台灣昆蟲學會 第44屆年會

蟲零開始

淨零排放與永續發展

中西化學工業股份有限公司
Chung Hsi Chemical Plant, Ltd.

中西化學 70th

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第四十四屆台灣昆蟲學會年會
The 44th Annual Meeting of Taiwan Entomological Society

2023 年 10 月 21 - 22 日

台灣 | 嘉義 | 國立嘉義大學蘭潭校區

Oct. 21 - 22, 2023

Lantan Campus of National Chiayi University

主辦單位: 台灣昆蟲學會、國立嘉義大學植物醫學系、國立臺灣大學昆蟲學系

各位會員、昆蟲界大家庭的先進們，大家好：

歡迎參加第 44 屆台灣昆蟲學會年會。很開心能與各位在嘉義大學相聚共同探討昆蟲學的各個發展面向，在這個學術與創新的場合，彼此激盪、相互交流。

今年的年會主題是「蟲零開始－淨零排放與永續發展」，我們很榮幸邀請到國內四位傑出的學者：石正人博士（國立臺灣大學昆蟲學系）、石憲宗博士（農業部農業試驗所應用動物組）、沈聖峰博士（中央研究院生物多樣性研究中心）及陳一菁博士（國立成功大學生命科學系），他們將從不同尺度和切入點帶來專題演講。

近年各國為減緩氣候急遽變遷造成對全球的衝擊，陸續提出「2050 淨零排放」的宣示與行動，以達到減排、增匯的目標，而昆蟲在其中扮演隱微但關鍵的角色，不可也不應缺席。作物相關的授粉昆蟲、害蟲影響到的是農業生產及糧食安全，透過病蟲害整合管理 IPM，降低化學農藥使用、建構負碳農法等，可減少土壤中甲烷等排放；黑水虻為近年來快速發展且推廣成效極佳的資源昆蟲，幼蟲分解不同的有機資源物，可以有效降低溫室氣體排放，產生的虻糞亦可成為良好的土壤資材；而近年來歐盟大力推動以昆蟲作為動物飼料或是食用蛋白質來源，除了具有高營養價值外，昆蟲蛋白更可降低能源需求與碳排放。以上種種都顯示昆蟲可在淨零排放及循環農業上做出重大貢獻。

本次也將頒發首屆鄭清煥農業昆蟲學學術獎，獲獎者為苗栗區農業改良場吳怡慧博士。其在荔枝椿象的生物防治研究以及天敵昆蟲的應用技術推廣方面表現優異，對永續農業與環境保護有重要貢獻。已故鄭清煥博士的女兒鄭如茜教授也將親臨頒獎，學會亦將頒贈榮譽會員予吳博士。

本次年會的工作坊內容相當多元，植物醫學工作坊中，學者專家將分享植物醫學所肩負的任務和植物醫師所面臨的挑戰，並討論未來植物醫師法的立法願景。淨零排放工作坊中，學者專家將探討森林昆蟲碳排和土壤碳匯，以及如何透過自然解方及食用昆蟲應用達到淨零排放的目標。台日黑水虻工作坊邀請到台灣產業界及學界的專家進行跨領域交流，促進黑水虻研究與產業發展。國土綠網工作坊將分享嘉南地區臺灣爺蟬的生態研究及保育成效。與學生對談場次由曾於海外求學、求職的師生進行經驗交流，提供未來計畫出國深造的學生方向和建議。

今年共收到 115 篇論文摘要投稿，議程相當豐富精采。場外活動也不容小覷，我們邀請到今年在全國科展獲得「台灣昆蟲學會昆蟲研究獎」的中小學師生團隊參加本次年會，分享其科展成果，歡迎與會者蒞臨指導並不吝給予鼓勵；晚間活動我們安排了在地總舖師的辦桌料理，在北迴歸線溫暖的秋天，希望能帶給與會者一個難忘的夜晚。

最後，我們要感謝贊助廠商對學會的支持愛護，使年會得以順利舉辦。再次歡迎各位朋友參加昆蟲年會，祝福大家在心靈和知識上都能有所收穫。

理事長
蕭旭峰
敬上
2023 年 10 月 20 日

第 44 屆昆蟲學會幹部

理事長 President	蕭旭峰 Shiuh-Feng Shiao	國立臺灣大學昆蟲學系 Department of Entomology, NTU
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	蔡偉皇 Wei-Huang Tsai	農業部科技處 Department of Science and Technology, Ministry of Agriculture
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	方怡婷 Yi-Ting Fang	國立臺灣大學昆蟲學系 Department of Entomology, NTU
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	林韋宏 Peter Lin	艾爾生態有限公司 A.I.R Ecological Education
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會計組 Accounting section	黎瑞鈴 Jui-Ling Lee	國立臺灣大學昆蟲學系 Department of Entomology, NTU
總務組 General affair section	王詩儀 Shih-Yi Wang	國立臺灣大學昆蟲學系 Department of Entomology, NTU
台灣昆蟲期刊主編 Formosan Entomologist editor in chief	路光暉 Kuang-Hui Lu	國立中興大學昆蟲學系 Department of Entomology, NCHU
台灣昆蟲副總編輯 Formosan Entomologist deputy editor in chief	吳明城 Ming-Cheng Wu	國立中興大學昆蟲學系 Department of Entomology, NCHU
海外昆蟲學者召集人 International academic convenor	蕭昀 Yun Hsiao	國立臺灣大學生態學與演化生物學研究所 Institute of Ecology and Evolutionary Biology, NTU

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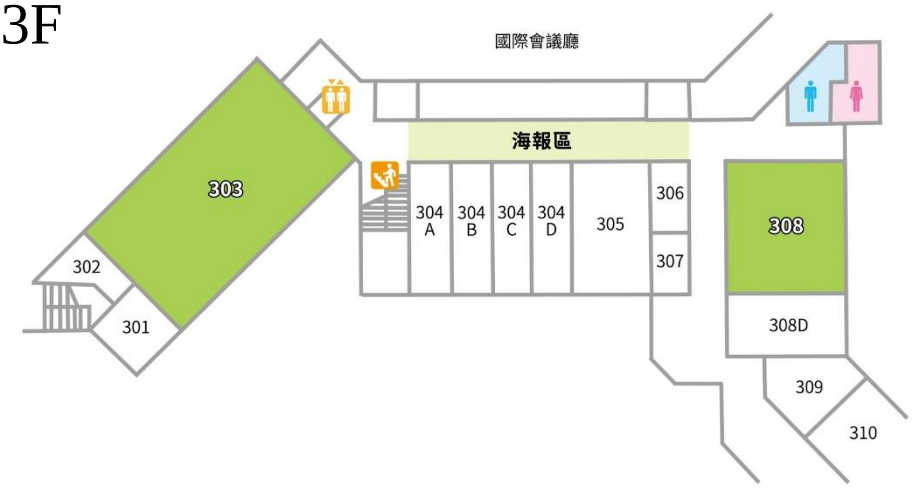
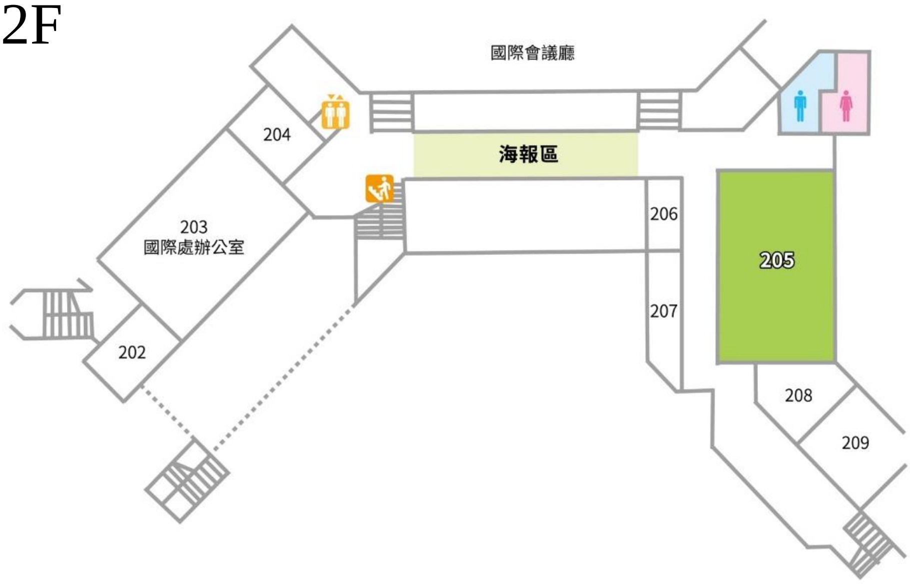
會場平面圖 Floor Plan

3F



2F



🟩 會場教室

🟩 海報區

🟪 攤位區

🟧 報到處

ⓘ 服務台

🚻 廁所

電梯

主要樓梯

1F

大會資訊 Meeting Information

大會地點 Meeting Venue

本屆大會於國立嘉義大學蘭潭校區國際交流學園 (嘉義市鹿寮里學府路300號) 舉行。主要場地包括1F國際會議廳、普通教室 (303、205、111)、2F & 3F長廊。

The conference will be held at National Chiayi University, NCYU. The venue includes 1F International conference hall; Classroom 303, 205, 111 and the 2F & 3F Gallery.

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20日前將檔案上傳至雲端。若大會當日需更新檔案，請至報到櫃檯，由工作人員協助檔案抽換。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. 20. Staff will be available at the registration counter to assist with updating files on-site. 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

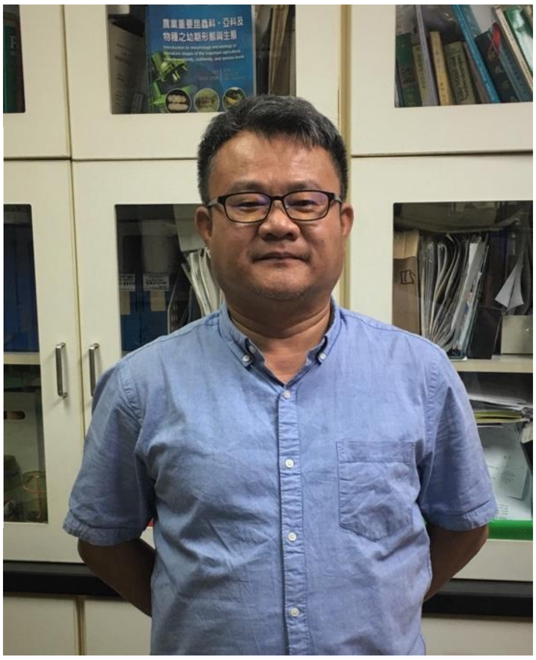
請自行準備您的海報，並於第一天10月21日報到後至2F & 3F長廊依編號張貼。現場備有黏貼工具，務必於海報時間之前張貼完畢。請宣讀者於海報時間 (15:15-16:15) 在海報旁介紹研究內容並回答問題，並務必於10月22日15:30 前自行將海報撤下。

The posters should be mounted at 2F & 3F Gallery before the poster session on Oct. 21. Pushpins are provided on site. During the poster sessions (15:15-16:15), presenters are requested to stand close to their boards, answer questions and facilitate discussions on their work. All posters must be removed by the presenters themselves before 15:30 on Oct. 22.

