚集以口器刮食葉肉出現短條狀食痕，且多留下一層表皮薄膜，造成被害葉片乾枯變形，影響植株正常生長。被害園區附近之山苦瓜亦有被害現象，調查臺東縣其他鄉鎮之木虌果園及野生山苦瓜暫未發現該蟲為害。另，調查瓜裂臀瓢蟲天敵，採得寄生蜂-釉小蜂（Entedoninae）及粗腿小蜂（*Brachymeria* sp.），並觀察到貓蛛科蜘蛛有捕食成蟲的行為。未來將進一步進行寄主範圍試驗，以評估對葫蘆科作物為害的重要性。

關鍵詞（Keywords）：木虌果（*Momordica cochinchinensis*）、瓜裂臀瓢蟲（*Henosepilachna septima*）、生活史（life cycle）、天敵（natural enemies）

PA07

叩頭蟲 (*Aeoloderma* spp.)在落花生田的發生情況
Occurrence of Click Beetles (*Aeoloderma* spp.) in Peanut Fields

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背景/研究問題/材料方法

叩頭蟲幼蟲為台灣早期造成地下部莢果蟲孔的害蟲之一，前人研究指出叩頭蟲幼蟲(金針蟲)會鑽入落花生果莢內進行取食，造成果莢空洞影響收成，但國內少有關於該類害蟲發生資料。本研究為建立落花生地下部害蟲基礎資料，自 2023 年春作起至台中霧峰區落花生田設置田間設置土壤陷阱 (5 個/區) 誘引叩頭蟲的成、幼蟲，目前每週調查 1 次共蒐集 3 作的發生資料，除此在 2024 春作每週設置有色黏紙各 10 張誘引成蟲，比較黃藍兩色黏紙對叩頭蟲誘引效果的差異。

結果/結論/應用啟示

地下部調查結果顯示無論是春作或秋作均可誘得叩頭蟲，以春作誘集密度較高。成蟲經鑑定種類為 *Aeoloderma brachmana*，該種亦危害甘藷、玉米等作物。以 2024 年春作有色黏紙數據進行資料分析，全期分別在黃色及藍色黏紙誘得 74 隻和 52 隻成蟲，將每週誘引數以獨立樣本進行 t 檢定分析，兩種顏色無顯著差異 ($t=1.63$, $df=258$, $p=0.105>0.05$)。由此可知，該種叩頭蟲在霧峰地區落花生田區域性週年發生，對於以黃或藍色黏紙監測方式無顏色偏好差異，但是否會影響落花生收成則需進一步評估。

關鍵詞（Keywords）：落花生（Peanut）、叩頭蟲（Click beetle）、土壤陷阱（Soil traps）、有色黏紙（Color sticky traps）、金針蟲（Wireworms）

PA08

修剪對無人植保機噴霧效果及防治芒果薊馬之研究探討

Research on the Effects of Pruning on Spray Efficiency and Control of Mango Thrips Using Unmanned Aerial Vehicles (UAVs)

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背景/研究問題/材料方法

芒果（*Mangifera indica* L.）為臺灣重要經濟果樹之一，生育階段中，以新梢抽芽及開花結果期為重要藥劑防治階段。薊馬為嚴重危害害蟲之一，會經由取食新芽及幼葉，造成葉片皺縮變形及褐化萎凋，亦會銼吸幼果造成表皮受傷褐化。本研究透過樹勢調整來探討無人植保機噴霧效果對芒果薊馬防治之影響。以不修剪作為樹冠緊密、有修剪者為樹冠稀疏兩種修剪模式，兩種樹勢修剪模式各 4 棵，修剪後於果樹抽梢期利用無人植保機進行噴霧效果及藥劑防治試驗。於開花期及小果期以多旋翼無人植保機噴灑防治藥劑 11.7%賜諾特水懸劑，每周進行一次防治，兩生育期期間各兩次防治，對照組不進行防治，每株芒果設置四張黃色黏紙，於每次噴藥前及最後一次噴藥後 7 d 調查 1 次，調查黃色黏紙上的薊馬數量，再以 Henderson & Tilton’s 公式計算防治率。另於修剪後第一次噴藥時，將每棵果樹樹冠分為上、中及下 3 層，每一層以靠近無人植保機前進方向一側最左端為採樣起始點，順時針方向將樹冠設置 8 個採樣點，並於樹冠中心同時設置一個採樣點，每層 9 個採樣點，每棵樹共 27 個採樣點，每個採樣點於葉面及葉背固定水試紙，每棵樹共 54 張水試紙，噴藥後回收水試紙以軟體 Image J (National Institutes of Health)分析藥劑噴灑至水試紙上之藥液沉積量及藥液覆蓋率(% area)。

結果/結論/應用啟示

結果顯示藥液沉積量於不同樹冠位置時，修剪對噴霧效果未造成顯著差異。而藥液覆蓋率僅於樹冠上層緊密程度之樹冠顯著少於稀疏程度之樹冠，其他樹冠位置皆無顯著差異。防治試驗結果顯示，開花期進行兩次防治，於防治後一週，樹冠稀疏程度之薊馬數量維持在每張黏紙 50 隻以下，防治率為 50.3%；而樹冠緊密程度之薊馬數量於防治後一週為每張黏紙 85 隻以上，與對照組數量無顯著差異，且防治率為 0%。開花期防治之蟲數以修剪程度與防治與否進行雙因子分析，結果顯示修剪程度不具顯著差異，防治與否具有顯著差異，兩因子間不具交感效應，表示修剪程度對防治的反應是一致的。小果期進行兩次防治之結果，防治後兩週樹冠稀疏之薊馬數量為 50 隻左右，防治率有 72.7%，樹冠緊密之薊馬數量為 85 隻以上，防治率僅 31.7%，小果期防治後一到兩週之蟲數以修剪程度與防治與否進行雙因子分析，結果與花期相同，修剪程度不具顯著差異，防治與否具有顯著差異，兩因子間不具交感效應。經過以上結果顯示，不同的修剪程度對於小黃薊馬族群密度未造成影響，然而修剪程度確實影響無人植保機藥液覆蓋率，進而影響薊馬防治率。未來建議果樹若應用無人植保機進行病蟲害防治，需進行樹勢修剪，提高藥液的附著度，方能提高對小型害蟲的防治效果。

關鍵詞（Keywords）：無人植保機（Unmanned Aerial Vehicle, UAV）、賜諾特（Spinetoram）、薊馬（Thrips）、沉積量（Deposition）、覆蓋率（Coverage）

PA09

危害柑橘類果實椿象飼養技術初探

Preliminary Study on the Rearing Techniques of Citrus Fruit Stink Bugs

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背景/研究問題/材料方法

角肩椿象(*Rhynchocoris humeralis*)為柑橘類果樹害蟲之一。椿象為半翅目，口器為刺吸式，主要吸食植物葉、枝、果實為主，其中尤其偏好未成熟青果，吸食果實後會使果實表面坍塌及轉色異常，造成外觀和口感不佳及出現提早落果現象，導致作物失去經濟價值，在金柑青果上危害情況最為明顯。為利角肩椿象相關防治試驗的進行，本研究目的是建立椿象人工飼養流程來維持試驗蟲源，並減少野外蟲源對試驗結果帶來的不確定性。建立飼養流程前需從野外採集野生蟲源(F0)並定期提供枝條及鮮果，目前已飼養到 F1 成蟲階段。

結果/結論/應用啟示

角肩椿象生活史為卵、若蟲(共五齡)及成蟲階段，在試驗初期，野外採集椿象(F0)會交尾並產卵，但其孵化(F1)之子代僅有低於 2%的個體能成長至三齡，因此對飼養方式進行優化；例如減少環境擾動、成若蟲分籠、增加食物選擇、改變飼養空間及環境，經過約 3 個月的調整，F1 約有 30%可成功蛻皮為成蟲。因此椿象飼養並非單純提供食物源即可，尚需適當環境調整才能提高羽化率。野外蟲源取得可能受作物生長時間、昆蟲生長情況影響，容易因數量不足影響試驗進行，因此掌控足夠適合齡期及健康的蟲源是相當重要的，期望未來能透過人工飼養方式建立足夠的椿象族群，進而開發出有效的防治方法或資材。

關鍵詞（Keywords）：角肩椿象（*Rhynchocoris humeralis*）、柑橘類果樹（citrus fruit trees）、飼養技術（rearing techniques）

PA10

織羅部落捕食水稻田飛蝨類及葉蟬類之四種瓢蟲發生調查

The investigation of the occurrence of four species of lady beetles that prey on planthoppers and leafhoppers in rice fields of the Ceroh Tribe

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背景/研究問題/材料方法

往昔研究顯示，部分瓢蟲種類是水稻田重要害蟲天敵，實驗室內的研究結果顯示發現六條瓢蟲 (*Cheilomenes sexmaculata* Fabricius)、波紋瓢蟲（*Coccinella transversalis* Fabricius）、八條瓢蟲 (*Harmonia octomaculata* Fabricius)及橙瓢蟲（*Micraspis discolor* Fabricius）等四種瓢蟲之成蟲及三齡幼蟲皆有取食褐飛蝨（*Nilaparvata lugens* Stal)、白背飛蝨（*Sogatella furcifera* Hovarth)及綠葉蟬 (*Nephotettix* spp.）等重要水稻害蟲之行為。織羅部落位於花蓮縣玉里鎮春日里，水稻是部落主要種植農作物之一，花蓮縣有機耕作面積全國第一，有機耕作不能使用化學合成農藥，生物天敵具有調節田區害蟲族群功能，為利於織羅部落有機耕作水稻田害蟲之防除，明瞭水稻田害蟲生物天敵資源，是不可或缺之工作。因此，於 2021 年至 2023 年間，每 2 個月以黃色黏蟲紙搭配掃網法，分別調查織羅部落 5 處有機農耕水稻田區及 5 處慣行農耕水稻田區瓢蟲發生之種類及豐度，為後續利用將瓢蟲納入有機水稻田害蟲防治管理系統建立基礎。

結果/結論/應用啟示

織羅部落有機水稻田中橙瓢蟲是數量最多的瓢蟲，平均每次每塊水稻田可調查到 19.3 隻、其次是六條瓢蟲的 1.4 隻、八條瓢蟲 0.2 隻及波紋瓢蟲 0.01 隻。橙瓢蟲於每次調查均可發現，但橙瓢蟲主要發生於 7、9 及 11 月份，若能加強水稻田生態營造於 1 月、3 月及 5 月間維持田區有開花植物及禾本科雜草存在，有助於提升橙瓢蟲發生數量.，提高對 1 期作水稻田飛蝨類及葉蟬類害蟲族群調節。

關鍵詞（Keywords）：瓢蟲（lady beetle）、織羅部落（Ceroh Tribe）、水稻田（rice field）、飛蝨（planthoppers）、葉蟬（leafhoppers）

PA11

東方蜂微粒子感染精選熊蜂與其微族群食量消耗表現
Infection of *Vairimorpha* (*Nosema*) *ceranae* on *Bombus eximius* and food consumption in the microcolonies

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背景/研究問題/材料方法

東方蜂微粒子（*Vairimorpha* (*Nosema*) *ceranae*) 為一種廣泛存在於西洋蜂（*Apis mellifera*) 的真菌性病原，導致蜜蜂產生下痢等症狀，而影響蜂群健康。商業化精選熊蜂（*Bombus eximius*) 的人工飼養需大量使用西洋蜂所收集之新鮮花粉做為其食料，因此瞭解熊蜂食料是否受到交叉感染，對其生產便成為重要關鍵。本研究使用西洋蜂蜂群分離東方蜂微粒子，於實驗室利用蜜蜂活體繼代培養。以人工餵食法，接種低、中、高 (5×10^4、10^5 及 10^6 (spore/10μl)) 東方蜂微粒子濃度感染精選熊蜂，後續以分子方法檢出確定感染情況。此外，誘導熊蜂工蜂組成微族群群 (microcolonies) (n = 8) 以 1.25×10^5 (spore/g) 微粒子濃度之花粉處理組，進行餵食並觀察蜂群食料消耗。

結果/結論/應用啟示

人工餵食東方蜂微粒子處理下，對於精選熊蜂成蜂存活與對照組並無顯著影響。低、中、高之劑量皆呈現低感染率 (10%, n = 10)；不同日齡與花粉之處理之檢出率僅 8.3% (n = 54)。在微族群試驗中，含 1.25×10^5 (spore/g) 微粒子之花粉處理組別，在第 1 – 7 天花粉消耗量較對照組上升 30.5%，而幼雛 (卵及幼蟲) 數顯著則下降 47.5%，顯示東方蜂微粒子感染增加蜂群的能量消耗。綜上所述，東方蜂微粒子對於精選熊蜂有低感染率，然而感染東方蜂微粒子仍會影響蜂群表現，是否存在其他負面影響值得後續研究。

關鍵詞（Keywords）：熊蜂（bumble bee）、微粒子病（Nosema disease）、微族群（microcoloines）

PA12

農業害蟲防治中的 RNAi 技術：創新應用與法規框架

RNAi Technology in Agricultural Pest Control: Innovative Application and Regulatory Framework

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背景/研究問題/材料方法

許多半翅目昆蟲利用刺吸式口器吸取植物汁液，導致植物枯萎。儘管化學農藥能有效控制，但可能導致抗藥性及環境風險性增加。RNA 干擾技術 (RNAi) 已成為防治農業害蟲的一種潛在策略。美國已成功使用 RNAi 製成的生物農藥 Ledprona 來防治科羅拉多馬鈴薯甲蟲，並獲得美國國家環境保護局核准。因此，本研究旨在利用 RNAi 技術誘導基因沉默防治半翅目害蟲，並進行 dsRNA 與奈米載體合成後的效果評估。同時，我們也蒐集國外相關研究文獻以及 RNAi 藥劑的申請流程與風險評估方法，以利後續建立脫靶效應風險檢測平台。

結果/結論/應用啟示

本研究選定 *ecdysone receptor* (*EcR*) 和 *ultraspiracle* (*usp*) 作為 RNAi 的標靶基因，合成之 dsRNA 與奈米顆粒結合應用於植株害蟲防治上，進行後續的防治評估。在比較國內外生物農藥法規時，我們發現台灣的過程相對快速，而美國則強調科學性、透明度和公眾參與。台灣風險評估包括文獻回顧、實驗數據分析及專家評估，過程相對較短，透明度和公眾參與較低。而美國風險評估則包括多階段審查、公開意見徵集及多次科學評估，可能需要數年完成，並定期監測已核准農藥。這種嚴謹的審查程序有助於提高農藥使用的安全性和公眾信任。

關鍵詞（Keywords）：RNA 干擾技術（RNAi）、生物農藥（Biopesticide）、奈米顆粒（Nanoparticle）

PA13

昆蟲接種技術之接種器設計
The Design of Dispenser for Entomovector Technology

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背景/研究問題/材料方法

過去研究顯示，授粉昆蟲如蜜蜂除了能傳遞花粉外，還可能散佈病原菌。研究人員便開始探討授粉昆蟲是否可用來傳播有益微生物，以達生物防治的目的。為實現此目標，需挑選適當的載體昆蟲、合適的微生物製劑，以及能使載體昆蟲有效黏附微生物的接種器。本研究聚焦於接種器的開發，並參考現有文獻中記載的數種蜜蜂接種器設計，以 3 種較符合實際需求的設計進行在地化調整。本實驗使用 3D 繪圖軟體 Tinkercad 設計接種器，並以聚乳酸（Polylactic Acid, PLA）作為列印材質，透過 3D 列印機 Ping 300+進行製作，並將接種器安裝於蜂巢出入口紀錄蜂群使用情形。另為確認蜜蜂是否可將接種器內粉末攜出接種盒，以染色石松子花粉放置於出口處進行測試，觀察蜜蜂是否可將染色花粉攜出接種盒。

結果/結論/應用啟示

實驗結果顯示，有 2 種接種器在放置後 24 小時內，蜜蜂進出蜂箱的數量緩步上升，在 48 小時後進出數趨於穩定不再增加，且蜜蜂正確使用接種器的比率達到 90%以上。此外蜜蜂進出接種器時能攜帶染色石松子花粉，顯示這 2 種接種器在傳遞微生物製劑方面具有應用潛力，惟接種器需在使用前 2 天安裝以穩定蜜蜂活動。未來可進一步測試蜜蜂在田間環境中散佈粉狀生物製劑的效果，並評估其實際應用價值。

關鍵詞（Keywords）：昆蟲接種技術（Entomovector Technology）、接種器（Dispenser）、授粉昆蟲（pollinating insects）、蜜蜂（honeybee）、植物保護（crop protection）

PA14

鳳梨果園內之紋翅蛾科成蟲生態調查

Ecological investigation of adult Cosmopterigidae insects in pineapple orchards

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背景/研究問題/材料方法

鳳梨 (*Ananas comosus*) 為臺灣重要熱帶果樹且深具外銷潛力，臺灣輸日鳳梨邊境檢疫於2022年由日方檢疫出紋翅蛾科 (Cosmopterigidae) 昆蟲，被檢疫出此昆蟲之鳳梨需進行燻蒸處理，除增加農民成本外，亦影響果實品質及儲架壽命。於2023年之田間調查結果發現，鳳梨果園中之紋翅蛾科昆蟲有2種，經分生鑑定，分別為 *Anatrachyntis rileyi* 及 *Labdia* sp.。*A. rileyi* 之幼蟲喜藏於鳳梨果目內取食萎凋之花器，蛹可在果目內或果實基部之果皮發現。2024年為探討紋翅蛾科昆蟲於田間發生之種類與族群分布概況，於屏東縣枋寮鄉及長治鄉兩地區之鳳梨園，自鳳梨開花初期至果實採收期，每2週採集鳳梨果實攜回實驗室內觀察，待成蟲開始羽化後，收集成蟲並進行形態鑑定。期能藉由族群調查探討紋翅蛾科昆蟲於鳳梨園之好發時期與幼蟲發育時間之生態資訊，進而建立最佳防治管理策略。

結果/結論/應用啟示

本研究調查之紋翅蛾科昆蟲種類，僅於枋寮鄉調查到 1 隻 *Labdia* sp.，其餘皆為 *A. rileyi*，然而，是否有其他相似種仍需再鑑定。於成蟲羽化數方面，枋寮鄉及長治鄉每顆鳳梨平均分別為 27.15 及 51.90 隻。各時期採樣之果實羽化為成蟲之高峰期，枋寮鄉為開花末期至謝花期，長治鄉則為果實發育初期。採樣後至成蟲羽化而出所需時間，分別為 2~92 天及 9~78 天，變化幅度甚大。調查結果顯示，於鳳梨開花末期至果實發育初期採集之果實，其成蟲羽化數量相對較高，故推測此時期應為紋翅蛾昆蟲於田間之重點防治階段。

關鍵詞（Keywords）：鳳梨（*Ananas comosus*）、紋翅蛾科（Cosmopterigidae）、檢疫害蟲（Quarantine pest）

PA15

Can we trust host plant records in literature? Re-evaluation of the reliability of oviposition selection assays for *Phthorimaea absoluta*

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背景/研究問題/材料方法

Phthorimaea absoluta (South American tomato pinworm, SATP) poses a significant threat to agriculture due to its substantial impact on global tomato production. Understanding the oviposition preferences of female SATP is critical for developing effective pest control measures. Laboratory experiments designed to simulate natural conditions are commonly employed to study these preferences; however, the extent to which these experiments accurately reflect natural behaviors remains uncertain. This study provides a thorough evaluation of the consistency of oviposition preferences across various experimental conditions by reviewing literature from the past 10 years (2014-2024). We systematically gathered and analyzed data from numerous studies, examining key experimental variables such as temperature, photoperiod, relative humidity, methodology, cage dimensions, number of host plants, substrate type, number of adult pairs, and caging duration. Our objective was to determine whether oviposition preferences remain stable or show variability under different experimental conditions and to evaluate the degree to which these laboratory conditions replicate natural oviposition behaviors.

結果/結論/應用啟示

Our analysis uncovered notable inconsistencies in both the design and results of oviposition preference assays. These discrepancies indicate that current laboratory setups frequently may not accurately replicate natural environments, leading to over-interpretations in the observed behaviors. This study highlights the necessity for improved experimental designs to enhance the ecological relevance of laboratory studies. We advocate for standardizing experimental conditions to reduce variability and better simulate field conditions, thereby achieving more reliable results.

關鍵詞（Keywords）： Experiment design, Oviposition preferences, Polyphagous insects, *Phthorimaea absoluta*, Host plants

PA16

油劑類資材與蟲生真菌對水稻禾蛛緣椿象防治效果評估
Evaluation of control effectiveness of the oil reagents and entomopathogenic fungi against rice paddy bug (*Leptocorisa acuta* (Thunberg))

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背景/研究問題/材料方法

禾蛛緣椿象（*Leptocorisa acuta*）係近年危害臺東縣關山地區第 1、2 期稻作抽穗期穀粒之害蟲，於孕穗期至開花期間，該區鄰近山邊或雜木林之田區，陸續發現其成蟲及若蟲刺吸乳熟期至糊熟期的稻穀，導致穀粒發生黑斑，產生斑點米，碾米時受害穀粒常斷碎，影響米質。為開發防治水稻禾蛛緣椿之有機資材，本試驗自感病蟲體與稻田土壤中，分別分離培養出白殭菌及黑殭菌後，再將菌株以孢子懸浮液濃度為 10^8 conidia/ml 接種於禾蛛緣椿象成蟲，進行室內致病力測試，計算接種 7 日後的平均死亡率。進一步以高致病力的菌株進行不同濃度的致死試驗，計算接種 7 日後禾蛛緣椿象成蟲及若蟲之平均感染率，評估其防治應用的潛力。此外，亦於室內比較 4.5%印楝素乳劑 1,000 倍、99%窄域油乳劑 200 倍及 95%印度苦楝油乳劑 200 倍等 3 種油劑類資材，對於禾蛛緣椿象成蟲致死效果。

結果/結論/應用啟示

結果顯示在 4 個分離菌株的初步篩選後，以白殭菌（*Beauveria bassiana* BB1031）與黑殭菌（*Metarhizium anisopliae* MA1012）等 2 種菌株對禾蛛緣椿象之校正死亡率較高，分別達 100%及 80%以上；後續選用致病力最高之 BB1031 進行不同濃度的致死試驗中，3 種濃度 10^6、10^7 與 10^8 conidia/ml 施用 7 天後，顯示感染成蟲後之平均死亡率分別為 80、90 及 90%以上；而感染若蟲後之平均死亡率分別為 60、70 及 80%以上。此外，油劑類資材室內藥效測試結果，3 種油劑施用 7 日後致死率均未達 50%以上。相較之下，此次篩選之蟲生真菌具備較高之感染致死效果，顯示其對防治禾蛛緣椿象具發展潛能。

關鍵字（Keywords）：禾蛛緣椿象（*Leptocorisa acuta*）、油劑類資材（oil reagents）、蟲生真菌(entomopathogenic fungi)、白殭菌（*Beauveria bassiana*）、黑殭菌（*Metarhizium anisopliae*）

壁報展示: 生物多樣性、族群與群聚生態學

Posters: Biodiversity, Population and Community Ecology

PB01

台灣白蟻的分飛季節

Dispersal flight seasons of termites in Taiwan

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背景/研究問題/材料方法

白蟻是多年生的真社會性昆蟲，分飛是白蟻擴散的主要方式，當巢群成熟後，會產生有翅生殖蟻，並等待適宜的氣候條件下飛出蟻巢，飛行落地後，雌雄蟲藉由費洛蒙溝通配對，再一起尋覓築巢地點，隨後交配與產卵。目前對於台灣 23 種白蟻分飛行為的資訊仍相當有限。本研究的目的是調查台灣白蟻物種的分飛季節性，利用國立自然科學博物館和國立中興大學於 1988 至 2023 年間採集的有翅生殖蟻樣本，根據各物種採集時間進行分飛季節性的分析，並將各物種白蟻的分飛事件分布擬合入高斯模型，以評估分飛高峰及集中程度。