大會專題演講 Keynote Speech

石憲宗 博士
農業部農業試驗所 研究員兼組長

Dr. Hsien-Tzung Shih
Senior Entomologist & Director
Taiwan Agricultural Research Institute,
Ministry of Agriculture



昆蟲作為人類食品與動物飼料原料及其他新穎性終端產品之永續發展

Sustainable development of insects as raw materials for human food, animal feed, and other novel end products

時間(Time): 2023. 10. 21 (Sat.) 10:00 - 11:00
地點(Venue): 國際會議廳 International conference hall

大會專題演講 Keynote Speech

沈聖峰 博士
中央研究院生物多樣性研究中心 研究員

Dr. Sheng-Feng Shen
Research Fellow
Biodiversity Research Center, Academia Sinica

氣候變遷下的挑戰：以地區性適應的觀點開創昆蟲保育新視角
Climate Change Challenges: Redefining Insect Conservation through the Lens of Local Adaptation

時間(Time): 2023. 10. 21 (Sat.) 11:00 - 12:00

地點(Venue): 國際會議廳 International conference hall

大會專題演講 Keynote Speech

吳怡慧 博士
苗栗區農業部農業改良場生物防治研究中心
副研究員

Dr. Yi-Hui Wu
Associate Research Fellow
Biological Control Research Center, Miaoli District Agricultural Research and Extension Station, Ministry of Agriculture

從一到無限–荔枝椿象與稻黑椿象生物防治之成效
Effectiveness of biological control of litchi stink bug and black rice bug

時間(Time): 2023. 10. 22 (Sun.) 09:00 - 10:00
地點(Venue): 國際會議廳 International conference hall

大會專題演講 Keynote Speech

石正人 博士
臺灣大學昆蟲學系 名譽教授

Dr. Cheng-Jen Shih
Emeritus Professor
Department of Entomology, National Taiwan University

昆蟲在低碳淨零之貢獻與利用

The contributions and applications of insect in carbon net zero

時間(Time): 2023. 10. 22 (Sun.) 14:45 - 15:45
地點(Venue): 國際會議廳 International conference hall

陳一菁 博士
成功大學生命科學系 副教授

Dr. I-Ching Chen
Associate Professor
Department of Life Sciences, National Cheng Kung University

全球生物多樣性變遷之台灣觀點與社會適應

Taiwan's perspective and social adaptation to global biodiversity changes

時間(Time): 2023. 10. 22 (Sun.) 15:45 - 16:45
地點(Venue): 國際會議廳 International conference hall

議程大綱

10 月 21 日 (六)

<table>
<tr><th>時間/地點</th><th colspan="4">國際會議廳</th></tr>
<tr><td>08:30 – 09:30</td><td colspan="4">報到(國際交流學園門口)、海報張貼(2 & 3 樓走廊)</td></tr>
<tr><td>09:30 – 10:00</td><td colspan="4">開幕致詞、合照</td></tr>
<tr><td>10:00 – 11:00</td><td colspan="4">大會專題演講: 石憲宗博士
昆蟲作為人類食品與動物飼料原料及其他新穎性終端產品之永續發展</td></tr>
<tr><td>11:00 – 12:00</td><td colspan="4">大會專題演講: 沈聖峰博士
氣候變遷下的挑戰：以地區性適應的觀點開創昆蟲保育新視角</td></tr>
<tr><td>12:00 – 13:30</td><td colspan="4">休息用餐／12:10-13:30 理監事會 (B1 會議室)</td></tr>
<tr><th>時間/地點</th><th>國際會議廳</th><th>303 教室</th><th>205 教室</th><th>111 教室</th></tr>
<tr><td>13:30 – 14:30</td><td>植物醫學工作坊</td><td rowspan="2">農業昆蟲學
OA01-OA07</td><td rowspan="2">生物多樣性、族群與群聚生態學
OB01-OB07</td><td>醫學與都市昆蟲學
OM01-02/OU01-02</td></tr>
<tr><td>14:30 – 15:15</td><td>國土綠網工作坊：以爺蟬保育為例</td><td>行為、生理、個體生物學
OE01-OE03</td></tr>
<tr><td>15:15 – 16:15</td><td colspan="4">茶敘(一樓中庭) / 海報時間 (2, 3 樓走廊)</td></tr>
<tr><td>16:15 – 17:45</td><td>淨零排放工作坊</td><td rowspan="2">農業昆蟲學
OA08-OA14</td><td>系統分類、族群遺傳、演化
OS01- OS06</td><td rowspan="2">行為、生理、個體生物學
OE04- OE10</td></tr>
<tr><td>17:45 – 18:00</td><td></td><td></td></tr>
<tr><th>時間/地點</th><th colspan="4">國際交流學園大樓外</th></tr>
<tr><td>18:00 – 20:00</td><td colspan="4">晚宴</td></tr>
</table>

議程大綱

10 月 22 日 (日)

時間/地點	國際會議廳			
08:30 – 09:00	報到(國際交流學園門口)			
09:00 – 10:00	鄭清煥農業昆蟲學學術獎頒獎 (國際會議廳) 大會專題演講: 吳怡慧博士 從一到無限-荔枝椿象與稻黑椿象生物防治案例之分享			
10:00 – 10:10	換場			
時間/地點	國際會議廳	303 教室	205 教室	111 教室
10:10 – 11:10	與學生對談-海外合作與工作經驗談	農業昆蟲學 OA15-OA22	生物多樣性、族群與群聚生態學 OB08-OB15	行為、生理、個體生物學 OE11-OE15
11:10 – 12:10				
12:10 – 13:10	休息用餐 / 12:20 – 13:10 會員大會 (國際會議廳)			
13:10 – 14:25	台日黑水虻工作坊: 產業現況及國際合作之必要性	農業昆蟲學 OA23-27	系統分類、族群遺傳、演化 OS07-OS09	醫學昆蟲學 OM03-OM05
14:25 – 14:45	茶敘(一樓中庭)			
時間/地點	國際會議廳			
14:45 – 15:45	大會專題演講: 石正人博士 昆蟲在低碳淨零的貢獻與利用			
15:45 – 16:45	大會專題演講: 陳一菁博士 全球生物多樣性變遷之台灣觀點與社會適應			
16:45 – 17:25	閉幕暨頒獎典禮／抽獎			

Program at a Glance

Oct. 21, 2023 (Sat.)

Time/Place	International conference hall
08:30 – 09:30	Registration (Gate of International Networking Academy Building)/ Poster mounted (2F & 3F Gallery)
09:30 – 10:00	Opening Welcome/ Group Photo
10:00 – 11:00	Keynote Speech: Dr. Hsien-Tzung Shih Sustainable development of insects as raw materials for human food, animal feed, and other novel end products
11:00 – 12:00	Keynote Speech: Dr. Sheng-Feng Shen Climate change challenges: redefining insect conservation through the lens of local adaptation
12:00 – 13:30	Lunch Break ／12:10-13:30 Board of Directors Meeting (B1 council hall)

Time/Place	International conference hall	303 room	205 room	111 room
13:30 – 14:30	Plant Doctor Workshop	Agricultural Entomology OA01-OA07	Biodiversity, Population and Community Ecology OB01-OB07	Medical Entomology/ Urban Entomology OM01-02/OU01-02
14:30 – 15:15	Ecological Network Workshop: The case of *Formotosena seebohmi*			Ethology, Physiology and Organismic Biology OE01-OE03
15:15 – 16:15	Tea Break (1F) / Poster Time (2F & 3F Gallery)			
16:15 – 17:45	Workshop on Net Zero	Agricultural Entomology OA08-OA14	Systematics, Population Genetics and Evolution OS01- OS06	Ethology, Physiology and Organismic Biology OE04- OE10
17:45 – 18:00				

Time/Place	Outside of International Networking Academy Building
18:00 – 20:00	Conference Banquet

Program at a Glance

Oct. 22, 2023 (Sun.)

Time/Place	International conference hall			
08:30 – 09:00	Registration (Gate of International Networking Academy Building)			
09:00 – 10:00	Ching-Huan Cheng Agricultural Entomology Research Award Ceremony Keynote Speech: Dr. Yi-Hui Wu Effectiveness of biological control of litchi stink bug and black rice bug			
10:00 – 10:10	Room Switching			
Time/Place	International conference hall	303 room	205 room	111 room
10:10 – 11:10	Conversations with Students: Overseas Collaboration and Job Search Experience	Agricultural Entomology OA15-OA22	Biodiversity, Population and Community Ecology OB08-OB15	Ethology, Physiology and Organismic Biology OE11-OE15
11:10 – 12:10				
12:10 – 13:10	Lunch Break / 12:20 – 13:10 Annual General Meeting (International conference hall)			
13:10 – 14:25	Fostering Taiwan-Japan Collaboration in the Black Soldier Fly Industry	Agricultural Entomology OA23-27	Systematics, Population Genetics and Evolution OS07-OS09	Medical Entomology OM03-OM05
14:25 – 14:45	Tea Break (1F)			
Time/Place	International conference hall			
14:45 – 15:45	Keynote Speech: Dr. Cheng-Jen Shih The contributions and applications of insect in carbon net zero			
15:45 – 16:45	Keynote Speech: Dr. I-Ching Chen Taiwan's perspective and social adaptation to global biodiversity changes			
16:45 – 17:25	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

10 月 21 日 (六)

*底線為論文宣讀者，粗體為參加競賽

時間/地點	國際會議廳
08:30 – 09:30	報到(國際交流學園門口)、海報張貼(2 & 3 樓走廊)
09:30 – 10:00	開幕致詞、合照
10:00 – 11:00	大會專題演講: 石憲宗博士 昆蟲作為人類食品與動物飼料原料及其他新穎性終端產品之永續發展 【主持人:楊恩誠博士】
11:00 – 12:00	大會專題演講: 沈聖峰博士 氣候變遷下的挑戰：以地區性適應的觀點開創昆蟲保育新視角 【主持人: 孫烜駿博士】
12:00 – 13:30	休息用餐／12:10-13:30 理監事會 (B1 會議室)

時間/地點	國際會議廳	303 教室	205 教室	111 教室
主題	工作坊	農業昆蟲學 【主持人:譚景文博士、吳怡慧博士】	生物多樣性、族群與群聚生態學 【主持人:許峰銓博士、蕭昀博士】	醫學昆蟲學/都市昆蟲學 【主持人:杜武俊博士、曾書萍博士】 行為、生理、個體生物學 【主持人:郭祺筠博士、曾惠芸博士】
13:30 – 13:45	植物醫學工作坊 【主持人:蕭旭峰博士】 與談人：	**OA01** **Sublethal effects of Spirodiclofen on life history traits and population parameters of *Tetranychus urticae* (Acari: Tetranychidae)** **Angela Huang, Ming-Ying Lin**	**OB01** **以誘引巢體進行南投濁水溪流域蜂類調查之測試** **扶尚睿、陳韻如、謝祥文、黃冠瑋、曾惠芸、楊恩誠**	**OM01** **Detection of *Anaplasma, Babesia, Ehrlichia,* and *Neoehrlichia* in ticks from small mammals in Kinmen, Taiwan** **Chia-Yi Lin, Tsai-Ying Yen, Yin-Wen Wu, Hsi-Chieh Wang, Kun-Hsien Tsai**