結果/結論/應用啟示

總共收集到 21 種白蟻，2551 筆分飛紀錄，其中 7 個物種樣本數少於 10 筆。大部分的物種分飛高峰位於四至六月，而散白蟻屬(*Reticulitermes*)的分飛高峰發生在一月中旬，白足樹白蟻(*Glyptotermes albofemoralis*)的分飛高峰發生在十月下旬。霧社華歪白蟻(*Sinocapritermes mushae*)的分飛分布不符合高斯模型，呈現兩個高峰，分別位於一月中旬及六月下旬。未來可進一步探討不同氣候因子對各種白蟻分飛行為的影響，建構更完整的白蟻分飛物候學。

關鍵詞（Keywords）：白蟻（termite）、分飛（dispersal flight）、季節性分布（seasonal distribution）

PB02

以共域與非共域攀蜥之捕食行為探討球背象鼻蟲與擬硬象天牛之擬態關係

Exploring the mimetic relationship between *Pachyrhynchus* and *Doliops* species by testing the preying behavior of sympatric and allopatric agamid lizards

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背景/研究問題/材料方法

在自然界中，昆蟲發展出許多防禦策略以避免遭受捕食者攻擊，如用鮮艷的警戒訊號警告掠食者；而模仿其他物種的警戒色以嚇阻天敵的行為則被稱作擬態。堅硬的球背象鼻蟲(*Pachyrhynchus* spp.)已被證實運用其翅鞘上的花紋作為警戒色禦敵，與球背象鼻蟲共域的擬硬象天牛(*Doliops* spp.)則演化出與象鼻蟲相似的斑紋，而被認為是球背象鼻蟲的貝氏擬態者；同時，共域的球背象鼻蟲也會因相似的翅鞘花紋使彼此受到保護，亦被認為擁有穆氏擬態關係。為釐清球背象鼻蟲種間、以及球背象鼻蟲和擬硬象天牛間的擬態關係，本研究的第一部分檢驗斷紋球背象鼻蟲(*P. nobilis yamianus*)與擬硬象天牛(*D. similis*)翅鞘上花紋對共域的捕食者–斯文豪氏攀蜥(*Diploderma swinhonis*)而言是否確實具有警戒功能。第二部分則測試非共域攀蜥在捕食斷紋球背象鼻蟲後的經驗後，再看到斷紋球背象鼻蟲、條紋球背象鼻蟲(*P. sonani*)與擬硬象天牛時的攻擊反應，以確認捕食者能否辨認此三種具有潛在擬態關係之獵物。

結果/結論/應用啟示

研究結果指出，在共域蜥蜴的試驗中，有較高比例(37.04%)的攀蜥會攻擊天牛；而觀察斷紋球背象鼻蟲的組別中則僅有少數比例(9.30%)攻擊象鼻蟲。非共域蜥蜴的測試中，經捕食斷紋球背象鼻蟲訓練後的攀蜥攻擊天牛之比例(39.44%)仍高於攻擊象鼻蟲之比例(30.56%)。研究結果顯示，對於斯文豪氏攀蜥而言，擬硬象天牛與球背象鼻蟲的擬態效果較球背象鼻蟲種間的擬態效果更差，未來將持續增加樣本數，以確認三種共域甲蟲的擬態關係。

關鍵詞（Keywords）：球背象鼻蟲（*Pachyrhynchus*）、擬硬象天牛（*Doliops*）、警戒色（aposematic color）、擬態關係（mimetic relationship）

PB03

微觀視角檢測捕食者與食餌攝入之塑膠微粒
Detection of microplastic ingestion by predator and prey from a micro-perspective

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背景/研究問題/材料方法

塑膠微粒(< 5 mm)具有多種化學成分(PE、PP、Rayon…)及外觀(纖維、碎塊、薄膜、圓珠…)，現今在生物體內的研究以顯微鏡目視法檢測為主並以光譜儀分析為輔。顯微鏡目視法判斷 1000µm 以下的塑膠有困難，利用 µFTIR 最小能檢測到 20µm。本研究利用 µFTIR 搭配陣列式相機加快掃描速度，檢測微米級塑膠微粒並獲得化學成分資訊。

結果/結論/應用啟示

捕食者 *Rhyacophila nigrocephala* (Trichoptera: Rhyacophilidae)及食餌 *Chironomidae* sp. (Diptera: Chironomidae)檢測到的塑膠微粒類型由多至少依序排列為聚乙烯(PE)、聚脂纖維(Polyester)及縲縈(Rayon)，且碎塊比例高於纖維，塑膠微粒大小多集中於 50-100µm。以塑膠微粒豐度(塑膠微粒/個體)來看，捕食者體內塑膠微粒多於食餌(3: 0.714)；塑膠微粒濃度(塑膠微粒/乾重)則相反(9.868: 368.421)。由於食餌的體型遠小於捕食者，換算濃度時數據放大，因此在研究生物體內的塑膠微粒時需要同時參考豐度及濃度，避免誤判。未來以目視法為主的試驗應同時使用 µFTIR 檢測，精準判斷是否具有生物放大或累積效應。

關鍵詞（Keywords）：水棲昆蟲（Aquatic insect）、塑膠微粒（Microplastics）、微觀視角（Micro-perspective）

PB04

苗栗南庄露露蛾相分析

Analysis of the moth fauna of Lulu camping site, Nanchuang, Miaoli

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背景/研究問題/材料方法

截至 2024 年 8 月 31 日止，已知分布於臺灣的鱗翅目昆蟲種類高達 83 科 2180 屬 5232 種，其中有 78 科 2052 屬 4795 種在傳統上被視為蛾類，也就是說已知蛾類種數佔臺灣鱗翅目物種高達 91.6%，然而在台灣的生物資源與物種調查上，蛾類被調查的強度遠遠不如蝶類，這使得我們對大多數地區蛾類相的了解局限於少數的科或中大型物種。物種調查的強度與鑑定的精確性也會影響我們對該地區自然資源品質的評估，進而影響保育措施或開發利用的方向。苗栗南庄為苗栗縣第二大鄉鎮，海拔範圍從 120 至 2,200 公尺，由於自荷治時期以後樟腦業為南庄最重要之產業，因此低海拔森林在過去曾受樟腦業與造林之干擾，目前為次生林狀態。涉及南庄地區的物種調查甚少，過去僅有向天湖濕地調查報告提及有 5 科 12 種蛾類。為瞭解南庄地區的蛾類資源，第一作者自 2018 年 2 月起以夜間燈光誘集與白天目視採集的方式調查位於蓬萊溪流域的南庄露露營地之蛾類。所有物種之紀錄與位點紀錄皆在拍照後上傳至飛蛾資訊分享站(twmoth.tbri.gov.tw)，並依據文獻與專家討論鑑定至種或形態種。

結果/結論/應用啟示

根據共計 5 年 55 個月 182 次的調查結果顯示，南庄露露營地已被記載之蛾類共計有 57 科 752 屬 933 種。就已知物種總數來說，佔台灣已知科的 73%、已知屬的 37%，以及已知種的 19%。大異角類(Macroheterocera)中以裳蛾科、尺蛾科、草螟科所佔比重最高。就幼蟲寄主來說，取食維管束植物、苔蘚、地衣、藻類、真菌以及腐植質之類群皆有相當豐富之多樣性，足可反映南庄潮濕溫暖的森林特性。本研究也顯示高強度的公民科學普查可以大幅增進我們對物種多樣性之了解，彌補公部門執行計畫成果之不足。

關鍵詞（Keywords）：鱗翅目（Lepidoptera）、物種多樣性（Species diversity）、蛾相調查（Moth fauna survey）、植食性昆蟲（Herbivorous insects）、公民科學（Citizen science）

PB05

113 年雪霸國家公園臺灣寬尾鳳蝶棲地調查計畫
2024 Investigation on the Habitat of Taiwan Broad-tailed Swallowtail Butterfly in Shei-Pa National Park

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背景/研究問題/材料方法

臺灣寬尾鳳蝶 (*Papilio maraho*) 過去承受採集販賣等壓力，依據農業部公告為瀕臨絕種保育動物。其幼蟲唯一寄主臺灣檫樹 (*Sassafras randaiense*) 亦為稀有植物，因此臺灣寬尾鳳蝶的生存與臺灣檫樹的族群生存息息相關。雪霸國家公園境內為臺灣寬尾鳳蝶重要的活動區域，轄區內有「觀霧寬尾鳳蝶野生動物重要棲息環境」是國內唯一以昆蟲為保育對象所設立保護區，同時亦為「臺灣檫樹生態保護區」。然而經過多次的臺灣檫樹及臺灣寬尾鳳蝶之調查及評估，認為目前雪霸國家公園轄區內的臺灣檫樹生長處於弱勢，且臺灣檫樹族群有呈現萎縮趨勢。為了解當前臺灣檫樹生長情況及分布，進行無人航空載具 (UAV) 對臺灣檫樹的分布進行影像拍攝與辨識、野外實地進行臺灣檫樹與臺灣寬尾鳳蝶生態調查、對觀霧及武陵地區適合種植臺灣檫樹的地點進行評估、亦進行臺灣檫樹種子採集與處理，作為後續人工栽植苗木準備工作。

結果/結論/應用啟示

截至今年 7 月，雖然尚未發現轄區內寬尾鳳蝶的踪影，但對於觀霧及武陵地區臺灣檫樹及合適造林地點進行評估，期望擴大臺灣寬尾鳳蝶可利用棲地，以利保育行動計畫的執行。冀望透過具體的調查與保育規劃，確保轄區內的臺灣檫樹與臺灣寬尾鳳蝶在自然棲息地中的永續生存。

關鍵詞（Keywords）：臺灣寬尾鳳蝶（*Papilio maraho*）、瀕臨絕種野生動物（endangered species）、臺灣檫樹（*Sassafras randaiense*）、觀霧寬尾鳳蝶野生動物重要棲息環境（Guanwu Broad-tailed Swallowtail Major Habitat）、臺灣檫樹生態保護區（*Sassafras randaiense* ecological protected area）

PB06

Asymmetric introgression and intraspecific variation in the cryptic invasive ant *Dolichoderus thoracicus* in Taiwan

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背景/研究問題/材料方法

Elucidating the factors underlying the proliferation of invasive pests is crucial for developing effective management and containment strategies. The role of intraspecific variation in contributing to pest invasiveness and ecological disruption is often overlooked, despite its potential to influence diverse ecological outcomes significantly. In this study, we focus on the black cocoa ant (*Dolichoderus thoracicus*) in Taiwan, where a cryptic invasive population has recently been identified. To address this knowledge gap, we utilized 22 microsatellite markers and distribution records to assess gene flow between native and invasive populations, comparing key characteristics of the two populations, including reproductive modes, breeding structure, and suitable niche.

結果/結論/應用啟示

Both the native and invasive populations primarily exhibit sexual reproduction, possess polygynous colonies, and have queens that engage in multiple mating. However, the native populations exhibit higher intracolonial worker relatedness and queen relatedness compared to the invasive populations. Genetic structure analysis revealed two distinct clusters corresponding to the native and invasive populations, with evidence of asymmetric introgression from the invasive population into the native one. Although the suitable niches of both populations appear similar, the invasive population demonstrates greater variation in its niche variation. This introgression, coupled with differences in breeding structure and niche variation, suggests that intraspecific invasion could threaten the genetic integrity of the native population and disrupt its ecological stability.

關鍵詞（Keywords）： Black cocoa ant, Breeding system, Genetic introgression, Niche modeling

PB07

Temporal transition of pollination networks driven by flowering phenology and bees' diet decision

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背景/研究問題/材料方法

Pollination underpins the reproductive success of numerous flowering plants and thus fosters biodiversity and ecosystem services crucial for human well-being. Therefore, understanding pollination ecology and the dynamics of pollination networks in nature is vital in elucidating the functioning and stability of ecosystems. Our study delves into the intricate temporal transitions within these pollination networks, focusing on the dynamic interplay between flowering phenology and bees' dietary preferences. Our study was conducted in Fushan Botanical Garden, Taiwan, encompassing 5 months in 2022. We specifically focused on a subset of the plant-pollinator community: Melastomataceae plants (4 species) and their pollinating bees (14 species or species complexes). We empirically recorded pollinating interactions in the sampling spots we set across the study area, thereby reconstructing the pollination networks (formed by our target species) therein over time. We employed simulated resampling based on empirical data to generate period-specific networks with a standardized sampling effort. We then conducted the principal component analysis and calculated functional distances among plants according to their visiting bee composition.

結果/結論/應用啟示

We discovered that not all bees passively feed on whatever flowers in the environment; instead, some preferred certain plants over others when multiple plants were co-blooming in the study area. Mapping with phenological data of the flowering Melastomataceae plants, we derived the temporal transition in the structure of pollination networks, which was driven collectively by flowering phenology and the bees' foraging preference. While the availability of food flowers has been considered a main driver of pollination network formation and their temporal dynamics, our findings highlight the complex nature of interactions within pollination networks, where the behaviors of the pollinators also play key roles. This study offers insights into the adaptive strategies employed by both plants and pollinators in response to ongoing environmental changes.

關鍵詞（Keywords）： 授粉網絡（Pollination network）、野牡丹科（Melastomataceae）、花蜂（Anthophila）、福山研究中心（Fushan Research Center）、物候學（Phenology）

PB08

復野溪流底棲大型無脊椎動物群集結構與生物多樣性之時間變化
Temporal variation of benthic macroinvertebrates community structure and biodiversity from rewilded river

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背景/研究問題/材料方法

2023 年，位南投國姓鄉的種瓜溪啟動了溪流復野計畫。透過拆除幾處「地坎」（低水平混凝土屏障）以及改造兩道堰，並著手復育植被，使溪流本身變得適合水生動物，溪流本身得到了解放。自然流動的溪流正在重建河床，形成不同結構的沙洲、水池和湍賴、淺灘，創造出多樣化的棲息地。這些水床在溪流水文系統中發揮關鍵作用並提供有價值的生態功能，尤其是對大型無脊椎動物和魚蝦類的生命週期和生物多樣性。儘管這是臺灣史上極其重要且難得的溪流復育示範工程，但對該溪仍缺乏詳細的水生生物學研究。本研究選定底棲大型無脊椎動物為監測復野行動效果的「工具」，2024 年每個月以定面積的舒伯氏水網在種瓜溪三樣點各採三網樣本，瞭解水棲昆蟲群集結構組成與生物多樣性並探討時間變化。

結果/結論/應用啟示

研究期間共採集了來自 9 目 46 科 65 分類群 11,317 隻的個體，水泥牆拆區後端的物種組成及生物多樣性（樣站 1 及樣站 2)較樣站 3(左右岸水泥高牆)為高，表明溪流恢復具成效，但在 2024 年 7 月工程影響及下旬受凱米颱風與西南氣流影響，降雨時間較多且長，惟河川採樣不受影響，物種組成及生物多樣性顯著下降。溪流復野後的水生昆蟲監測為復野評估提供有效的資訊，可更好地了解溪流復野狀況。透過水生昆蟲監測為溪流復野後維持生物多樣性提供支持，加上濱岸植物群集和生態系功能的能力，整體瞭解復野溪流的生態完整性。

關鍵詞(Key words)：溪流復野 (Rewilded river)、種瓜溪 (Zhong Gua Xi)、底棲大型無脊椎動物 (Benthic Macroinvertebrates)、生物多樣性 (Biodiversity)

PB09

塑膠微粒與底棲大型無脊椎動物的生物多樣性：以台灣中部大甲溪為例

Microplastics and biodiversity of benthic macroinvertebrates: A case study in the Dajia River in central Taiwan

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背景/研究問題/材料方法

塑膠微粒(< 5 mm)由於其微小且不可生物降解的特性，各種環境中無處不在，並被生物取食，對生態系或甚至人類的潛在危害風險引起全球關注。大多數研究都是聚焦在以海洋環境為主的研究，直到最近淡水生態系統研究才引起大家關注。調查台灣中部重要流域中水棲昆蟲幼蟲體內的塑膠微粒污染情況，評估塑膠微粒對淡水溪流生態系統之潛在衝擊。大甲溪流域下游設置 3 個測站，以定面積的舒伯氏水網採樣調查 3 次。

結果/結論/應用啟示

總體而言，收集 7 目 32 科 46 分類群 3765 隻水蟲，萃取到 56 個塑膠微纖維。各測站水質特性(包括水溫、pH、溶氧量、導電度、鹽度、濁度)在季節上皆呈差異，其中溶氧量及水溫最為明顯。Two-way ANOVA(採樣時間、測站)分析四種群聚指數(Family richness index、Simpson’s index、Shannon-Wiener’s index 及 Pielou’s evenness index)，採樣時間及測站間無交互作用，科級豐富度受時間及測站顯著影響、Shannon 受時間影響、均勻度及 Simpson 在時間及測站間都沒有顯著差異。塑膠微粒豐度(particles/individuals)及濃度(particles/mg dw) three- way ANOVA(採樣時間、測站及昆蟲目級)顯示時間對豐度($P = 0.0111$)及濃度($P=0.0228$)皆有顯著性差異，但測站及各目昆蟲皆無差異且彼此之間無交互作用。此外，微塑膠存在的形式有碎片、薄膜、纖維和泡沫且環境塑膠微粒的化學成分多種多樣，檢測到最豐富的微塑膠類型是聚乙烯(PE)。提議基於當前的科學知識，並通過為重要河流系統中的塑膠微粒污染狀況提供可用資訊，為塑膠微粒控制政策奠定基礎。

關鍵字（Keywords）：塑膠微粒（Microplastics）、底棲大型無脊椎動物 (Benthic Macroinvertebrates)、生物多樣性 (Biodiversity)

PB10

雪霸國家公園溪流中微塑膠的垂直通量和底棲大型無脊椎動物的生物多樣性

Vertical flux of microplastics and biodiversity of benthic macroinvertebrate from streams in the Shei-Pa National Park

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背景/研究問題/材料方法

塑膠微粒（Microplastics, MPs）是無所不在普遍存在的污染物，在水生環境中也日益受到關注，除了破壞水質也危害水生生物並藉由生物體進入食物網，對全球健康影響重大。本研究在國寶魚台灣櫻花鉤吻鮭(*Oncorhynchus masou formosanus*)棲息地之三條溪流以泊集網於溪流左、中、右岸設置一天，於 2023/6/28、2023/10/2、2024/1/17 三次採集評估溪流動態下水棲昆蟲組成、生物多樣性與塑膠微粒垂直通量。

結果/結論/應用啟示

研究期間共採獲 6 目 29 科 44 分類群 6039 隻水蟲，萃取到 27 個塑膠微纖維，two- way ANOVA(採樣時間、測站)分析四種群聚指數(Family richness index、Simpson’s index、Shannon-Wiener’s index 及 Pielou’s evenness index)，顯示沒有交互作用，Simpson 指數在時間及測站間沒有顯著差異，其他三種指數皆受測站影響，多樣性以高山溪測站最高、有勝溪測站最低。塑膠微粒豐度(particles/individuals)及濃度(particles/mg dw) 以 three- way ANOVA(採樣時間、測站及昆蟲目級)分析，顯示彼此間無差異且無交互作用，以捕食者與非捕食者進行 *t* 檢定無顯著差異，暗示塑膠微粒目前沒有生物放大與累積效應。雪霸國家公園溪流由上而下塑膠微粒通量不受時空及水棲昆蟲影響，顯示無固定塑膠污染來源。

關鍵字（Keywords）：水棲昆蟲（Aquatic insect）、塑膠微粒垂直通量（Vertical flux of microplastics）、淡水生態系（Freshwater ecosystems）、生物多樣性（Biodiversity）

PB11

大甲溪流域水棲昆蟲攝入塑膠微粒之時空變化

Temporal-spatial variations of microplastics ingested by aquatic insects in the Dajia River Basin

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背景/研究問題/材料方法

塑膠微粒已是 21 世紀新興的全球污染物，正在對淡水生態系構成威脅。溪流扮演傳播塑膠微粒至海洋的主要媒介。台灣目前生物體內塑膠微粒相關研究相對國際少，本研究調查 2023 年 8 月(濕季) 和 2024 年 1 月(乾季)水棲昆蟲攝入塑膠微粒污染狀況，旨在分析大甲溪流域的時空變化。該研究在大甲溪流域由源頭自下游設置十樣點以定面積的舒伯氏水網各採三網樣本，檢驗兩個假設：1）水棲昆蟲樣本中塑膠微粒有顯著差異；2）乾季和濕季塑膠微粒有顯著差異。

結果/結論/應用啟示

採集時間為 2023 年濕季及 2024 年乾季，共採集到 7 目 49 科 12,339 之水棲昆蟲，顯微鏡目視檢出 204 個塑膠微粒。塑膠微粒豐度(塑膠微粒/個體)於時間上有顯著差異($p=0.0035, p<0.05$)，濕季比乾季高，空間及各目級則無顯著差異；塑膠微粒濃度(塑膠微粒/乾重)則於時間、空間及各目級皆無顯著差異。季節影響塑膠微粒於河川中的量，但沒有匯集累積在下游，水棲昆蟲攝入的機會沒有增加。此外，由於搖蚊耐污染的特性，被各國作為塑膠微粒相關研究之試驗生物材料，且各樣站皆可採集到及易鑑定到科級，適合作為塑膠微粒污染的指標生物。這對評估塑膠微粒的環境影響和生態效應是非常有用的信息及提高了對塑膠微粒威脅的認識。

關鍵字（Keywords）：水棲昆蟲（Aquatic insect）、塑膠微粒（Microplastics）、淡水生態系（Freshwater ecosystems）

PB12

台灣地區馬祖列島產螳螂(昆蟲綱：螳螂目)名錄

Checklist on Mantises (Insecta: Mantodea) of Matsu Islands, Taiwan

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背景/研究問題/材料方法

馬祖列島位於中國福建省閩江口沿海，鄰近中國，大小島嶼共計 35 座，主要島嶼有南竿、北竿、東引、東莒及西莒等 5 個島。馬祖列島早期受軍事管制，生物多樣性資訊鮮為人知，昆蟲相及昆蟲多樣性相關資料，多僅能參考吳文哲等著作的《馬祖昆蟲生態導覽》(Wu et al. 2003)；然該書中對螳螂相關資訊描述有限，僅提及有大刀螳屬物種存在。本研究綜合 2019-2024 年間馬祖列島採集資料、標本檢視與文獻回顧，建立馬祖列島的螳螂名錄。瞭解馬祖列島螳螂的物種組成及分布狀況外，亦有助於了解臺灣地區的螳螂多樣性的起源。

結果/結論/應用啟示

透過標本檢視、歷年採集成果發現，馬祖列島的螳螂包含 1 科 4 屬 5 種，均為馬祖列島的新記錄種；包含寬腹斧螳 *Hierodula patellifera* (Serville, 1838)、薄翅螳 *Mantis religiosa* (Linnaeus, 1758)、棕靜螳 *Statilia maculata* (Thunberg, 1784)、狹翅大刀螳 *Tenodera angustipennis* (Saussure, 1869)及枯葉大刀螳 *Tenodera aridifolia* (Stoll, 1813)。在檢視過台灣大學、中興大學、屏東科技大學、農業試驗所及國立自然科學博物館等單位的昆蟲標本館藏後，發現馬祖列島乃至金門、澎湖等各離島的螳螂標本相當稀少，顯示過往各離島的昆蟲調查相當有限，無法協助深入探討台灣地區昆蟲多樣性的分佈特性及遷移分化，也凸顯各離島昆蟲相調查的重要性，才能據以分析臺灣昆蟲的起源及多樣特性。

關鍵詞（Keywords）：螳螂目(Mantodea)、生物多樣性(Biodiversity)、新記錄(new record)

PB13

台灣地區蘭嶼產螳螂(昆蟲綱：螳螂目)名錄

Checklist on Mantises (Insecta: Mantodea) of Orchid Island, Taiwan

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背景/研究問題/材料方法

熱帶島嶼-蘭嶼，位於台灣和菲律賓之間，有黑潮經過，生物多樣性豐富，在生物地理學上的重要地理位置，也與台灣地區部分昆蟲的起源有關聯。蘭嶼的昆蟲多樣性調查可追溯至日治時期學者，如鹿野忠雄(1929)、楚南仁博(1927)及中條道夫(1930)，他們對多個昆蟲類群皆有調查記錄，如重要保育類大葉螽斯 *Phyllophorina kotoshoensis* Shiraki, 1930 和珠光裳鳳蝶 *Troides magellanus sonani* Matsumura, 1932 等都是當時蘭嶼常見昆蟲，但未有關螳螂目的相關資訊，直至 Yang et al. (2000)等才有寬腹斧螳 *Hierodula patellifera* (Serville, 1838)一種螳螂。本研究綜合 2016-2024 年間的採集資料、標本檢視與相關文獻回顧，建立蘭嶼的螳螂名錄。