13:45 – 14:00	・陳文華博士(國立屏東科技大學植物醫學系) ・郭章信博士 (國立嘉義大學植物醫學系) ・唐政綱博士 (國立中興大學植物保健學位學程) ・蕭旭峰博士 (國立臺灣大學昆蟲學系)	**OA02** **本土產蟲生線蟲於番茄防治番茄夜蛾 *Helicoverpa armigera* (Hübner) 之潛力評估** **李筠婷、曾慶慈**	**OB02** **全球暖化對台灣家白蟻和格斯特家白蟻食物資源競爭的影響** **楊尚恩、李後鋒**	**OM02** **臺北市立動物園廄刺蠅對白犀牛之危害調查** **洪可安、蔡昀陵、吳立信**
14:00 – 14:15		**OA03** **Post-harvest quarantine cold treatment for 'Golden Sweet' and 'Jade Girl' cherry tomatoes infested with fruit flies (Tephritidae)** **Prakriti Regmi, Kao-Wei Lin, Wen-Bin Yeh**	**OB03** **A taxonomic review of Japanese *Aprostocetus* Westwood, 1833 (Hymenoptera: Eulophidae), with notes of potential significance of *Aprostocetus* in evolutionary research** **Miki Hisano, Kazunori Matsuo**	**OU01** **Contact toxicity and repellent effects of clove powder, clove oil, and is major bio-active compounds against destroyer ants, *Trichomyrmex destructor* (Hymenoptera: Formicidae), under laboratory conditions** **Rosy Gurung, Lekhnath Kafle**
14:15 – 14:30		**OA04** **小猿葉蟲 (*Phaedon brassicae* Baly, 1987)(Coleoptera: Chrysomelidae) 室內大量飼育流程建立** **林柏丞、陳家安、陳巧燕、莊國鴻、陳雅苓、林彥伯**	**OB04** **利用 CLIMEX 預測長足捷蟻 *Anoplolepis gracilipes* 在台灣的物種分布模型–以土壤溫度建立預測模型** **戴正、葉錦紘、吳立心**	**OU02** **A field study on the effects of EM probiotic supplements on honeybee, *Apis mellifera* (Hymenoptera: Apidae), productivity** **Simran Kayastha, Lekhnath Kafle**
14:30 – 14:45	國土綠網工作坊：以螽蟬保育為例 【主持人: 宋一鑫博士】 與談人： ・施怡伸技佐 (林業及自然保育署嘉義分署)	**OA05** **使用數學方法，探究授粉昆蟲減少導致植物豐度下降之情形** **李奕德、仲澤剛史**	OB05 以幼蟲期發育表現探討瓜實蠅 (*Zeugodacus cucurbitae*) (Diptera: Tephritidae)白蛹品系的大量飼養條件 洪傳捷、周明儀、黃紹毅、黃毓斌、范姜俊承	**OE01** **以幾丁質為基質純化大腸桿菌表現系統中的 Galectin1-melittin 融合蛋白** **曾瑤光、吳岳隆、黃榮南**

14:45 – 15:00	・翁榮顯理事長 (草山社區發展協會)	**OA06** **蟲生真菌對黃條葉蚤成蟲的防治效果評估** **洪欽麟、唐政綱、莊益源**	**OB06** **人類世的生物加速反應** **陳怡玟、陳一菁、Malin Pinsky、Jonathan Lenoir**	**OE02** **亞致死劑量益達胺誘發工蜂早熟之生理機制探究** **陳琬鎰、楊恩誠**
15:00 – 15:15		**OA07** **黑殭菌 MA721 菌株對二點葉蟎防治效果評估** **黃閔軍、莊益源**	**OB07** **A study on the effects of organic acids and probiotics supplements on insecticide toxicity in honeybees (*Apis mellifera*)** **Ramita Prajapati, Lekhnath Kafle**	**OE03** **黃原鼻白蟻的生殖階級發育途徑** **李宛眞、邱奕寧、李後鋒**
15:15 – 16:15	茶敘(一樓中庭) / 海報時間 (2, 3 樓走廊)			
主題	工作坊	農業昆蟲學 【主持人:譚景文博士、吳怡慧博士】	系統分類、族群遺傳、演化 【主持人:蔡正隆博士、韋家軒博士】	行為、生理、個體生物學 【主持人:郭祺筠博士、曾惠芸博士】
16:15 – 16:30	淨零排放工作坊 【主持人:葉文斌博士】 與談人： ・趙榮台博士 (農業部林業試驗所) ・石憲宗博士 (農業部農業試驗所) ・李後鋒博士 (國立中興大學昆蟲學系) ・王巧萍博士 (農業部林業試驗所)	**OA08** **光波長對番茄潛旋蛾 *Phthorimaea absoluta* 誘捕效果探討** **許雅涵、吳宗澤、莊益源**	**OS01** **臺灣產黑殭菌屬 12 菌株之系統學研究** **林貝容、林彥伯、郭章信**	**OE04** **消除 PI-*Wolbachia* 誘導漿黑卵蜂 *Telenomus remus* 之雌性功能性童貞突變** **涂宜呈、賴慶庭、吳立心**
16:30 – 16:45		**OA09** **Different target-site mutations associated with diamides resistance in *Plutella xylostella* (Lepidoptera: Plutellidae)** **Rameshwor Pudasaini, Cheng Chang, Mu-Hsin Chen, Shu-Mei Dai**	**OS02** **穿山甲木鼻白蟻 (蜚蠊目：木鼻白蟻科) 的生態棲位與階級發育** **劉人翰、梁維仁、邱俊禕、廖浩全、林志銓、葉信廷、李後鋒**	**OE05** **東方果實蠅對甲基丁香油反應之關鍵氣味結合蛋白特性分析** **張維展、徐駿森、呂彥儒、許如君**

16:45 – 17:00		**OA10** **感染 SBV 的東方蜂幼蟲之發育與病毒複製相關的關鍵基因調控** **Zih-Ting Chang, Yu-Feng Huang, Tzu-Han Chen, Chung-Yu Ko,Yu-Shin Nai, Yue-Wen Chen**	**OS03** **利用粒線體基因體探討臺灣產竹節蟲的親緣關係** **王柏澂、吳立偉**	**OE06** **共生蟎透過比例辨識法選擇埋葬蟲宿主** **吳奕達、林暐鈞、Tanmay Dixit、Nicholas Horrocks、孫烜駿**
17:00 – 17:15		**OA11** **影響菸草粉蝨取食獲得 begomoviruses 的生物因子** **黃雅郁、李威樺、蔡志偉**	**OS04** ***Pseudalomya* 屬(膜翅目：姬蜂科：姬蜂亞科)於臺灣之首次發現及其族級分類地位探討** **陳玄樸、菊地 波輝、蕭旭峰**	**OE07** **Comparative genomics of *Purpureocillium lilacinum* NCHU-NPUST-175 and molecular marker development** **Zhi-Yu Yeh, Pei-Hsin Lo, Chuen-Fu Lin, Yu-Shin Nai**
17:15 – 17:30		**OA12** **Whole genomic sequencing and analysis of *Rhagastis binoculata* nucleopolyhedrovirus (NPV) in Taiwan** **Yu-Yun Kuo, Ju-Chun Chang, Yi-Hsuan Li, Yu-Feng Huang, Tzong-Yuan Wu, Yu-Shin Nai**	**OS05** **臺灣跳蟲 (彈尾綱) 之多樣性** **Hsin-Ju Cheng, Frans Janssens, Bruno Bellini, Taizo Nakamori, Chih-Han Chang**	**OE08** **Transcriptome analysis of entomopathogenic fungi, *Beauveria bassiana* infected coffee berry borer *Hypothenemus hampei* (Ferrari)** **Fang-Min Chang, Yi-Hao Huang, Hsiao-Ling Lu, Yu-Shin Nai**
17:30 – 17:45		OA13 麵包蟲幼蟲蟲糞的理化特性評估 林柏文、段浩文、林祐丞、李裕娟、張淑貞、石憲宗	**OS06** **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**	**OE09** **白蟻不對稱彈性大顎最佳幾何比例：二維模型探究** **劉子嘉、關貫之、王翊語、邱俊禕、李後鋒、紀凱容**
17:45 – 18:00		OA14 麵包蟲幼蟲蟲糞添加廢菇包介質之設施栽培應用初探 李裕娟、林柏文、王朝儀、段浩文、石憲宗		**OE10** ***Wolbachia* 感染對漿黑卵蜂適應高溫的影響** **郭思彤、吳立心**
時間/地點	國際交流學園大樓外			
18:00 – 20:00	晚宴			

10 月 22 日 (日)

時間/地點	國際會議廳			
08:30 – 09:00	報到(國際交流學園門口)			
09:00 – 10:00	鄭清煥農業昆蟲學學術獎頒獎 (國際會議廳) 大會專題演講: 吳怡慧博士 從一到無限-荔枝椿象與稻黑椿象生物防治案例之分享【主持人:蕭旭峰博士】			
10:00 – 10:10	換場			
時間/地點	國際會議廳	303 教室	205 教室	111 教室
主題	工作坊	農業昆蟲學 【主持人: 宋一鑫博士】	生物多樣性、族群與群聚生態學 【主持人: 陸聲山博士】	行為、生理、個體生物學 【主持人: 李後鋒博士】
10:10 – 10:25	與學生對談-海外合作與 工作經驗談 【主持人: 陳宣汶博士】 與談人： ・陳宣汶博士 (國立嘉義大學生物資源學系) ・吳倩誼碩士生 (國立臺灣大學昆蟲學系) ・黃悠然博士 (九州大學比較社會文化研究院) ・劉家銘博士 (國立研究開發法人農業・食品產業技術綜合研究機構)	OA15 原民部落作物害蟲調節服務功能調查及原民植物對有益天敵之助益 李忠泰、林立、游之穎、林少晴	OB08 授粉者之性別對共花植物間的競爭和共存有其重要性 仲澤剛史、岸茂樹	OE11 一種喜白蟻性隱翅蟲的擬寄生性隱翅蟲 梁維仁、丸山宗利、李後鋒
10:25 – 10:40		OA16 運用本土天敵於有機田區成功控制稻黑椿象 蔡恕仁、王誌偉	OB09 台灣東方蜜蜂高度適應性之分子層次研究：基因表現與單核苷酸多態性的關聯 陳韻如、扶尚睿、謝祥文、董致韡、林詩舜、楊恩誠	OE12 顯微斷層掃描 (Micro CT) 在昆蟲學研究的應用 廖浩全、 蔡漢祥、 陳妤欣、 吳佳倩、 陳慕璇、 李後鋒
10:40 – 10:55		OA17 殺蟎劑對臺東地區鳳梨釋迦葉蟎類之抗藥性評估 許育慈、陳姿岑	OB10 台北植物園與中和四號公園授粉網絡與其時間動態 謝藹、葉文琪、陸聲山	OE13 利用桿狀病毒表面展示技術建立呼吸道病毒感染血清檢測系統 王麒瑋、陳祥恩、潘正宇、蔡智瑄

10:55 – 11:10		OA18 黑水虻與魚粉胺基酸組成之變異程度比較 施則均、錢柏綸	OB11 獨角仙、外米擬步行蟲及長角象鼻蟲之幼蟲腸道菌分離、鑑定及菌相差異。 姚美吉、葉千榕、王泰權、張淑貞、林柏文	OE14 解析 vasa 基因在孤雌胎生豌豆蚜的發育表現以及演化意涵 林季瑋、張俊哲
11:10 – 11:25		OA19 國高中生對食用昆蟲的態度及可能影響因素之探討-以臺中市區為例 吳幸珊、黃紹毅	OB12 台灣青蔥甜菜夜蛾的抗藥性調查 申屠萱、江明耀、黃毓斌、戴淑美	OE15 多樣寡家蟻探索行為與集體覓食行為之初探 游羽暄、林欣誼、陳依淇、陳鑫樟、趙子嫣、賴麗娟
11:25 – 11:40		OA20 環境降溫對於青蔥甜菜夜蛾防治效果研究 林俊成、林立	OB13 嬌小、大量且多樣：臺灣落葉層甲蟲計劃啟動！ Martin Fikáček, Fang-Shuo Hu, Bin-Hong Ho, My-Hanh Le, Jen-Pan Huang	
11:40 – 11:55		OA21 應用無人植保機噴施淡紫菌 TNZZS6 發酵產物之田間防治試驗 林慧婷、陳盈丞、蔡小涵	OB14 台灣鋏蠓 (*Forcipomyia taiwana*) 幼蟲棲地偏好與環境因子研究 黃政學、林姿佑、范姜俊承、蔡正隆、羅怡珮、黃榮南、詹美鈴	
11:55 – 12:10		OA22 落花生土壤害蟲調查與草螟蛾 *Sufetula* sp.發生概述 張淳淳、戴宏宇、陳怡如	OB15 國立自然科學博物館園區蠓科物種多樣性 林姿佑、蔡正隆、賀毓翔、羅怡珮、詹美鈴	
12:10 – 13:10	休息用餐 / 12:20 – 13:10 會員大會 (國際會議廳)			