結果/結論/應用啟示

本研究透過標本檢視及歷年採集成果發現，蘭嶼的螳螂含 2 科 6 屬 6 種，有 3 個已知種、2 個新記錄種及一個未知種。經標本比對及生殖器解剖分析顯示，Yang et al. (2000)記錄之寬腹斧螳應為錯誤鑑定，可能為身分未知的新種或菲律賓系的物種。過往對各離島的螳螂調查相當有限，本研究結果顯示，蘭嶼的螳螂多樣性遠大於過往的調查結果，並訂正先前錯誤鑑定；凸顯各離島昆蟲調查的需求特性，得已正確了解臺灣地區的螳螂多樣性及可能起源。

關鍵詞（Keywords）：螳螂目(Mantodea)、生物多樣性(Biodiversity)、新紀錄(new record)

壁報展示: 行為、生理、個體生物學

Posters: Ethology, Physiology and Organismic Biology

PE01

以表觀遺傳學的角度探討咖啡因影響西方蜂的學習記憶
Caffeine enhanced the memory ability of honey bee by epigenetic regulation

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背景/研究問題/材料方法

西方蜂為世界上最重要的授粉昆蟲，對植物繁殖和維持生態平衡的貢獻舉足輕重。西方蜂在授粉時，花蜜是主要的獎勵之一，其中含有許多次級代謝物，例如咖啡因。咖啡因除了是植物預防植食動物取食的防禦物質外，更擁有吸引蜜蜂造訪的功能，前人研究顯示咖啡因能夠增強西方蜂的學習記憶能力與相關基因表現，使其記得該花朵位置更快且更久，但其機制尚不明瞭。在哺乳動物，學習記憶可被 DNA 甲基化、組蛋白乙醯化等表觀遺傳機制調控，進而影響神經功能與行為反應；在小鼠也已經證實咖啡因會影響組蛋白的乙醯化，但在蜜蜂上還並未被證實，綜觀上述研究為咖啡因提升蜜蜂記憶能力的機制提供新的可能性。本研究將針對咖啡因能否以表觀遺傳的方式調控蜜蜂的基因表現與學習記憶探索，透過即時定量聚合酶連鎖反應及西方墨點法等方式，觀察組蛋白修飾及學習記憶相關基因的表現，驗證咖啡因是否通過調控西方蜂大腦中的表觀遺傳標記來改變基因表達模式，進而提升其學習記憶的效率。

結果/結論/應用啟示

本研究以表觀遺傳學的角度理解西方蜂的咖啡因偏好行為的生理機制，拓展表觀遺傳學在學習記憶功能中的應用潛力，亦對未來利用咖啡因提升蜜蜂生理與行為表現提出貢獻。

關鍵詞（Keywords）：蜜蜂（Honeybee）、咖啡因（Caffeine）、表觀遺傳學（Epigenetic）、記憶能力（memory ability）

PE02

初探臺灣直黃斑蜂(*Trachusa formosanum*)之繁殖生態學
Preliminary Study on the Reproductive Ecology of *Trachusa formosanum*

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背景/研究問題/材料方法

臺灣直黃斑蜂(*Trachusa formosanum*)是目前臺灣已知最大的切葉蜂，過往認知屬於地棲穴居型的獨居蜂。繁殖期為六月初至七月下旬，由雌蜂負責築巢和採集繁殖用的資源，包含花粉、葉片及樹脂。目前關於此物種基本生活史與繁殖生態學所知甚少，因此，本研究針對福山植物園(Fushan Botanical Garden)中的三個鄰近巢區進行初步探究，欲釐清其資源利用模式、築巢模式以及巢穴結構。我們透過現場觀察、標放、採集以及對目標巢穴進行錄影及灌模，記錄臺灣直黃斑蜂繁殖相關的行為細節。

結果/結論/應用啟示

資源利用方面，我們發現臺灣直黃斑蜂偏好採集青葉楠和樟科植物的葉子、茶科植物的花粉，但樹脂來源仍未確定。三個巢區的蜂群採集資源的往返時長相近，推測在巢區間個體在此空間尺度下所利用植株並無分化。築巢方面，一個巢穴大約在三天內就可從開挖進入資源採集階段，且同一個體會築多個巢穴；研究期間沒有由上標個體觀察到換區築巢的情形。巢穴結構由長於 15 公分的主通道與一或多個巢室組成，巢室由長條葉子包裹、以樹脂黏合，內含花粉。我們在繁殖季後期觀察到未標記個體進出上標個體的巢穴的情形，因此推測可能存在共用巢穴或托卵寄生的現象。這些發現為我們對此物種提供了新的認識，並加深了對其繁殖生態學的理解。

關鍵詞（Keywords）：臺灣直黃斑蜂（*Trachusa formosanum*）、繁殖生態學（Reproductive ecology）、切葉蜂（Leaf-cutting bees）、築巢行為（Nesting behavior）、地棲穴居蜂（Ground-nesting bees）

PE03

Cryptic strategies of *Trachyzulpha formosana* (Orthoptera: Tettigoniidae): background matching and masquerade

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背景/研究問題/材料方法

Many organisms can avoid detection from predators through camouflage. Background matching is one type of camouflage in which organisms choose a background that matches their appearance to reduce predation rate. Another type of camouflage is masquerade, which the organism mimics an item in which the predator has no interest. In this study, we used an endemic katydid in Taiwan, *Trachyzulpha formosana*, which exhibits two distinct morphs: one resembling moss and the other resembling lichen. We hypothesize that katydids with different morphs choose backgrounds that match their own appearance; or alternatively, the katydid itself masquerades as lichen or moss, without the need to stay on specific background. In the first experiment, we evaluated whether katydids choose a specific background based on visual cues. We used boxes with printed moss and lichen background images glued to the inner walls, along with cameras to record the time each katydid spent on either background. In the second experiment, real moss and lichen were attached to the images in the boxes to evaluate whether the non-visual cues of the real moss and lichen may influence background selection. Each katydid was placed inside the box at night and left until the following morning.

結果/結論/應用啟示

Our analyses showed that moss-morph katydids placed in boxes with printed images only have an overall preference for moss background. When splitting the data into day and night, this preference was only present during the day. Moss-morph katydids placed in boxes with real moss and lichen showed a preference for lichen background at night, but there was no preference during the day. Initial data from lichen-morph katydids show no preference. These results suggest that background matching may be influenced by the type of morph, time of day, as well as whether colored background or real substrate is used in the experiment.

關鍵詞（Keywords）： Background matching, Color morph, Camouflage, Orthoptera

PE04

Identification of mycoviruses from the transcriptomic data of entomopathogenic fungi, *Beauveria bassiana* NCHU-271 and *Metarhizium pinghaense* NCHU-125

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背景/研究問題/材料方法

Mycoviruses have recently been described widespread across fungal species, including entomopathogenic fungi (EPF). Mycovirus can affect the phenotype of fungal species. From the transcriptomic data of *Beauveria bassiana* NCHU-271 (Bb-NCHU-271) and *Metarhizium pinghaense* NCHU-125 (Mp-NCHU-125), the contigs associated with mycoviruses were identified. Herein, this study aims to analyze the mycoviral genomes features and perform the phylogenetic a nalysis, investigate the present of mycoviruses in EPF by RT-PCR.

結果/結論/應用啟示

In our transcriptomic data, we also found 15 contigs in Bb-NCHU-271 and 5 contigs in Mp-NCHU-125 that match with mycoviruses. In Bb-NCHU-271, it was found to be infected by a narnavirus (BbNV-271), which has one RNA genome of 1,720 bp in size, and has putative polypeptide encodes the RdRP. Besides, BbNV-271 has three subviral RNAs (SRs), and the SRs termini showed high identities to those of BbNV-271. Interestingly, Bb-NCHU-271 was also infected by a partitivirus (BbPV-271), which has two RNA genomic segments (dsRNA1= 1,790 bp and dsRNA= 1598 bp). The dsRNA1 has putative ORF1 encodes the RdRP. The dsRNA2 has putative ORF2 encodes the coat protein (CP). In Mp-NCHU-125, a polymycovirus (MpPmV-125) was found. The RNA genome consists of four dsRNAs with the sizes of 2400bp (ORF1, RdRP), 2332bp (ORF2), 1920bp (ORF3, Methyltransferase) and 1351bp (ORF4, PAS-rich protein). The RdRP of three mycoviruses phylogenetically clustered with *Beauveria bassiana* narnavirus, *Beauveria bassiana* partitivirus 1 and Metarhizium anisopliae polymycovirus 1. The presenting of mycoviruses in EPF isolates were validated by RT-PCR. In the future, the prevalence of mycoviruses among the EPF isolates and the epigenetically rregulation of mycoviruses to the Bb-NCHU-271 and Mp-NCHU-125 will be further evaluated.

關鍵詞（Keywords）： *Beauveria bassiana*, *Metarhizium pinghaense*, narnavirus, partitivirus, polymycovirus

PE05

老化對果蠅視神經功能的影響
Aging effects on *Drosophila* visual neuronal function

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背景/研究問題/材料方法

Various neurons change in synaptic numbers with age; however, little is known whether these age-related changes in synapses affect neuronal activities. The *Drosophila* visual neuron Dm8, downstream of UV-sensing photoreceptor R7, is critical in UV preference behavior. Applying 2-photon calcium imaging in the 3, 6 and 9 days-old flies, we monitored neural activities of Dm8s responded toward different UV light intensities. By fitting with the Naka-Rushton function, we quantified Dm8’s changes in dynamic range and sensitivity to UV light with age.

結果/結論/應用啟示

Dm8s displayed inhibitory responses during UV light-on and excitatory responses during light-off. We found that stronger light stimulation led to larger UV-off excitation but smaller UV-on inhibition. The opposite effect on response amplitudes implied that the decrement of light-on inhibition and increment of light-off excitation have the same origin, and most likely, it is excitatory inputs. The 3 days-old Dm8 had smallest UV-on inhibition but largest UV-off excitation. It implied the strength of excitatory inputs to Dm8 reduced with age. Moreover, according to response-light intensity functions, the 3 days-old Dm8s had better UV sensitivity and the 9 days-old Dm8s were less sensitive to UV light, indicating Dm8’s UV sensitivity declined with age. Taken together, our results suggests that aging has significant impacts on visual functions in Dm8s.

關鍵詞（Keywords）：年齡（Age）、鈣離子影像（Calcium imaging）、果蠅（Drosophila melanogaster）、神經活性（Neuronal activity）、視神經（Visual neuron）

PE06

蜂翅變形病毒感染影響西方蜜蜂（*Apis mellifera*）的碳水化合物代謝並導致免疫功能受損
Deformed wing virus infection affects carbohydrate metabolism in *Apis mellifera* and leads to immune impairment.

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背景/研究問題/材料方法

Western honeybees (*Apis mellifera*) are crucial pollinators in nature, playing an indispensable role in ecosystems and ensuring global food security. These bees facilitate the reproduction of flowering plants, which directly impacts biodiversity and agricultural productivity. However, in recent years, honeybee diseases and parasites have severely threatened bee survival, leading to alarming declines in bee populations worldwide. For instance, the Varroa mite (*Varroa destructor*) is a common pest that endangers bees and spreads diseases such as Deformed Wing Virus (DWV), exacerbating colony collapse disorder. Bees infected by DWV often experience weakened immune systems, rendering them more vulnerable to other pathogens and environmental stressors. Yet, the precise mechanisms through which this virus influences immune function remain unclear. Previous studies have suggested that immune capacity is closely linked to carbohydrate metabolism, which provides the necessary energy for maintaining immune responses. In this study, carbohydrate metabolism levels of bees infected with DWV were assessed to observe the extent of immune impairment. Glucose and trehalose concentrations in hemolymph will be measured using enzymatic assays, while glycogen content in bee tissues will be analyzed to assess energy reserves. Additionally, gene expression levels of key enzymes involved in carbohydrate metabolism, such as hexokinase, will be evaluated using real-time PCR (qPCR).