主題	工作坊	農業昆蟲學 【主持人: 陳美娥博士】	系統分類、族群遺傳、演化 【主持人: 吳立偉博士】	醫學昆蟲學 【主持人: 蔡坤憲博士】
13:10 – 13:25	台日黑水虻工作坊: 產業現況及國際合作之必要性 【主持人: 劉家銘博士】 與談人： ・石正人博士 (國立臺灣大學昆蟲學系) ・譚景文博士 (國立中興大學昆蟲學系) ・吳孟昆先生 (昆億生物科技股份有限公司) ・錢柏綸先生(循創生物科技股份有限公司) ・霜田政美博士 (東京大學大學院農學生命科學研究科) ・大木碩仁博士候選人 (東京大學大學院農學生命科學研究科) ・小林徹也博士 (國立研究開發法人農業・食品產業技術綜合研究機構生物機能利用部門) ・武田晃司博士 (國立研究開發法人農業・食品產業技術綜合研究機構生物機能利用部門)	OA23 稻黑椿象 (半翅目：蝽科) 卵寄生蜂-黑卵蜂 (膜翅目：緣腹細蜂科) 於不同溫度下之寄生表現 蔡餘慶、江旻柔、吳怡慧	OS07 系統分類成果與在地知識流通的距離ー分類群地方名稱的關鍵橋樑角色與推動策略 吳士緯、李興漢	OM03 Progress of proposing ecology-based control measure against the stable fly in Japan Kazunori Matsuo, Yu-Zen Huang, Wei-Ren Liang, Miki Hisano, Koshi Asami, Makito Shindo, Yume Kawano, Hirona Nakazato, Yuka Sakai, Haruho Kodama, Tatsuo Fujioka
13:25 – 13:40		OA24 葫蘆科作物主要產區菸草粉蝨(*Bemisia tabaci*)對 16 種國內登記殺蟲劑之感受性監測研究 林映秀、饒聖慈	OS08 An undescribed species of Australian gall-inducing soft scale (Hemiptera: Coccidae) Michael Gorton, Yen-Po Lin, Penny J. Gullan	OM04 Survey of the sand fly population in the urban city of Taipei Botanical Garden Yu-Feng Tsai, Shiuh-Feng Shiao, Kun-Hsien Tsai
13:40 – 13:55		OA25 農業長期生態樣區指標生物族群與環境因子之關聯性探討：以六條瓢蟲為例 楊婉秀、董耀仁、許北辰、石憲宗	OS09 20 年未解之謎—台灣的半板竹節蟲(Phasmatodea: Lonchodidae: Necrosciinae: *Hemiplasta*)的分類地位? 張書銘、蕭旭峰	OM05 台灣病媒蚊感染沃爾巴克氏菌調查與其對節肢病毒之效果評估 陳秀玲、鍾瀚璿、鄧華真
13:55 – 14:10		OA26 Establishment of high potential entomopathogenic fungi selection markers by aligning phenotype and gene expression levels Nian-tong Ni, Yu-Shin Nai		

14:10 – 14:25		OA27 新式蜂球應用於施放赤眼卵蜂防治玉米秋行軍蟲 謝佳宏、張光華、林立、郭東禎、莊玉祥		
14:25 – 14:45	茶敘(一樓中庭)			
時間/地點	國際會議廳			
14:45 – 15:45	大會專題演講: 石正人博士 昆蟲在低碳淨零的貢獻與利用 【主持人: 黃榮南博士】			
15:45 – 16:45	大會專題演講: 陳一菁博士 全球生物多樣性變遷之台灣觀點與社會適應 【主持人: 呂曉鈴博士】			
16:45 – 17:25	閉幕暨頒獎典禮／抽獎			

Conference Agenda

Oct. 21, 2023 (Sat.) * Underline denotes speakers, Bold denotes competition

Time/Place	International conference hall
08:30 – 09:30	Registration (Gate of International Networking Academy Building)/ Poster mounted (2F & 3F Gallery)
09:30 – 10:00	Opening Welcome/ Group Photo
10:00 – 11:00	Keynote Speech: Dr. Hsien-Tzung Shih Sustainable development of insects as raw materials for human food, animal feed, and other novel end products 【Hosts: Dr. En-Cheng Yang】
11:00 – 12:00	Keynote Speech: Dr. Sheng-Feng Shen Climate Change Challenges: Redefining Insect Conservation through the Lens of Local Adaptation 【Hosts: Dr. Syuan-Jyun Sun】
12:00 – 13:30	Lunch Break ／12:10-13:30 Board of Directors Meeting (B1 council hall)

Time/Place	International conference hall	303 room	205 room	111 room
Topics	Workshop	Agricultural Entomology 【Hosts: Dr. Ching-Wen Tan, Dr. Yi-Hui Wu】	Biodiversity, Population and Community Ecology 【Hosts: Dr. Feng-Chuan Hsu, Dr. Yun Hsiao】	Medical Entomology/ Urban Entomology 【Hosts: Dr. Wu-Chun Tu, Dr. Shu-Ping Tseng】 Ethology, Physiology and Organismic Biology 【Hosts: Dr. Chi-Yun Kuo, Dr. Hui-Yun Tseng】
13:30 – 13:45	Plant Doctor Workshop 【Host: Dr. Shiuh-Feng Shiao】 Panelists: ・Dr. Wen-Hua Chen (Department of Plant Medicine, National Pingtung University of Science and Technology)	**OA01** **Sublethal effects of spirodiclofen on life history traits and population parameters of *Tetranychus urticae* (Acari: Tetranychidae)** **Angela Huang, Ming-Ying Lin**	**OB01** **Using trap nests for bee/wasp survey at Zhuoshui River, Nantou** **Shang Jui Fu, Yun-Ru Chen, Hsiang-Wen Hsieh, Guan-Wei Haung, Hui-Yun Tseng, En Cheng Yang**	**OM01** **Detection of *Anaplasma, Babesia, Ehrlichia,* and *Neoehrlichia* in ticks from small mammals in Kinmen, Taiwan** **Chia-Yi Lin, Tsai-Ying Yen, Yin-Wen Wu, Hsi-Chieh Wang, Kun-Hsien Tsai**

13:45 – 14:00	・Dr. Chang-Hsin Kuo (Department of Plant Medicine, National Chiayi University) ・Dr. Cheng-Kang Tang (Plant Health Care Program, National Chung Hsing University) ・Dr. Shiuh-Feng Shiao (Department of Entomology, National Taiwan University)	**OA02** **Potential of indigenous entomopathogenic nematodes against a Lepidopteran pest of Tomato, *Helicoverpa armigera* (Hübner)** **Yun-Ting Lee, Ching-Tzu Tseng**	**OB02** **Impact of global warming on food resource competition between Formosan and Asian subterranean termites (Blattodea: Rhinotermitidae)** **Shang-En Yang, Hou-Feng Li**	**OM02** **The survey of infestation of *Stomoxys calcitrans* (Diptera: Muscidae) on *Ceratotherium simum* in Taipei Zoo** **Ke-An Hong, Yun-Ling Tsai, Li-Hsin Wu**
14:00 – 14:15		**OA03** **Post-harvest quarantine cold treatment for 'Golden Sweet' and 'Jade Girl' cherry tomatoes infested with fruit flies (Tephritidae)** **Prakriti Regmi, Kao-Wei Lin, Wen-Bin Yeh**	**OB03** **A taxonomic review of Japanese *Aprostocetus* Westwood, 1833 (Hymenoptera: Eulophidae), with notes of potential significance of *Aprostocetus* in evolutionary research** **Miki Hisano, Kazunori Matsuo**	**OU01** **Contact toxicity and repellent effects of clove powder, clove oil, and its major bio-active compounds against destroyer ants, *Trichomyrmex destructor* (Hymenoptera: Formicidae), under laboratory conditions** **Rosy Gurung, Lekhnath Kafle**
14:15 – 14:30		**OA04** **A mass rearing method of *Phaedon brassicae* Baly,1987 (Coleoptera: Chrysomelidae)** **Po-Cheng Lin, Jia-An Chen, Chiao-Yen Chen, Kuo-Hung Chuang, Ya-Ling Chen, Yen-Po Lin**	**OB04** **Predicting the species distribution model of the yellow crazy ant *Anoplolepis gracilipes* in Taiwan using CLIMEX – a predictive model base on soil temperature** **Jheng Dai,Ching-Hong Yeh,Li-Hsin Wu**	**OU02** **A field study on the effects of EM probiotic supplements on honeybee, *Apis mellifera* (Hymenoptera: Apidae), Productivity** **Simran Kayastha, Lekhnath Kafle**
14:30 – 14:45	Ecological Network Workshop: The case of *Formotosena seebohmi* 【Host: Dr. I-Hsin Sung】 Panelists: ・Ms. Yi-Sheng Shih (Chiayi Branch, Forestry and Nature Conservation Agency)	**OA05** **When does pollinator crisis cause plant crisis? A mathematical approach** **Yi-De Lee, Takefumi Nakazawa**	OB05 Studies on the mass rearing requirements for the larval stage of white pupa melon fly strain (*Zeugodacus cucurbitae*) (Diptera: Tephritidae) Chuan-Jie Hong, Ming-Yi Chou, Shaw-Yhi Hwang, Yu-Bing Huang, Chung-Cheng Fanjiang	**OE01** **Chitin as a matrix for the purification of Galectin1-Melittin fusion protein expressed in *Escherichia coli*.** **Yao-Kuang Tseng, Yueh-Lung Wu, Rong-Nan Huang**

14:45 – 15:00	・Mr. Jung-Hsien Weng (Caoshan community development association)	**OA06** **Evaluation of the entomopathogenic fungi for control of *Phyllotretra striolata* (Fabricius) adults** **Chin-Lin Hung, Cheng-Kang Tang, Yi-Yuan Chung**	**OB06** **Acceleration of biological responses in Anthropocene** **Yi-Wen Chen, I-Ching Chen, Malin Pinsky, Jonathan Lenoir**	**OE02** **Investigating physiological mechanisms of sublethal imidacloprid-induced precocious foraging in honey bee workers** **Wan-Yi Chen, En-Cheng Yang**
15:00 – 15:15		**OA07** **Evaluation of control effectiveness of *Metarhizium* sp. MA721 strain against *Tetranychus urticae*** **Min-Jun Huang, Yi-Yuan Chuang**	**OB07** **A study on the effects of organic acids and probiotics supplements on insecticide toxicity in honeybees (*Apis mellifera*)** **Ramita Prajapati, Lekhnath Kafle**	**OE03** **Reproductive castes development of *Prorhinotermes flavus* (Blattodea: Rhinotermitidae)** **Wan-Jen Li, Yi-Ning Chiu, Hou-Feng Li**
15:15 – 16:15	Tea Break (1F) / Poster Time (2F & 3F Gallery)			
Topics	Workshop	Agricultural Entomology 【Hosts: Dr. Ching-Wen Tan, Dr. Yi-Hui Wu】	Systematics, Population Genetics and Evolution 【Hosts: Dr. Cheng-Lung Tsai, Dr. Chia-Hsuan Wei】	Ethology, Physiology and Organismic Biology 【Hosts: Dr. Chi-Yun Kuo, Dr. Hui-Yun Tseng】
16:15 – 16:30	Workshop on Net Zero 【Host: Dr. Wen-Bin Yeh】 Panelists: ・Dr. Jung-Tai Chao (Taiwan Forestry Research Institute, Ministry of Agriculture)	**OA08** **Discussion of trapping effects of different light wavelength against tomato leafminer, *Phthorimaea absoluta* (Lepidoptera:Gelechiidae)** **Ya-Han Hsu, Tsung-Tse Wu, Yi-Yuan Chuang,**	**OS01** **The systematic study of 12 strains of *Metarhizium* (Ascomycota: Sordariomycetes) in Taiwan** **Pei-Jung Lin, Yen-Po Lin and Chang-Hsin Kuo**	**OE04** **Induction of female functional virginity mutations in the wasp *Telenomus remus* by eliminating PI -*Wolbachia*** **I-Chen Tu, Ching-Ting Lai, Li-Hsin Wu**