結果/結論/應用啟示

These measurements will provide insights into how DWV infection disrupts carbohydrate metabolism and compromises immune function. Clarifying the underlying mechanisms will shed light on the physiological impacts on infected bee populations, ultimately contributing to better strategies for managing honeybee health and ensuring the sustainability of their critical ecological role.

關鍵詞（Keywords）： *Apis mellifera*, Deformed wing virus, Carbohydrate metabolism of bees, Immune impairment of bee

壁報展示: 醫學昆蟲學

Posters: Medical Entomology

PM01

蚊蟲血紅蛋白基因之表現及功能性分析

Expression and Functional Analysis of Mosquito Hemoglobin Gene

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背景/研究問題/材料方法

蚊幼蟲透過呼吸管自水面獲得氧氣，然而前期實驗使用單分子膜隔絕空氣， 6 小時後觀察孑孓的死亡率僅達 22%，因此假設蚊幼蟲有其他獲得氧氣的機制。根據文獻顯示搖蚊科幼蟲可以表現血紅蛋白基因，藉此血紅蛋白擷取水中氧氣，蚊幼蟲是否具有血紅蛋白則沒有相關文獻或證據。本研究分析六種蚊科幼蟲體內是否具有血紅蛋白基因，並以登革熱病媒蚊為主，探討蚊幼蟲血紅蛋白基因的表現及功能。首先彙整 NCBI 資料庫中昆蟲綱血紅蛋白之 mRNA 序列，以及已解序之蚊蟲基因體序列，利用 DNA Star 設計引子對。抽取蚊幼蟲 RNA 進行反轉錄，以巢式 PCR 偵測血紅蛋白基因。同時透過缺氧的處理，以即時定量 PCR 檢測白線斑蚊和埃及斑蚊幼蟲血紅蛋白基因表現，並以西方墨點法確認血紅蛋白表現量的差異。

結果/結論/應用啟示

所設計的引子對成功增幅 6 種蚊幼蟲血紅蛋白基因，親緣關係樹呈現其基因之歧異性。缺氧處理使埃及斑蚊幼蟲血紅蛋白 RNA 基因相對表現量增高為 3.9 倍，白線斑蚊些微增加至 1.5 倍，但統計上無差異。以西方墨點法確認二種斑蚊血紅蛋白在缺氧時均大量表現。未來將進一步探討血紅蛋白基因在蚊蟲體內不同細胞之分布、血紅蛋白之具體功能，以及血紅蛋白表現與環境變因之相關性。

關鍵詞（Keywords）： 血紅蛋白（hemoglobin）、登革熱（dengue fever）、斑蚊（*Aedes mosquito*）

PM02

Prevalence of tick-borne *Anaplasma phagocytophilum*, *Neoehrlichia mikurensis* and a novel *Rickettsia* sp. in ticks in Hualien

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背景/研究問題/材料方法

Ticks are the primary ectoparasites of animals and serve as vectors for multiple bacteria, including *Anaplasma*, *Babesia*, *Ehrlichia*, and *Rickettsia* spp. which make threats to human health and animal health. Moreover, as the number of people raising companion animals and increasing frequency of visiting wild field have raised health concerns of neglected infectious diseases. The aim of the study was to determine the prevalence rate and identified species of Anaplasmataceae, and *Rickettsia* in ticks from both companion animals and small mammals in Hualien in eastern Taiwan by PCR.

結果/結論/應用啟示

In 2021 and 2023, a total number of 115 and 23 ticks were collected from companion animals and small mammals, respectively. Species of 41 small mammals were *Apodemus agrarius* (n=8), *Rattus losea* (n=11), *Rattus norvegicus* (n=6), and *Suncus murinus* (n=16) were collected. Of the 115 ticks, the prevalence rate of Anaplasmataceae, and *Rickettsia* were 84.3% and 2.6%, respectively. Moreover, gene pairwise comparison suggested a putative new species, *Rickettsia* sp. HH-1, in *Haemaphysalis hystricis*. Of the 41 small mammals' spleens and 23 ticks collected in 2023, 0% (0/23) of ticks and 19.5% (8/41) of small mammals were infected with Anaplasmataceae. *Anaplasma phagocytophilum* and *Neoehrlichia mikurensis* were detected in 5 and 3 small mammals, respectively. The *16S* rDNA amplicons showed 100% identical to *A. phagocytophilum* clone 10699S (Accession no.: MK394178.1) isolate from spleen in *R. losea* in Taiwan and 100% identical to *N. mikurensis* strain JXRLSY-59 (Accession no.: MH722225.1) isolate from spleen in *R. losea* in China. These results demonstrate that ticks and small mammals infected with *Rickettsia*, *Ehrlichia* and *Anaplasma* spp. In eastern Taiwan. Under the One Health concept, the high prevalence of Anaplasmataceae and more species of pathogens indicating that people in Hualien should notice tick biting may cause tick-borne infectious diseases.

Keywords: Anaplasmataceae, One Health, *Rickettsia*, small mammals, tick

PM03

積溫作為登革熱病媒蚊密度預測潛在防治指標的探討

Exploring Accumulated Temperature as a Potential Indicator for Predicting Dengue Vector Density to Support Control Strategies

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背景/研究問題/材料方法

白線斑蚊 (*Aedes albopictus*) 是傳播登革熱、屈公病等傳染病的重要媒介。臺北市存在白線斑蚊，且也曾發生多起登革熱疫情，控制病媒是阻斷疾病傳播的關鍵手段。白線斑蚊的生長、發育和活動易受溫度影響，其發育零點溫度約為 11.40 ±0.37℃，隨著溫度上升，幼蟲期、蛹期及羽化後至吸血產卵的時間皆會縮短。本研究初步探討積溫是否可以作為預測病媒蚊密度的指標，為防治病媒蚊提供科學依據。研究期間為 2020 年至 2024 年，病媒蚊的數據依據本中心的誘卵桶監測標準作業流程於臺北市部分里別進行收集；溫度數據則取自監測區域附近的氣象觀測站。

結果/結論/應用啟示

結果顯示，於 2021、2023 及 2024 年，當日低溫皆高於 11 度後，誘卵桶陽性率超過 10%的時間約為 6 週。通過計算誘卵桶陽性率超過 10%之週數的前 4 週累積溫度，我們能夠推算出蚊蟲數量快速增長的時間點。藉此預測蚊蟲數量上升的關鍵時期，此預測參數作為防治病媒蚊的具體參考數據。透過計算積溫預測病媒蚊密度變化，不論當地有無誘卵桶監測的地點，防治單位皆能更準確地掌握蚊蟲數量增長趨勢，並提前採取有效的控制措施，從而提高防治效能，減少傳染病的傳播風險。但由於目前尚未驗證此方法對蚊蟲控制的實際效能，其應用仍需謹慎，並在未來進行更進一步的研究與驗證。

關鍵詞（Keywords）：*Aedes albopictus*, Accumulated Temperature, Ovitrap Surveillance, Control Strategies

PM04

The Diversity of Ectoparasites from Wildlife and their Implications for the One Health Approach

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背景/研究問題/材料方法

Ectoparasites play a crucial role in the wild animal community. The composition of ectoparasite species reflects not only the biodiversity of their hosts but also their population dynamics and environmental factors of habitats. Ectoparasites uptake bloodmeals from animal hosts and carry pathogens that might affect the health of wildlife, humans, and domestic animals, posing a One Health concern. Therefore, studying these ectoparasites’ diversity helps clarify the interactions between wildlife hosts, habitats, and human activities. Based on previous reports, eastern Taiwan harbors a high diversity of wildlife and habitats. For example, Argasidae and Ixodidae (Acari: Ixodida) may play biological roles in the bridges of disease transmission in this area. The WildOne is the major wildlife rescue center in eastern Taiwan and is responsible for wildlife’s protection and welfare. In this study, ectoparasites were collected from 127 rescued wild animals from 2021 to 2024, and samples from the above hosts were morphologically identified and grouped for future pathogen screening.

結果/結論/應用啟示

A total of 33 species of wildlife were reported and delivered to the WildOne. Grouping of ectoparasites was Ixodidae (65%), lice (13%), hippoboscid flies (10%), mites (8%), maggots (2%) and fleas (2%) were recorded. Avian is mainly parasitized by feather lice (n=14) and hippoboscid flies (n=13), while mammals and reptiles are primarily infested by *Haemaphysalis* spp. (n=33). Notably, all ticks (n=9) found on reptiles were *Amblyomma geoemydae*, demonstrating a preference of specific ticks for reptiles. The genus *Dermacentor* was only found on Formosan black bears, possibly due to their larger body size. The geographic distribution of wildlife was clustered in green land and edge of agricultural areas in Hualien and Taitung County. These preliminary results show the interaction among diverse wildlife, ectoparasites, and the geographic distribution of land use. Future study will perform the molecular analysis of microbes upon ectoparasites and provide insights for wildlife management, public health education and One Health framework formulation.

關鍵詞（Keywords）： ectoparasite, One Health, wildlife, Ixodida

PM05

探討外寄生蟲群落在台灣鼠形動物宿主中漢他病毒傳播之潛在角色

Exploring the potential role of ectoparasite communities on hantavirus transmission of murine-like mammals in Taiwan

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背景/研究問題/材料方法

Recently, the human cases of hantavirus infection is getting higher after COVID-19 pandemic based on Taiwan CDC statistic. The main route of hantavirus infection is through inhalation or ingestion of aerosolized virus which shed in excreta of murine-like mammals, such as Rodentia and Eulipotyphla species. In hantavirus transmission, understanding the factors which play role in infection dynamics of reservoir populations is essential to assess the exposure risk of hantavirus and to identify the risk factors of infection. For public health concern, this study aims to evaluate potential hantavirus transmission role of ectoparasites in murine-like mammals surround human infection cases. This study conducted 37 sample sites, including new hanta cases between 2023 to 2024 (n = 9), old hanta cases between 2016 to 2022 (n = 17), control area without case (n = 7), and wild field (n = 4) to sample murine-like mammals from Feb., 2023 to Aug., 2024. The environment of sites were recorded by photo. Every site was placed 100 life traps lasting 2 night and the baits were slice of sausage or sweet potato covered peanut butter. The blood, lung and ectoparasites were collected. The infection rates of hantavirus in each site were calculated based on molecular and serological analysis.

結果/結論/應用啟示

A total of 807 murine-like mammals were captured and 37% had ectoparasites. The species with rank of ectoparasite incidence were *Rattus losea* (71%), *Rattus tanezumi* (70%), *Bandicota indica* (67%) and *Rattus norvegicus* (53%). According to the ectoparasite family, Laelapidae was the most abundant, followed by Pulicidae. For the RT-PCR detection, 413 samples from lung were tested and the positive rate was 12.8% (53/413), of which all sequences from *Rattus norvegicus* were identical to *Ortohantavirus seoulense* (SEOV). The correlation between ectoparasite load and positive infection rate of *Rattus norvegicus* showed load of Laelapidae and Pulicidae had a weak-moderate negative correlation, but had no correlation in incidence rate of ectoparasite. To sum up, this study provides a new insight on ectoparasite load and communities of murine-like mammals in environmental epidemiology of hantavirus.

關鍵詞（Keywords）：漢他病毒（Hantavirus）、體外寄生蟲（ectoparasite）、鼠形動物（murine-like mammals）、厲蟎科（Laelapidae）、蚤科（Pulicidae）

PM06

New emerging tick-borne *Anaplasma*, *Ehrlichia*, and *Neoehrlichia* spp. in ticks and small mammals in Kinmen County, an offshore island of Taiwan

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背景/研究問題/材料方法

Symptoms of rickettsiosis are mostly non-specific, which makes the disease difficult to diagnose correctly. Kinmen County, an offshore island of Taiwan, is one of the most affected areas by scrub typhus. However, with only less than 20% of reported cases being confirmed with scrub typhus, it is reasonable to consider that other vector-borne rickettsioses play a part in causing fever of unknown origin. Previous studies have identified human granulocytic anaplasmosis (HGA) and human monocytic ehrlichiosis (HME) in Kinmen County, but their transmission in the natural environment remained to be clarified. Small mammals and ticks parasitizing small mammals were collected around Kinmen County from August 2018 to June 2022. PCR was carried out with primer sets of 16S rRNA and *p44/msp2* genes to detect *Anaplasma*, *Ehrlichia*, and *Neoehrlichia* spp.