16:30 – 16:45	・Dr. Hsien-Tzung Shih (Taiwan Agricultural Research Institute, Ministry of Agriculture) ・Dr. Hou-Feng Li (Department of Entomology National Chung Hsing University) ・Dr. Chiao-Ping Wang (Taiwan Forestry Research Institute, Ministry of Agriculture)	**OA09** **Different target-site mutations associated with diamides resistance in *Plutella xylostella* (Lepidoptera: Plutellidae)** **Rameshwor Pudasaini, Cheng Chang, Mu-Hsin Chen, Shu-Mei Dai**	**OS02** **Ecological niches and caste development of *Stylotermes halumicus* (Blattodea: Stylotermitidae)** **Ren-Han Liu, Wei-Ren Liang, Chun-I Chui, Hau-Chuan Liao, Chih-Chuan Lin, Hsin-Ting Yeh, Hou-Feng Li**	**OE05** **Study of key odorant-binding proteins associated with methyl eugenol responsiveness in *Bactrocera dorsalis*** **Wei-Chan Chang, Chun-Hua Hsu, Yen-Ju Lu, Ju-Chun Hsu**
16:45 – 17:00		**OA10** **Regulation of core developmental and virus-replication related genes of *A. cerana* larvae infected with SBVs** **Zih-Ting Chang, Yu-Feng Huang, Tzu-Han Chen, Chung-Yu Ko,Yu-Shin Nai, Yue-Wen Chen**	**OS03** **Using mitogenome reconstructing phylogeny of Taiwan stick insects** **Bo-Cheng Wang, Li-Wei Wu**	**OE06** **Proportional processing of burying beetle host selection in the phoretic mite** **Yi-Ta Wu, Wei-Jiun Lin, Tanmay Dixit, Nicholas Horrocks, Syuan-Jyun Sun**
17:00 – 17:15		**OA11** **Biological factors affecting the acquisition of begomoviruses by *Bemisia tabaci*** **Ya-Yu Huang, Wi-Hau Li, Chi-Wei Tsai**	**OS04** **Discovery of the genus *Pseudalomya* (Hymenoptera: Ichneumonidae: Ichneumoninae) from Taiwan and the implication on its tribal placement** **Hsuan-Pu Chen, Namiki Kikuchi, Shiuh-Feng Shiao**	**OE07** **Comparative genomics of *Purpureocillium lilacinum* NCHU-NPUST-175 and Molecular Marker Development** **Zhi-Yu Yeh, Pei-Hsin Lo, Chuen-Fu Lin, Yu-Shin Nai**
17:15 – 17:30		**OA12** **Whole genomic sequencing and analysis of *Rhagastis binoculata* nucleopolyhedrovirus (NPV) in Taiwan** **Yu-Yun Kuo, Ju-Chun Chang, Yi-Hsuan Li, Yu-Feng Huang, Tzong-Yuan Wu, Yu-Shin Nai**	**OS05** **Diversity of Collembola in Taiwan** **Hsin-Ju Cheng, Frans Janssens, Bruno Bellini, Taizo Nakamori, Chih-Han Chang**	**OE08** **Transcriptome analysis of entomopathogenic fungi, *Beauveria bassiana* infected coffee berry borer Hypothenemus hampei (Ferrari)** **Fang-Min Chang, Yi-Hao Huang, Hsiao-Ling Lu, Yu-Shin Nai**

17:30 – 17:45		OA13 Assessment of the physicochemical characteristics of mealworm (*Tenebrio molitor* L.) larvae frass Bo-Wen Lin, Hao-Wen Duan, Yu-Cheng Lin, Yuh-Jyuan Lee, Shu-Chen Chang, Hsien-Tzung Shih	**OS06** **A taxonomic study of Dacinae fruit flies (Diptera: Tephritidae) of Taiwan with description of male genitalia** **Chien-Yu Huang, Shiuh-Feng Shiao**	**OE09** **Optimal shapes for termite's asymmetric elastic mandibles: 2D geometric models** **Tzu-Chia Liu, Kuan-Chih Kuan, Yi-Yu Wang, Chun-I Chiu, Hou-Feng Li, Kai-Jung Chi**
17:45 – 18:00		OA14 Yellow mealworm added to spent shiitake substrates and rice husk to cultivate lettuce and seedling of strawberry in facilities Yuh-Jyuan Lee, Bo-Wen Lin, Chao+Yi Wang, Hao-Wen Duan, Hsien-Tzung Shih		**OE10** **The effects of *Wolbachia* infection on thermal adaptation in *Telenomus remus*** **Si-Tone Guo, Li-hsin Wu**
Time/Place	Outside of International Networking Academy Building			
18:00 – 20:00	Conference Banquet			

Oct. 22, 2023 (Sun.)

Time/Place	International conference hall			
08:30 – 09:00	Registration (Gate of International Networking Academy Building)			
09:00 – 10:00	Ching-Huan Cheng Agricultural Entomology Research Award Ceremony Keynote Speech: Dr. Yi-Hui Wu Effectiveness of biological control of litchi stink bug and black rice bug【Host: Dr. Shiuh-Feng Shiao】			
10:00 – 10:10	Room Switching			
Time/Place	International conference hall	303 room	205 room	111 room
Topics	Workshop	Agricultural Entomology 【Host: Dr. I-Hsin Sung】	Biodiversity, Population and Community Ecology 【Host: Dr. Sheng-Shan Lu】	Othology, Physiology and Organismic Biology 【Host: Dr. Hou-Feng Li】
10:10 – 10:25	Conversations with Students: Overseas Collaboration and Job Search Experience 【Host: Dr. Hsuan-Wien Chen】 Panelists: ・Dr. Hsuan-Wien Chen (Department of Biological Resources, National Chiayi University) ・Ms. Chien-Yi Wu (Department of Entomology, National Taiwan University) ・Dr. Yu-Zen Huang (Faculty of Social and Cultural Studies, Kyushu University) ・Dr. Chia-Ming Liu (National Agriculture and Food Research Organization)	OA15 Investigation of pest regulation service function of aboriginal tribal crops and the benefit of aboriginal plants to beneficial natural enemies Zhong-Tai Li, Lily Lin, Chih-Ying Yu, Shau-Ching Lin	OB08 Pollinator sex matters in competition and coexistence of co-flowering plants Takefumi Nakazawa, Shigeki Kishi	OE11 A staphylinid parasitoid of a staphylinid termitophile Wei-Ren Liang, Munetoshi Maruyama, Hou-Feng Li
10:25 – 10:40		OA16 Using native natural enemies to control rice black bugs in organic paddy rice Shu-Jen Tsai, Chih-Wei Wang	OB09 Molecular insights into the altitude adaptation of the Asian honey bee: Correlations between gene expression and SNPs Yun-Ru Chen, Shang-Jui Fu, Hsiang-Wen Hsieh, Chih-Wei Tung, Shih-Shun Lin, En-Cheng Yang	OE12 Micro computed tomography in entomological research Hauchuan Liao, Han-Hsiang Tsai, Yu-Hsin Chen, Chia-Chien Wu, Mu-Xuan Chen, Hou-Feng Li

10:40 – 10:55		OA17 Resistance evaluation of acaricides for controlling spider mite on atemoya in Taitung Yu-Tzu Hsu, Zi-Cen Chen	OB10 The pollination network and its temporal dynamic in Taipei Botanical Garden and Zhonghe No. 4 Park Tien Hsieh, Wen-Chi Yeh, Sheng-Shan Lu	OE13 Establishment of serological detection systems for respiratory virus infections using baculovirus surface display technology Chi-Wei Wang, Shiang-En Chen, Zheng-Yu Phan, Chih-Hsuan Tsai
10:55 – 11:10		OA18 Comparison of variation of amino acid profiles of black soldier fly and fishmeal Che-Chun Shih, Po-Lun Chien	OB11 Comparison of larval gut microbiota in Japanese rhinoceros beetle (*Trypoxylus dichotomus*), lesser mealworm (*Alphitobius diaperinus*) and coffee bean weevil (*Araecerus fasciculatus*) larva. Me-Chi Yao, Chien-Yong Yeh, Tai-Chuan Wang, Shu-Chen Chang, Bo-Wen Lin	OE14 Dissecting the developmental expression and evolutionary significance of vasa genes in the parthenogenetic and viviparous pea aphid *Acyrthosiphon pisum* Gee-Way Lin, Chun-Che Chang
11:10 – 11:25		OA19 The attitude of secondary school students towards edible insects and possible influential factors- take Taichung city for example Sing-Shan Wu, Shaw- Yhi Hwang	OB12 Investigation of insecticide resistance in *Spodoptera exigua* on green onion in Taiwan. Husan Shentu, Ming-Yao Chiang, Yu-Bing Huang, Shu-Mei Dai	OE15 Preliminary study of exploration behavior and collective foraging behavior by the marauder ant *Carebara diversa* Yu-Hsuan Yu, Xin-Yi Lin, Yi-Chi Chen, Xin-Zhang Chen, Tzu-Yen Chao, Li-Chuan Lai
11:25 – 11:40		OA20 The effect of environment cooling on the control of beet armyworm (*Spodoptera exigua*) Jyun-Cheng Lin, Lily Lin	OB13 Tiny, numerous and diverse: Taiwanese Leaf Litter Beetles Project has started! Martin Fikáček, Fang-Shuo Hu, Bin-Hong Ho, My-Hanh Le, Jen-Pan Huang	

11:40 – 11:55		OA21 Field trials of spraying fermentation products of *Purpureocillium takamizusanense* TNZZS6 for controlling *Tessaratoma papillosa* Drury with unmanned aerial vehicle Hui-Ting Lin, Ying-Cheng Chen, Hsiao-Han Tsai	OB14 Habitat preference and environmental factors of the biting midge, *Forcipomyia taiwana* Cheng-Hsueh Huang, Tsu-Yu Lin, Chun-Cheng Fan Chiang, Cheng-Lung Tsai, Yi-Pei Luo, Rong-Nan Huang, Mei-Ling Chan	
11:55 – 12:10		OA22 Survey of the soil pests affecting peanuts and the occurrence of Sufetula sp. Chun-Chun Chang, Hung-Yu Dai, Yi-Ju Chen	OB15 Diversity of Ceratopogonidae in the green space of National Museum of Natural Science Tsu-Yu Lin, Cheng-Lung Tsai, Yu-Hsiang Ho, Yi-Pei Luo, Mei-Ling Chan	
12:10 – 13:10	Lunch Break / 12:20-13:10 Annual General Meeting (International conference hall)			
Topics	Workshop	Agricultural Entomology 【Host: Dr. Mei-Er Chen】	Systematics, Population Genetics and Evolution 【Host: Dr. Li-Wei Wu】	Medical Entomology 【Host: Dr. Kun-Hsien Tsai】
13:10 – 13:25	Fostering Taiwan-Japan Collaboration in the Black Soldier Fly Industry 【Host: Dr. Chia-Ming Liu】 Panelists: ・Dr. Cheng-Jen Shih (Department of Entomology, National Taiwan University) ・Dr. Ching-Wen Tan (Department of Entomology, National Chung Hsing University) ・Mr. Meng-Kun Wu (Chairman, Kunyi Biotech INC) ・Mr. Po-Lun Chien (Chairman, InnoRs Biotechnology Co., Ltd.)	OA23 Parasitic preference under different tempertures in an egg parasitoid wasp (Hymenoptera: Scelionidae) of *Scotinophara lurida* Yu-Ching Tsai, Min-Rou Jiang, Yi-Hui Wu	OS07 The gap between systematics achievements and local knowledge dissemination - the important bridging role of taxon vernacular names and promotion strategies Shipher Wu, Hsing-Han Li	OM03 Progress of proposing ecology-based control measure against the stable fly in Japan Kazunori Matsuo, Yu-Zen Huang, Wei-Ren Liang, Miki Hisano, Koshi Asami, Makito Shindo, Yume Kawano, Hirona Nakazato, Yuka Sakai, Haruho Kodama, Tatsuo Fujioka
13:25 – 13:40		OA24 Monitoring on the field sensitivity of whiteflies against registered insecticides in Taiwan Ying-Shiou Lin, Sheng-Tsz Rau	OS08 An undescribed species of Australian gall-inducing soft scale (Hemiptera: Coccidae) Michael Gorton, Yen-Po Lin, Penny J. Gullan	OM04 Survey of the sand fly population in the urban city of Taipei Botanical Garden Yu-Feng Tsai, Shiuh-Feng Shiao, Kun-Hsien Tsai

13:40 – 13:55	・Prof. Masami Shimoda (Graduate School of Agricultural and Life Sciences, The University of Tokyo) ・Mr. Hiroto Oki (Graduate School of Agricultural and Life Sciences, The University of Tokyo) ・Dr. Tetsuya Kobayashi (Institute of Agrobiological Sciences, National Agriculture and Food Research Organization) ・Dr. Takeda Koji (Institute of Agrobiological Sciences, National Agriculture and Food Research Organization)	OA25 Exploring the correlation between indicator organism populations and environmental factors in an agricultural long-term ecological station: a case study of *Cheilomenes sexmaculata* Wan-Hsiu Yang, Yaw-Jen Dong, Pei-Chen Hsu, Hsien-Tzung Shih	OS09 A two-decade mystery of stick insects – What is the identity of the genus *Hemiplasta* (Phasmatodea: Lonchodidae: Necrosciinae) in Taiwan? Shu-Ming Chang, Shiuh-Feng Shiao	OM05 Investigation of *Wolbachia* infection in vector mosquitoes in Taiwan and assessment of its impact on arthropod viruses Shiu-Ling Chen, Han-Hsuan Chung, Hwa-Jen Teng
13:55 – 14:10		OA26 Establishment of high potential entomopathogenic fungi selection markers by aligning phenotype and gene expression levels Nian-tong Ni, Yu-Shin Nai		
14:10 – 14:25		OA27 Application of the new wasp ball for releasing *Trichogramma* wasps to control the fall armyworm in the corn field Chia-Hung Hsieh, Kuang-Hua Chang, Li Lin, Dong-Jhen Guo, Yu-Hsiang Chuang		
14:25 – 14:45	Tea Break (1F)			

Time/Place	International conference hall
14:45 – 15:45	Keynote Speech: Dr. Cheng-Jen Shih The contributions and applications of insect in carbon net zero 【Host: Dr. Rong-Nan Huang】
15:45 – 16:45	Keynote Speech: Dr. I-Ching Chen Taiwan's perspective and social adaptation to global biodiversity changes 【Host: Dr. Hsiao-Ling Lu】
16:45 – 17:25	Award Ceremony & Farewell / Raffle

壁報展示總表 Poster List

農業昆蟲學 【評審: 林彥伯博士、曾慶慈博士】

Agricultural Entomology 【Judges: Dr. Yen-Po Lin, Dr. Ching-Tzu Tseng】

編碼 Code	論文標題 Title	作者 Authors
PA01	**The role of new invasive plants as alternative hosts for *Phthorimaea absoluta* (Lepidoptera: Gelechiidae) and the implication for tomato pest management**	**Manupa Pabasara Wickramasinghe, Shen-Horn Yen**
PA02	**利用機器模擬熊蜂振動評估番茄授粉效能** **Assessment of tomato pollination efficiency through machine-mimicked bumblebee vibrations**	**郭耘、曾惠芸** **Yun Kuo, Hui-Yun Tseng**
PA03	**馬尼拉小繭蜂病毒中 microRNA 調節影響斜紋夜蛾胰島素脂肪代謝途徑** **S*nellenius manila* bracovirus microRNAs regulate insulin lipid metabolism pathways in *Spodoptera litura***	**蘇榆娟、林鈺淳、吳岳隆** **Yu-Juan Su,Yu-Chun Lin,Yueh-Lung Wu**
PA04	研製海藻酸鈉凝膠餌劑應用於長腳捷蟻防治 Development of alginate hydrogel baits for management of *Anoplolepis gracilipes*	呂明益、林宗岐 Ming-Yi Lu, Chung-Chi Lin
PA05	11 種殺蟎劑對鳳梨釋迦二點葉蟎毒性測試 Toxicity of 11 acaricides for *Tetranychus urticae* on atemoya	許育慈、陳姿岑 Yu-Tzu Hsu, Zi-Cen Chen
PA06	實驗室飼育顯示紫背草為秋行軍蟲的潛在替代性寄主植物（鱗翅目：夜蛾科） Laboratory rearing reveals red tasselflowers as a potential alternative host plant of fall armyworms (Lepidoptera: Noctuidae)	蕭昀、許峰銓、謝侑廷、林暐鈞、黃薰逸、何傳愷 Yun Hsiao, Feng-Chuan Hsu, You-Ting Hsieh, Wei-Jiun Lin, Xun-Yi Huang, Chuan-Kai Ho
PA07	台灣野生與栽培種大豆對嚙食性害蟲之轉錄體分析與相關化學防禦代謝物分析 Transcriptome and metabolome analyses to study the defense mechanisms of Taiwan soybean plants against chewing herbivore	張淵云、林禎祥、陳賢明 Yuan-Yun Zhang, Chen-Hsiang Lin, Hieng-Ming Ting
PA08	免耕與耕犁下玉米田地表節肢動物相差異 Differences in arthropod assemblages and insect pest occurrence between no-tillage and Plowed corn fields	董耀仁、楊婉秀、許北辰 Yaw Jen Dong, Wan-Hsiu Yang and Pei-Chen Hsu
PA09	豆科雜糧小型害蟲相初步調查 Preliminary surveillance of small pests in upland legume crops	陳怡如、張淳淳、陳泓銘、戴宏宇 Yi-Ju Chen, Jen-Pan Huang, Hong-Ming Chen, Hui-Yun Tseng
PA10	東方蜂微粒子於精選熊蜂腸道的滯留與取食反應 The retention of *Nosema ceranae* in the intestines and feeding response on *Bombus eximius*	黃英泓、宋一鑫 Ying-Hong Huang, I-Hsin Sung
PA11	無人植保機噴灑不同劑型農藥之霧滴分布情形 Droplets distribution of different pesticide formulations by unmanned aerial vehicle	陳盈丞、黃美靜 Ying-Cheng Chen, Mei-Jing Huang

PA12	評估殺蟲劑與蟲生真菌對檬果褐葉蟬藥效試驗初探 Evaluation of efficacies of insecticides and entomogenous fungi against mango leafhoppers (*Idioscopus nitidulus* (Walker))	陳盈丞`蔡翰沅 Ying-Cheng Chen, Han-Yuan Tsai
PA13	檳榔蟲害安全用藥暨農藥減量示範 Demonstration of safe use of pesticides for Areca nut pests and pesticides reduction	陳盈丞、林宇盛 Ying-Cheng Chen, Yu-Sheng Lin
PA14	Molecular identification of a microsporidia from cucumber moth, *Diaphania indica* (Saunders)	Yu-Yun Kuo, Chun-Yan Lee, Yu-Shin Nai
PA15	**Oviposition preferences of the fall armyworm (*Spodoptera frugiperda*) in response to various potential push and pull plants, in Taiwan**	**Kervin Can, Tsui-Ying Chang, Lekhnath Kafle, Wen-Hua Chen**

生物多樣性、族群與群聚生態學 【評審: 孫烜駿博士、邱名鍾博士】

Biodiversity, Population and Community Ecology 【Judges: Dr. Syuan-Jyun Sun, Dr. Ming-Chung Chiu】

編碼 Code	論文標題 Title	作者 Authors
PB01	**臺灣櫻花鉤吻鮭大型水棲昆蟲食餌攝入塑膠微粒** **Microplastic ingestion in large aquatic insect prey of Taiwan salmon *Oncorhynchus masou formosanus***	**吳友誠、陳昭汝、丘明智、郭美華** **Yu-Cheng Wu ，Zhao-Ru Chen，Ming-Chih Chiu，Mei-Hwa Kuo**
PB03	**白足扁琉璃蟻族群結構與環境降雨量之關係** **The relationship between the *Technomyrmex albipes* colony and the environmental precipitation**	**翟珈葳、宋秉叡、林宗岐** **Chia-Wei Chai, Ping-Jui Sung, Chung-Chi Lin**
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行為、生理、個體生物學　　【評審: 吳立心博士、鄭任鈞博士】

Ethology, Physiology and Organismic Biology　　【Judges: Dr. Li-Hsin Wu, Dr. Ren-Chung Cheng】

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昆蟲作為人類食品與動物飼料原料及其他新穎性終端產品之永續發展
Sustainable development of insects as raw materials for human food, animal feed, and other novel end products

林柏文[1]、張淑貞[1]、王泰權[2]、林盈甄[1]、楊文欽[3]、李啟陽[1]、李裕娟[1]、蔡淑珍[1]、林宗俊[1]、李瑋崧[1]、李雅琳[1]、江秀娥[1]、姚美吉[1]、許北辰[1]、董耀仁[1]、陳昌岑[1]、余祥萱[1]、石憲宗[1]*
Bo-Wen Lin[1], Shu-Chen Chang[1], Tai-Chuan Wang[2], Ying-Chen Lin[1], Wen-Chin *Yang*[3], Chi-Yang Lee[1], Yuh-Jyuan Lee[1], Shwu-Jene Tsai[1], Tsung-Chun Lin[1], Wei-Sung Li[1], Ya-Lin Lee[1], Hsiu-E Chiang[1], Me-Chi Yao[1], Pei-Chen Hsu[1], Yaw-Jen Dong[1], Chang-Tsern Chen[1], Shiang-Shiuan Yu[1], Hsien-Tzung Shih[1]*
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Background

Facing major challenges such as global climate change, population growth, limited agricultural land, unbalanced use of natural biological resources, changes in food consumption patterns, and environmental sustainability, countries need innovative and compatible solutions to echo the resolution “shift the world onto a sustainable and resilient path” and its 17 sustainable development goals (SDGs) adopted by the General Assembly of the United Nations in September 2015. Among them, insects can potentially serve as human food and animal feed in achieving SDGs, such as eradicating poverty and hunger, achieving food security, and ensuring sustainable consumption and production patterns.

Applications

This keynote address mainly shares the challenges and trends of global consumers' acceptance of edible insects and the know-how of developing an insect farming and application industry that can fulfill environmental sustainability and meet production costs and food security. To reach this goal, the following guidelines and approaches are addressed: planning industry-scale production based on the end application, developing appropriate policy supporting tools, regulatory measures for each branch of the industry chain and corresponding competent authorities, developing friendly regulations that are in line with international standards, venture capital coaching mechanisms, and organization of cross-domain research alliances, etc. The speech also cites the relevant regulations, development status, and trends that the EU and other countries have formulated in recent years regarding insects as human food or farmed animal feed ingredients that provide some foundations for Taiwan to establish emerging industries that are both economically competitive and sustainably attainable.