結果/結論/應用啟示

A total of 692 small mammals belonging to five species of rodents (*Callosciurus erythraeus*, *Mus musculus*, *Rattus losea*, *Rattus norvegicus*, and *Rattus tanezum*) and one species of shrew, *Suncus murinus*, were captured. In addition, 928 ticks were collected, and the majority of which were *Ixodes granulatus*. Anaplasmataceae was detected in 44% (14/32) of spleen samples and 53% (106/200) of ticks. The positivity rates of *Anaplasma phagocytophilum*, *Ehrlichia*, and *Candidatus* Neoehrlichia mikurensis were 6.2% (2/32), 28.1% (9/32), and 9.4% (3/32) in spleens and 2.0% (4/200), 42.5% (85/200), and 8.5% (17/200) in *I. granulatus*, respectively. The sequences of *A. phagocytophilum*, *Ehrlichia*, and *Ca.* N. mikurensis shared high similarity with sequences from neighboring countries such as China, Japan, and Korea. This study gave us a better understanding of the ecology of Anaplasmataece in Kinmen County and highlighted the risk of tick-borne rickettsioses in the area. Although there hasn't been report of case of *Ca*. N. mikurensis in Taiwan, public awareness of the infection should be raised when encountering related clinical signs.

關鍵詞（Keywords）： Small mammals, Ticks, *Anaplasma*, *Neoehrlichia*, *Candidatus* Neoehrlichia mikurensis

壁報展示: 系統分類、族群遺傳、演化

Posters: Systematics, Population Genetics and Evolution

PS01

台灣落葉棲息卵蜣螂屬(*Panelus*)糞金龜（鞘翅目：金龜子科）的系統分類學與系統發育學

Leaf-litter inhabiting *Panelus* dung beetles (Coleoptera: Scarabaeidae) in Taiwan: systematics and phylogenetics

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背景/研究問題/材料方法

Taiwan exhibits diverse topography and climate that promote high species diversity and endemism. Many highly diverse and endemic groups are represented by arthropods inhabiting forest ground, soil and leaf litter. In this study, we focus on a tiny-sized dung beetle genus *Panelus* with four species reported from Taiwan, all endemic. *Panelus* is widely distributed in Taiwan, with highest diversity found in lowlands, but reaching forests up to c. 2000 m of altitude. However, the study of collection specimens and the DNA barcoding data of freshly collected specimens both indicate that the species diversity of Taiwanese *Panelus* is underestimated. The goal of our study is to revise the Taiwanese fauna of *Panelus* and understand its origin and age.

結果/結論/應用啟示

Previous studies of *Panelus* underestimated the species richness mainly because they only used characters of body shape and body color to diagnose the species. We revealed that surface punctation, hind wing development, and male genitalia are crucial for an accurate identification. The width of the 6th abdominal segment can be used to distinguish sexes. Two lineages of *Panelus* are found in Taiwan, clearly defined by DNA data as well as by the body shape, metaventral shield, and the form of male genitalia: *P. crenatus* group and *P. maedai* group. Despite most species are macropterous, they are often locally endemic and likely bad at dispersal. Moreover, more species may co-exist in the same area. DNA barcoding data available at the moment indicate that 8–12 species may be present in Taiwan. We are at the moment working on including additional DNA fragments to corroborate these results, and to reveal the species limits more accurately.

關鍵詞（Keywords）：鞘翅目（Coleoptera）、卵蜣螂屬（*Panelus*）、落葉（leaf litter）、DNA 條形碼（DNA barcoding）、台灣（Taiwan）

PS02

白蛹性狀的瓜實蠅基因分析

Genetic analysis of white pupal trait in melon flies (Diptera:Tephritidae)

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背景/研究問題/材料方法

白蛹性狀的瓜實蠅(*Zeugodacus cucurbitae*)個體相當罕見，目前對該品系的了解甚微。所以本研究針對台灣產的雙性白蛹品系進行孟德爾遺傳試驗與全基因定序。探討白蛹性狀本身的基因特性，比較與野生型蟲的褐蛹基因及國外白蛹品系的白蛹基因差異。

結果/結論/應用啟示

針對白蛹品系與野生型族群的親代，依性別配對共有 4 個組合產生 F_1 世代，結果顯示所有 F_1 世代皆為純色蛹，且雜交組合的處理都是褐蛹，初步推測白蛹基因為隱性。將 F_1 世代依性別配對產生 16 個組合的 F_2 世代，使用卡方適存度分析顯示其符合孟德爾遺傳定律的單基因座遺傳模式。針對性別比例將兩品系所有處理的雌雄蟲數量進行卡方檢定，確認白蛹基因並無性聯遺傳的特性。以全基因定序的結果表明白蛹基因位於 5 號體染色體上的 MFS transporter 位點突變，與國外的白蛹品系是相同的關鍵變異位置。未來可將白蛹基因導入性染色體建構具性聯遺傳的品系，以蛹色做為鑑定性別的表型標記，應用於昆蟲不孕性技術(SIT)。

關鍵詞（Keywords）：瓜實蠅（*Zeugodacus cucurbitae*）、白蛹（White pupae）、孟德爾定律（Mendel's laws）、全基因定序（Whole genome sequencing）、隱性基因（Recessive gene）

PS03

臺灣的長毛跗蟎屬蜂蟎
Bee mites of genus *Sennertia* from Taiwan

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背景/研究問題/材料方法

長毛跗蟎屬 (*Sennertia*) 的蜂蟎與蜜蜂科 (Apidae) 木蜂亞科 (Xylocopinae) 物種具有密切的寄生關係，該屬蜂蟎以異形第二若蟎的生命階段附著在蜂的體表進行攜播，其餘生命週期則在蜂巢中以花粉或巢內碎屑為食，對其寄主可能具有負面的影響。其中，木蜂屬 (*Xylocopa*) 的擴散能力強，易藉由國際貿易擴散到新的地區變為外來種，其攜播的蜂蟎亦會對當地的木蜂構成潛在威脅。本研究從臺灣和金門地區收集八種木蜂，經鏡檢木蜂採集其體表攜播的蜂蟎，製成玻片進行形態鑑定。另外，單隻萃取蜂蟎的 DNA，進行 COI 基因的序列分析，建構親緣樹以輔助形態鑑定結果。

結果/結論/應用啟示

本研究探討臺灣及金門地區之木蜂與其攜播的長毛跗蟎屬蜂蟎，進行物種鑑定與描述，進而了解此屬蜂蟎與木蜂寄主的關係，並確認物種分布情形。經形態鑑定與親緣樹分析結果確立臺灣分布五種本土及一種外來長毛跗蟎屬蜂蟎：*S. alfkeni*、*S. horrida*、*S. lauta*、*S. eximius*、*S. robusta* 和 *S. taiwanensis*。親緣樹分析中，不同物種間有明顯的序列分群，支持形態鑑定的結果。本研究更新臺灣及金門地區長毛跗蟎屬蜂蟎的分類現況，並期盼未來持續探討臺灣蜂蟎的多樣性。

關鍵詞（Keywords）：木蜂（carpenter bee）、蜂蟎（bee mite）、攜播（phoresy）

PS04

森林底層的枝條取食者：匿頸擬步行蟲屬 *Stenochinus* (鞘翅目：擬步行蟲科)幼蟲的特殊形態學與生物學

Forest twig-eaters: unusual morphology and biology of larvae of *Stenochinus*darkling beetles (Coleoptera: Tenebrionidae)

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背景/研究問題/材料方法

The soil and leaf litter in Taiwanese forests is extremely rich in beetles and other arthropods. Although they may be important for forest dynamics, biomass decomposition or nutrient cycling, nearly nothing is known about their identity, biology and role in the ecosystems. Here we report the identity and biology of the ‘twig-eaters’, the beetle larvae inhabiting dry pieces of twigs in forest leaf litter, that we commonly found in our samples across Taiwan. Using DNA barcoding, we associated these larvae with the adults of *Stenochinus* Motschulsky, 1860 (Coleoptera: Tenebrionidae, darkling beetles) that has six species known from Taiwan Island. In this study, we use macro photography and microscopy to document the detailed morphology of these larvae. We also report some basic biology data based on the observation of live larvae in the laboratory, and the preliminary data on species diversity of the genus in Taiwan, based on our DNA barcoding data.

結果/結論/應用啟示

The morphology of *Stenochinus* larva is strongly modified compared to ‘usual’ mealworm body form of darking beetles in (1) cylindrical very elongate body, (2) modification of the abdominal apex into a disc-like compact structure, and (3) rows of very long setae on thorax and abdomen. In characters (1) and (2), the larvae resemble those of the**related genus *Stongylium* that inhabit rotten wood. We document that larvae use dry twigs as protective cases: they actively bite the tunnel in the center of the twig and move into a new twig when necessary; they can leave the twig case and return into it. Hidden in the twig case, they move through the substrate and feed on wood particles. They can also feed on paper, indicating that they may be able to digest cellulose, but we did not find any protist symbionts in their intestines. The larvae are often very common in forest leaf litter and may hence be an important component of wood decomposition in Taiwanese forests. DNA data indicate the presence of 6–8 species candidates in the analyzed samples across Taiwan, indicating that unknown species are present in Taiwanese fauna.

關鍵詞（Keywords）：鞘翅目（Coleoptera）、森林（forests）、幼蟲形態學（larval morphology）、DNA 條碼（DNA barcoding）、臺灣（Taiwan）

PS05

Conservation Genetics and Phylogeography of Broad-tailed Swallowtail, *Papilio maraho*

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背景/研究問題/材料方法

The Taiwan Broad-Tailed Swallowtail (*Papilio maraho*) is an endemic butterfly listed as a Category I protected species under Taiwan’s Wildlife Conservation Act. This species is rare in the wild, and its larvae feed exclusively on the rare plant, *Sassafras randaiense*. Due to its rarity, there is a lack of scientific evidence to assess when this butterfly appeared in Taiwan, the historical population dynamics it has faced, and what the current effective population size is, to support current conservation efforts. To gather the necessary scientific data, we analyzed genomic data using double-digest restriction site-associated DNA sequencing (ddRAD-seq) and conducted comparative analyses of their population genetics and historical demography.

結果/結論/應用啟示

Our preliminary results show that *Papilio maraho* and its sister species, *Papilio elwesi*, belong to distinct clades, with the latter showed greater genetic variability and identified in four separate populations. Structure analysis indicates that *Papilio elwesi* exhibits an admixed ancestral population, with notable genetic components from *Papilio maraho*. In contrast, *Papilio maraho* shows a predominantly distinct ancestral population with only minimal genetic contributions from *Papilio elwesi*. This pattern likely reflects ancestral polymorphisms preserved in *Papilio elwesi*, while *Papilio maraho* has underwent more extensive lineage sorting since its ancestors settled in Taiwan. Demographic analysis suggests that *Papilio maraho* experienced an early population size increased during the Last Glacial Maximum (LGM), followed by a notable bottleneck. Future work will focus on estimating the current effective population size and mutation load for the conservation action plan of *Papilio maraho*.

關鍵詞（Keywords）：　conservation genetics, genome-wide analysis, phylogeography, population structure

PS06

Gene Flow and Introgression Across Elevational Ecotypes in Snail-Feeding Ground Beetle *Carabus nankotaizanus*

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背景/研究問題/材料方法

Ecotypes are populations of a species that adapt to local environments, which often show distinct traits in their morphology, physiology, behavior or ecology. However, these local adaptations do not always lead to genetic divergence of the populations, and the extent of gene flow among ecotypes remain unclear. Taiwanese snail-feeding carabid beetle, *Carabus nankotaizanus*, has two distinct elevational ecotypes (lowland and mountain), which exhibit substantial divergence in morphology, seasonality and ecology. Previous phylogenetic analyses of one mitochondrial and three nuclear genes suggested that parallel evolution of ecotypes in both southern and northern lineages. This study aims to investigate the phylogeographic patterns and gene flow of the two ecotypes of *C. nankotaizanus* based on genomic data of RAD-seq. Two alternative hypotheses were examined: 1) The altitudinal and geographical boundaries in Taiwan contribute to the divergence between ecotypes. 2) The level of gene flow varies across populations along altitudinal and geographical gradients.

結果/結論/應用啟示

The results showed significant genetic divergence between the two ecotypes, with the mountain ecotype being paraphyletic and the lowland ecotype monophyletic, which challenges the previous phylogenetic hypothesis of parallel elevational evolution between lowland and mountain ecotypes. The analyses of population genetic structures identified four distinct genetic populations, which correspond to four geographic regions: the Central Mountain Range, the northeastern lowland of Taiwan, the northern Central Mountain Range (Bilu + Mt. Taiping), and southeastern Taiwan. The results also indicated varying levels of genetic introgression across latitudinal gradients, particularly between the northeastern lowland and the lowlands of southeastern Taiwan, as well as between the Central Mountain Range and the mountains of southeastern Taiwan. The genetic divergence and the patterns of introgression among populations together suggest that both geographic isolation, genetic exchange and local adaptation have played pivotal roles in the divergence of the ecotypes.

關鍵詞（Keywords）： Central Mountain Range, elevational gradient, genome-wide analysis, introgression, local adaptation, phylogeography

PS07

Milionia 屬尺蛾(鱗翅目:尺蛾科，枝尺蛾亞科，雕尺蛾族)在羅漢松科上的拓殖與物種分化

Colonization and species divergence of the genus *Milionia* (Lepidoptera: Geometridae, Ennominae, Boarmiini) on Podocarpaceae

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背景/研究問題/材料方法

Milionia 屬的尺蛾是一個龐大的類群，包括 85 個日行性物種分佈於印度次大陸、中南半島、巽它大陸、華萊士區、新幾內亞島和澳大利亞東北部。牠們是為羅漢松(*Podocarpus*)的專一植食昆蟲。羅漢松葉片的代謝物能夠像脫皮激素一樣干擾昆蟲的正常發育，因此，*Milionia* 屬和羅漢松之間的專一性關係對昆蟲學家和植物生態學家都極具吸引力。此外，*Milionia* 屬在印太區也是許多鱗翅目擬態群的模式，但至目前為止此屬的親緣關係假說卻付之闕如，因此我們重建此屬的親緣關係以檢驗諸多生態學假說，例如幼蟲與寄主植物關係、該屬在東南亞物種爆發的形成，以及警戒與擬態翅紋的起源。由於 *Milionia* 的姊妹群關係沒有現存假說，因此我們使用 *Chiasmia* (Macariini)做為功能性外群，納入井上寬推測與其相近的所有屬，例如：*Paramilionia*、*Callhisita*、*Retromilionia*、*Pseudomilionia*、*Extramilionia*、*Praesos*、*Diomilionia*、*Eumilionia*、*Lobocraspeda*、*Ovimilionia*、以及 *Macromilionia*。我們採用細胞色素 c 氧化酶亞基 I(COI)序列，採用 IQ-TREE V1.6.10 進行了最大似然分析。我們亦將把感興趣的特徵進行編碼，然後在 Mesquite 中呈現特徵的分布與祖型重建結果。

結果/結論/應用啟示

根據初步的親緣關係重建結果顯示，*Milionia* 的姊妹群並非單一屬，而是一個屬群，而 *Milionia* 屬本身可能並非單系群，井上寬所建立的幾個小屬也並不全然是單系群，這也就是說 *Milionia* 屬虛要被重新定義。*Milionia* 屬內部具有三個多樣性中心，新幾內亞、菲律賓、以及蘇拉維西。三個地區的物種爆發為獨立發生，而此屬的起源可能出現在巽它古陸而非印度次大陸。在翅紋演化方面有些相當盛行的翅紋並非單一起源，這意味著 *Milionia* 除了成為其它鱗翅目在擬態上的模型之外，屬內也具有種間的擬態。

關鍵字（Keywords）：化學防禦（chemical defense）、警戒性（Aposematism）、趨同演化（Convergent evolution）、擬態（Mimicry）、專食性昆蟲（Specialist）

PS08

造成北海岸居民嚴重過敏的毒蛾是個新外來入侵物種嗎?
Is the tussock moth causing anaphylaxis in northern coast a new invasive species?

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背景/研究問題/材料方法

2024 年 7 月間三芝地區的居民通報受到毒蛾的侵擾，造成嚴重過敏。由於被發現的地點有大量的榕樹，因此初步被鑑定為榕透翅毒蛾(*Perina nuda*)。然而因為榕透翅毒蛾在台灣從未有引發大規模過敏的紀錄，高密度幼蟲發生的狀況也很稀少，因此我們遂前往勘查。結果顯示造成過敏的是一種從未被記錄過的大型靚毒蛾，聚集性的幼蟲僅取食榕樹葉片。為了釐清造成該種毒蛾的身分與來源，我們檢查了存放於倫敦自然史博物館與牛津大學動物學博物館中的相關模式標本並解剖其生殖器，然後以 *Albarracina* 屬為外群，加上 *Lacida*、*Bembina*、*Toxoproctis*、*Artaxa*、*Arna*、*Euproctis chrysorrhoea*、*Micromorphe*、*Orvasca*、*Sphrageidus*、*Kidokuga*、*Somena* 屬各一種，並納入所有具 COI 序列之 Nygmia 屬物種為內群。其中我們特別增加 *Nygmia plana*、*N. staudingeri*，以及 *N. nigricauda* 三個物種的取樣數量，以 Maximum Likelihood 以及 Bayesian inference 重建其親緣關係。

結果/結論/應用啟示

根據我們所重建的親緣關係顯示，在三芝地區所發現的物種很可能是廣泛分布於印度東北至華南的漫星靚毒蛾。由於這個物種在過往從未被任何調查發現過，且近年之目擊紀錄集中在沙崙至三芝，因此我們高度懷疑此種蛾類乃透過海運貨櫃進入台灣。由於許多黃色的毒蛾不易辨識，但對人類造成過敏的風險程度與症狀並不相同，因此我們認為未來將有必要連結毒蛾類的分類鑑定、臨床症狀、檢驗方式(例如毒毛微細形態)，並監測容易受燈光誘引進入交通工具之外來毒蛾在台灣的擴散與可能影響。

關鍵字（Keywords）：毒蛾（tussock moths）、毛蟲過敏（Lepidopterism）、系統分類（Systematics）、外來入侵物種（Invasive species）、針毛毒液（Spicule venom）

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Dengue beaters - Novel synergies of recombinant biolarvicidal proteins, naturally derived geosmin and gravid trap for *Aedes* spp.

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Background/ Questions/ Methods

The rise of dengue fever in recent years has become a significant issue in tropical and sub-tropical areas, inflicting serious socioeconomic and healthcare burdens. Various efforts at vector control rely heavily on the application of pesticides, source reduction, biological control, and physical control. In this study, we aim to produce a synergistic method to attract, trap, and kill *Aedes albopictus* by synthesizing recombinant biolarvicides, exploring beetroot peel as a new oviposition attractant, and potentially deploying a household-use sticky gravid trap. We produced recombinant mosquito-specific biolarvicides, namely Cyt2Ba, Xpp81Aa1, and BmK proteins under different induction conditions. The former two are originally from *Bacillus thuringiensis* whereas the latter is from the scorpion, *Buthus martensii* Karsh. Previous studies have shown that geosmin is a good oviposition attractant for *Aedes aegypti* and beetroot peel consists of a high concentration of geosmin. To further investigate the attractiveness of Taiwanese-grown beetroot (*Beta vulgaris*) peel towards gravid *Aedes albopictus*, we processed and obtained the dried beetroot peel powder. Then, we studied the attractive effect of beetroot peel, hay infusion and water on gravid mosquitoes. In addition, we designed a black, recyclable, and cylindrical sticky gravid trap with dimensions of 24 cm x 16.6 cm (height x diameter) to integrate the biolarvicidal proteins and beetroot peel-infused water. Two pieces of sticky paper were attached to the walls of the inner container. We experimentally tested our prototype for its ability to attract, trap, and adhere adult mosquitoes.

Results/ Conclusion/ Applications

We assessed the larvicidal activities of Cyt2Ba, Xpp81Aa1, and BmK recombinant proteins and found that Xpp81Aa1 has higher larvicidal efficacy as compared to Cyt2Ba and BmK. We experimentally determined that 2.5mg/ml significantly attracted more gravid mosquitoes compared to water and hay infusion. In conclusion, we successfully synthesized biolarvicidal proteins and incorporated naturally derived geosmin into our sticky gravid trap prototype.

Keywords: Dengue fever, Biolarvacidal protein, Beetroot peel, Gravid trap, *Aedes spp.*

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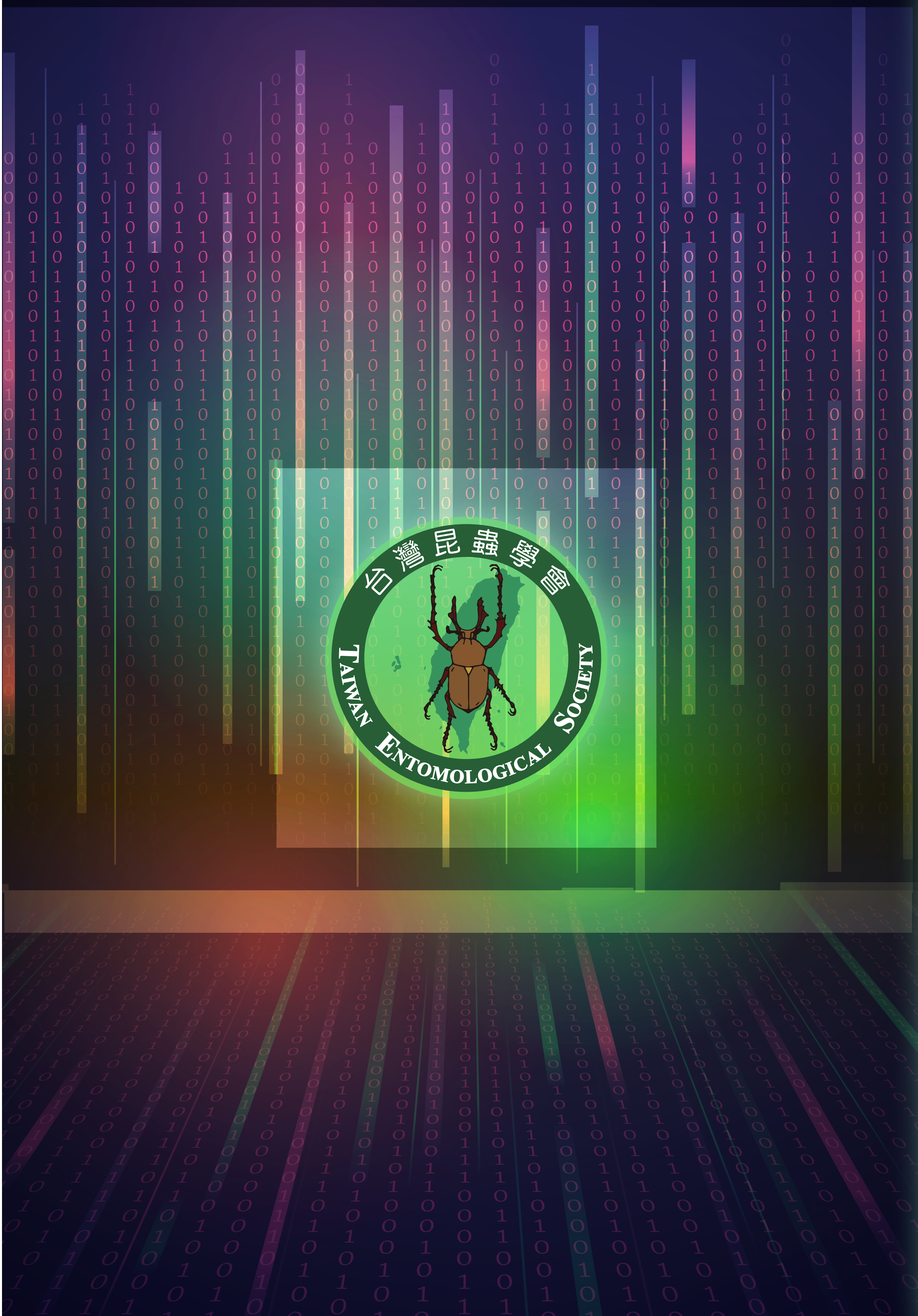
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