關鍵字(Keywords): 昆蟲 (insect)、人類食品 (human food)、動物飼料(animal feed)、永續發展目標 (sustainable development goals, SDGs)

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氣候變遷下的挑戰：以地區性適應的觀點開創昆蟲保育新視角

Climate Change Challenges: Redefining Insect Conservation through the Lens of Local Adaptation

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氣候變遷對許多生物的生態與適存度來顯著衝擊。為精確估算物種面對氣候變遷的脆弱度，須深究其在異質環境中的生理特質變化。然而，對於決定族群分佈的核心功能性狀以及背後的機制—是否為生理可塑性或是地區性適應—的認知，目前尚顯不足。我們的研究以分佈於亞洲，包含中國、日本與台灣的尼泊爾埋葬蟲 *Nicrophorus nepalensis* 為研究對象。發現於不同海拔和緯度的山區存在特定的溫度環境，在此情境下，兩大功能性狀—熱耐受度及繁殖光週期—彼此互動，進一步影響其繁殖節律。值得注意的是，雖然不同山區的族群在熱耐受度上展現相似性，但其繁殖光週期則有所差異。經由共同花園和互換移植實驗，確定該繁殖光週期性乃是基於地區性適應，而非單純的生理可塑性。我們的結果顯示，處於台灣中海拔且全年繁殖的族群於氣候暖化之下，可能面臨更大的適存壓力。因當此甲蟲於暖和環境下進行繁殖時，其原有的繁殖策略可能不再合適，導致族群容易受氣候變遷的衝擊。藉由深入探討物種的不同族群的功能性狀與其在各式環境中的地區性適應，我們得以更確切地估算氣候變遷對於生物的衝擊，並為昆蟲保育策略帶來新的啟示。

關鍵字(Keywords)：Local adaptation, burying beetles, species vulnerability

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荔枝椿象與稻黑椿象生物防治之成效

Effectiveness of biological control of litchi stink bug and black rice bug

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荔枝椿象 (*Tessaratoma papillosa*) 為臺灣入侵害蟲，危害農作物荔枝、龍眼，與原生樹種臺灣欒樹、無患子，且因受擾動時會分泌腐蝕性液體，對農民收成與一般民眾皆造成困擾。利用荔枝椿象卵寄生蜂平腹小蜂 (*Anastatus japonicus*) 進行卵期防治，可釋放於有機園、荒廢園或無法用藥之區域。目前完成建立平腹小蜂量產技術，並在商品儲存以低溫處理替代寄主與寄生完成的平腹小蜂，皆可有 5 個月的儲存期，除可進行提早生產，以供應足夠的田間釋放量，並增加出貨時間彈性；目前田間釋放可到達區域以盒裝釋放成蟲或吊掛卵片，無法到達之偏遠山區以無人機釋放卵片；於荔枝椿象交尾時開始釋放平腹小蜂，每次釋放 14,000 隻，10-14 天釋放一次，連續 4 次；在田間同時期調查有釋放平腹小蜂的 2 樣 區卵粒防治率可達 84%與 87%，無釋放樣區為 15%，經逐年釋放小蜂之樣區，荔枝椿象數量明顯降低。

稻黑椿象 (*Scotinophara lurida*) 為日治時期水稻五大害蟲之一，因藥劑的使用後轉為潛在害蟲，但於 110 年起造成臺東關山 100 公頃有機水稻田嚴重損失；臺東區農業改良場於 111 年採集田間黑卵蜂 (*Telenomus* sp.) 交由苗改場建立量產技術，於 112 年第一期稻作稻黑椿象產卵期 3 月中旬至 5 月初，每週進行大量釋放成蜂，共釋放 80 萬隻黑卵蜂，卵粒防治率可達 80%以上，與黑殭菌共同搭配使用下，已恢復過往收成數量。

關鍵字(Keywords)：生物防治 (biological control)、荔枝椿象 (*Tessaratoma papillosa*)、稻黑椿象 (*Scotinophara lurida*)、平腹小蜂 (*Anastatus japonicus*)、黑卵蜂 (*Telenomus* sp.)

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昆蟲在低碳淨零之貢獻與利用

The contributions and applications of insect in carbon net zero

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昆蟲，尤其是腐食性昆蟲，因低碳淨零的議題，越凸顯其應用價值。腐食性昆蟲的特殊食性，使其同時具有分解者與消費者的功能。他們能快速且大量取食動植物屍體（有機廢棄物），扮演清道夫及資源回收的角色。長大後的蟲體，可供其他消費者取食，是生態循環和循環經濟重要的一環。有機廢棄物經過生物轉換後，合成昆蟲蛋白質、脂肪、碳水化合物、幾丁質、礦物質等，將碳和能量儲存在蟲體內，再供其他動物取食，經由食物鏈，進入生態圈，形成龐大碳匯。近年來，有關黑水虻的研究噴出，主要在有機廢棄物處理，用以取代傳統堆肥、掩埋、焚化等方法，從而減少溫室氣體排放。長大的幼蟲可以萃取生質柴油，蟲乾作為飼料，用昆蟲蛋白取代魚粉和大豆蛋白，減少海洋捕撈或陸地濫墾造成的生態破壞和碳足跡的累積。蟲糞作為有機肥料，除了提供氮磷鉀肥料外，蟲蛻的幾丁質可以防治土壤線蟲並促進根部益生菌的增生，誘導植物產生抗性，減少病蟲害。在當前全球暖化、原物料短缺、永續能源開發等日益惡化的大環境下，昆蟲正以其獨特的生活習性，顯露其價值，是當前低碳淨零揭櫫的『以自然為本的解決方案』中，最具發展潛力的方法之一，值得我們近一步研究與開發應用。

關鍵字：腐食性昆蟲、黑水虻、低碳淨零、循環經濟、有機廢棄物處理

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全球生物多樣性變遷之台灣觀點與社會適應
Taiwan's Perspective and Social Adaptation to Global Biodiversity Changes.

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The 'insect apocalypse' debate has raged over the past five years, including significant geographical and taxonomic disparities and challenges in attributing causes. Most research has focused on temperate regions, leaving tropical, high-biodiversity areas underrepresented. However, many studies suggest that tropical fauna with narrower climate niches may be more vulnerable to climate change. Here, we applied one of the most comprehensive butterfly monitoring programs in the world's low-latitude regions in Taiwan, filling this significant knowledge gap. Spanning nearly three decades (1994-2021), the program collected 282 butterfly species, documenting over 50,000 individual specimens and providing insights into changes in butterfly diversity, community, and the impacts of climate and land use. Surprisingly, in the face of diverse environmental changes, butterfly diversity, biomass, and abundance seem to be increasing, mainly due to shifting temperatures aligning with the optimum for most species. The observed range shifts and community reshuffling display a clear climate fingerprint, with species moving toward higher latitudes and lower altitudes and communities showing a trend toward thermophilization. While species adapt to climate change in specific ways, the trait hypervolume leans towards smaller sizes and those adapted to disturbed habitats. The overall trait space is reduced by nearly a third, suggesting potential changes in ecological function. This research presents a different narrative of biodiversity change but is consistent with global findings of widespread species shifts in response to climate changes. The goal of preserving species compositions seems increasingly misaligned with conservation needs. In the Anthropocene, conservation strategies should consider "managing change," necessitating robust societal engagement, a shift in mindset, and effective monitoring systems.

Keywords：Insect apocalypse, climate niche, thermophilization, trait hypervolume, conservation

論文宣讀: 農業昆蟲學
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OA01

Sublethal effects of spirodiclofen on life history traits and population parameters of *Tetranychus urticae* (Acari: Tetranychidae)

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背景/研究問題/材料方法

Effects on individuals or populations that are biological, physiological, demographic, or behavioral that persist after exposure to a toxin at a sublethal dose or concentration are referred to as sublethal effects. When no apparent mortality is caused in the experimental population, a dose or concentration is considered sublethal. Pesticide doses and concentrations below the median lethal (LD_{50}/LC_{50}) level are typically regarded as sublethal. Alterations in life expectancy, development rates, population growth, fertility, behavior, feeding, oviposition, etc., may be manifestations of sublethal effects. In several insect orders, sublethal effects were noted on biological, physiological, and behavioral aspects; these effects may or may not cause issues with pest control. *Tetranychus urticae* is an agricultural pest mite with global distribution, a high level of pesticide resistance, and a wide range of host plants. The sublethal effects of spirodiclofen on *T. urticae* were investigated by treating protonymphs.

結果/結論/應用啟示

The results showed that the oviposition days were decreased by treatment with LC_{10} and LC_{30} of spirodiclofen. Furthermore, the transgenerational effects of spirodiclofen decreased the intrinsic rate of increase (r), finite rate of increase (λ), net reproductive rate (R_0), and survival rate of the next generation produced by females exposed to sublethal concentrations. Additionally, the mean generation time (T) and developmental time were increased. According to the findings, *T. urticae* may develop more slowly under sublethal concentrations of spirodiclofen, and the pest population is unlikely to rebound as a result. It may therefore be slightly helpful in the integrated pest management. The study of sublethal effects on pests is critical and must be taken into account when determining the total effect of a toxicant.

關鍵詞(Keywords)：*Tetranychus urticae*, spirodiclofen, sublethal effect, population parameters, life tabl

OA02

本土產蟲生線蟲於番茄防治番茄夜蛾 Helicoverpa armigera (Hübner)之潛力評估

Potential of indigenous entomopathogenic mematodes against a Lepidopteran pest of tomato, Helicoverpa armigera (Hübner)

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背景/研究問題/材料方法

番茄夜蛾 *Helicoverpa armigera* (Hübner) 為番茄上之主要大型鱗翅目害蟲，其幼蟲破壞性強，除啃食植株幼嫩部外，亦蛀食或鑽入果實；且幼蟲具自相殘殺習性，多為一蟲一果，易使作物失去商品價值，導致嚴重經濟損失。目前田間仍以化學農藥為主要防治方式，然番茄夜蛾已對多種作用機制之化學藥劑產生抗藥性。為因應農藥十年減半政策及全球環境友善趨勢，故以生物防治面探究本議題，而蟲生線蟲為一種蟲生病原，其特色為侵染期幼蟲 (Infective juvenile, IJ) 具尋找寄主之能力，並自昆蟲之口、氣孔、肛門等自然開口侵入，後於寄主血體腔中釋放體內之共生細菌，最終導致害蟲死亡，故具潛力防治鑽食入果之番茄夜蛾。本試驗從行為、致病力等方面探討本土產蟲生線蟲 *Steinernema taiwanensis* 與 *Oscheius sp.*對番茄夜蛾之防治潛力。

結果/結論/應用啟示

行為試驗分別測試兩種線蟲對番茄夜蛾活體與屍體之反應，*S. taiwanensis* 多往活體之番茄夜蛾移行；而 *Oscheius sp.* 則無固定之移行方向。致病力試驗則以 25、50、75 IJs/ml 之 *S. taiwanensis* 與 *Oscheius sp.* 線蟲懸浮液接種番茄夜蛾五齡幼蟲，結果顯示以 *S. taiwanensis* 處理之幼蟲於接種後 72 小時之死亡率皆高於 50%，且於 50、75 IJs/ml 濃度之幼蟲死亡率分別為 80%、92%；而 *Oscheius sp.* 處理之幼蟲死亡率於 72 小時後皆低於 50%。上述結果顯示 *S. taiwanensis* 對番茄夜蛾較具防治潛力，但其於田間之應用策略仍需進一步之研究。

關鍵詞(Keywords)：蟲生線蟲 (entomopathogenic nematodes)、番茄夜蛾(*Helicoverpa armigera*, *Steinernema taiwanensis*)

OA03

Post-harvest quarantine cold treatment for ‘Golden Sweet’ and ‘Jade Girl’ cherry tomatoes infested with fruit flies (Tephritidae)

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背景/研究問題/材料方法

Cherry tomatoes (*Solanum Lycopersicum* var. *cerasiforme*) serve as host plants for fruit fly species commonly found in Taiwan such as the oriental fruit fly (*Bactrocera dorsalis*), melon fly (*Zeugodacus cucurbitae*), and pumpkin fruit fly (*Zeugodacus tau*). These quarantine pests pose a threat to cherry tomatoes, limiting their export from Taiwan to other countries that are pest-free. Therefore, phytosanitary treatment is necessary before cherry tomatoes are exported. Different numbers of eggs of fruit flies per tomato were inoculated to observe the optimum inoculated egg number. The life cycle of fruit flies inside cherry tomatoes was observed for up to 10 days to find the growing time required for the development stages of fruit flies. The most cold-resistant developmental stages of the fruit fly were observed at 1.5-2 °C for up to 9 days. Small-scale and large-scale tests were performed at 1-1.5 °C for 15 days to obtain 100% mortality of fruit flies. Sensory evaluation and fruit quality of cherry tomatoes were measured in terms of peel color, firmness, and Brix.

結果/結論/應用啟示

The optimum inoculated number of eggs per cherry tomatoes was 10. Larvae of Melon fly in the third instar were the most cold-resistant. In 15 days, 1-1.5 °C provided complete disinfestation, resulting in a 100% mortality rate of fruit flies within cherry tomatoes. The cold treatment has a minor impact on the quality of the cherry tomatoes, though it is acceptable for market accessibility. The post-harvest cold disinfestation treatment proposed in this study serves as a standard quarantine protocol for the export of cherry tomatoes.

關鍵詞(Keywords)：cherry tomatoes, cold treatment, oriental fruit fly, melon fly, pumpkin fruit fly

OA04

小猿葉蟲 (*Phaedon brassicae* Baly,1987) (Coleoptera: Chrysomelidae) 室內大量飼育流程建立

A mass rearing method of *Phaedon brassicae* Baly,1987 (Coleoptera: Chrysomelidae)

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背景/研究問題/材料方法

小猿葉蟲為目前臺灣北部有機栽培十字花科 (Brassicaceae) 蔬菜田區重要害蟲，其成、幼蟲均啃食葉片呈穿孔破碎狀，影響作物商品價值甚鉅。此害蟲於土層化蛹，並以成蟲越夏，入秋後至隔年夏季前氣溫較低時好發，連續種植十字花科蔬菜田區常遭其危害，經濟重要性僅次於同科之黃條葉蚤 (*Phyllotreta striolata* Fabricius, 1801)。本研究欲建立小猿葉蟲室內大量飼育方法，期能穩定獲得足量蟲體供後續實驗所用。故從飼養蟲箱改良、食草育苗步驟及蟲源分區繼代等建構飼育流程，並以 30 隻成蟲接種 3 日之條件，計算每飼養蟲箱可獲得之幼蟲及成蟲總數，試驗共 3 重覆，每重覆 3 至 5 箱。

結果/結論/應用啟示

飼養蟲箱以 30×30×30 cm 壓克力箱進行設計，於箱體 3 面切割直徑 11 cm 圓形洞口，其上可更換 100 目鐵網或絹網調整內部濕度。利用 3 寸盆種植十字花科蔬菜，介質為 BVB 培養土混合珍珠石 (5:1)，每盆灑 0.08 g 種子，以細粒赤玉土覆土，再從底部給水並置於 25℃、80% RH 及 12 小時光照生長箱中，取 10 至 14 日齡菜苗供飼。蟲源分為成蟲 (長期蟲源) 及繼代區 (實驗材料)，以 30 隻成蟲接種 3 日之 3 次試驗結果顯示，每蟲箱幼蟲平均有 418 ± 126.7、351.4 ± 91.0 及 318.4 ± 98.7 隻；成蟲則平均有 138.3 ± 59.2、157.3 ± 25.4 與 165.3 ± 29.5 隻。未來將利用兩性生命表程式取得幼蟲齡別分化、成蟲壽命及繁殖力等資訊，以改善飼育條件，並做為小猿葉蟲綜合管理之參考。

關鍵詞(Keywords)：小猿葉蟲(*Phaedon brassicae* Baly,1987)、十字花科(Brassicaceae)、金花蟲科(Chrysomelidae)

OA05

使用數學方法，探究授粉昆蟲減少導致植物豐度下降之情形
When does pollinator crisis cause plant crisis? A mathematical approach

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背景/研究問題/材料方法

Loss of insect pollinators, known as the pollinator crisis, has raised serious concerns over biodiversity decline and food security. One of the stressors on pollinators is the pesticide usage, which is targeted at herbivorous pests but can also decrease pollinators. Considering that most pollinators are antagonistic herbivores at the juvenile stage, the long-term relation between pollinator crisis and plant abundance remain unclear and can be complicated. Specifically, the loss of adult pollinators may benefit plants due to a decrease in herbivorous juveniles, while pest control may reduce plant abundance because of less maturation, eventually leading to plant crisis. Here, we aim to theoretically investigate whether and under what conditions pollinator crisis can bring about plant crisis. We develop a model including functional groups of plant and pollinator, where pollinator has an herbivorous juvenile and a mutualistic adult stage. We then access the long-term effects of stage-specific death rates on plant abundance.

結果/結論/應用啟示

Our results offer a novel insight into the relation between pollinator crisis and plant crisis. Decline of pollinator can give rise to plant reduction, where pollinator and plant abundance show positive correlations. However, excessive pollinators suppress plants, in which pollinator crisis is beneficial. This study represents an initial step toward a better understanding of the impact of pollinator crisis, providing a more general perspective on biodiversity conservation and agricultural management.

關鍵詞(Keywords)：授粉者危機(pollinator crisis)、族群動態模型(population dynamics model)、層級結構(stage structure)、拮抗—互利共生耦合(antagonism-mutualism coupling)、混合族群動態(hybrid community dynamics)

OA06

蟲生真菌對黃條葉蚤成蟲的防治效果評估

Evaluation of the entomopathogenic fungi for control of *Phyllotretra striolata* (Fabricius) adults

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背景/研究問題/材料方法

黃條葉蚤為鞘翅目金花蟲科 (Chrysomelidae) 葉蚤屬的昆蟲，以十字花科 (Brassicaceae) 植物為寄主植物。台灣十字花科作物在2022年的總收量超過70萬公頓，種植面積超過20萬公頃。因成蟲與幼蟲皆會取食植株，而造成作物生產上嚴重的的經濟損失。慣行農法上目前多以化學農藥做為防治手段，而在高度依賴化學農藥的情況下，害蟲抗藥性的風險也隨之上升，同時容易造成環境汙染的問題。因此本研究應用自然界昆蟲病原的蟲生真菌，進行防治效果的初步試驗與評估。多種蟲生真菌菌株自土壤與感病蟲體分離並純化培養後，以0.05% Tween 80水溶液配置孢子懸浮液 (1×10^8 conidia/ml)，於高相對濕度環境下，分別接種於成蟲後，連續記錄7日的累積死亡率進行分析評估，再進一步分別以防治效果較佳的菌株進行不同濃度的致死試驗，評估其防治應用的潛力。此外，也對菌株進行形態與分子生物的鑑定，有助於未來研究方面與應用的延伸。

結果/結論/應用啟示

結果顯示在9個分離菌株的初步篩選後，以MA624與CCC901等二種菌株對黃條葉蚤成蟲之校正累積死亡率最高，分別達到90.0±2.8及76.8±8.3%；分別在此兩種菌株不同的濃度的試驗當中，皆以最高濃度 (1×10^8 conidia/ml) 的校正累積死亡率為最高，分別可達到100.0及82.7±6.9%，與其他孢子濃度間呈顯著差異。菌株的形態與分子生物的鑑定結果，顯示此二菌株皆為黑殭菌 (*Metarhizium anisopliae* (Metsch.))。相關實驗結果，顯示此二菌株對防治黃條葉蚤具發展潛能。

關鍵詞(Keywords)：黃條葉蚤 (*Phyllotreta striolata*)、蟲生真菌(entomopathogenic fungi)、黑殭菌(*Metarhizium anisopliae*)、生物防治(biological control)、十字花科(Brassicaceae)

OA07

黑殭菌 MA721 菌株對二點葉蟎防治效果評估

Evaluation of control effectiveness of *Metarhizium* sp. MA721 strain against *Tetranychus urticae*

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背景/研究問題/材料方法

二點葉蟎 (*Tetranychus urticae*) 為一全球性之農業重要有害生物，寄主植物範圍極廣，可危害多種農作物。而因其體型小、生活週期短、繁殖力強等特點，時常造成嚴重的農業損失，並易對農藥產生抗藥性，使後續防治難度增加。本試驗先於實驗室內篩選出對二點葉蟎雌成蟎具有高致病力的菌株後，再測試其在不同濃度的孢子懸浮液下分別對雌成蟎及卵的感染能力，以評估此菌株後續應用於微生物防治此害物之潛力。

結果/結論/應用啟示

在室內進行 6 個菌株對二點葉蟎的致病力篩選試驗後，顯示黑殭菌 MA721 菌株之半致死時間 (Lethal time of 50%, LT_{50}) 最短，為 2.9 天，因此後續試驗選擇使用菌株 MA721 作為實驗材料。此菌株在不同濃度的孢子懸浮液對雌成蟎之致病力測試中，三種濃度 1 × 10^6、1 × 10^7 與 1 × 10^8 conidia/mL 施用 4 天後，顯示對雌成蟎之校正死亡率分別為 42.4 ± 4.5、98.7 ± 0.6 與 100%。另外，將不同濃度的孢子懸浮液直接噴施在二點葉蟎產卵的葉片上，7 日後統計卵的孵化率，顯示在三種孢子濃度由低至高分別為 88.4 ± 7.0、60.7 ± 8.9 與 22.4 ± 9.2%，而對照組之孵化率為 100%。由上述實驗結果顯示黑殭菌 MA721 菌株對二點葉蟎之雌成蟎具有高致病力，且對卵亦具有抑制孵化之能力，未來將進一步進行田間試驗探討其作為微生物防治資材之可行性。

關鍵詞(Keywords)：二點葉蟎(*Tetranychus urticae*)、蟲生真菌 (entomopathogenic fungus)、微生物防治(microbial control)

OA08

光波長對番茄潛璇蛾 Phthorimaea absoluta 誘捕效果探討

Discussion of trapping effects of different light wavelength against tomato leafminer, *Phthorimaea absoluta* (Lepidoptera:Gelechiidae)

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背景/研究問題/材料方法

近年入侵台灣的番茄潛旋蛾(*Phthorimaea absoluta* Meyrick)為全球番茄產業的重要害蟲之一，潛旋蛾幼蟲會潛入植體葉肉組織取食，在葉片上形成大面積窗格狀潛痕，防治不當可導致茄科作物產量的嚴重損失。本研究探討不同波長之 LED 燈管對於番茄潛旋蛾的誘捕效果，供試 LED 燈管波長分別為 365-380、380-400、400-420、420-430、440-460 及 465-475 nm 等共六組。田間試驗分別在南投縣仁愛鄉有機及慣行栽培番茄的網室中進行，分別於各網室中央間隔等距設置六組燈光誘捕器，將燈光誘捕器的黏蟲紙攜回實驗室，將誘捕之樣本以 10％氫氧化鈉進行透化處理，鑑定捕獲此蛾之性別及數量，並進行數據分析。結果/結論/應用啟示連續進行 6 週誘捕試驗後，將試驗數據換算為誘捕率再進行統計分析，在有機網室試驗中以波長 380-400 及 400-420 nm 二種處理組的誘捕效果最佳，平均誘捕率分別為 36.7±7.4 及 41.8±2.8%，和其他波長處理組均呈顯著差異，且對雌蛾的誘捕效果亦以此二種波長效果較佳。在慣行網室試驗中以波長 400-420 nm 處理組誘捕率為 50.5±5.5%最佳，與其他波長處理組均呈顯著差異。依據初步試驗結果，顯示波長 400-420 nm 的燈光誘捕裝置對番茄潛旋蛾具備較佳誘捕效果，相關結果可供田間防治應用參考。

關鍵詞(Keywords)：番茄潛旋蛾(*Phorimaea absoluta*)、燈光陷阱(light trap)、波長(wavelength)

OA09

Different target-site mutations associated with diamides resistance in *Plutella xylostella* (Lepidoptera: Plutellidae)

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背景/研究問題/材料方法

The diamondback moth, *Plutella xylostella* (Linnaeus) (Lepidoptera: Plutellidae), is a notorious pest of cruciferous crops globally in terms of damages and insecticide resistance development. Seven field populations of *P. xylostella* were collected, and a susceptible strain named SH_{ggt} was selected against chlorantraniliprole and tetraniliprole to obtain CHL~sel ~and TET~sel ~strains, respectively under laboratory conditions. After resistance development, both the lab-selected strains and a field population were reared without exposure to insecticides to analyze the decline of resistance and mutation frequencies.

結果/結論/應用啟示

The field-collected populations exhibited low to high levels of resistance to chlorantraniliprole and tetraniliprole. Similarly, continuous selection to 30 generations resulted in the development of the RRs 7,073.2 and 6,971.0 for CHL_{sel} and TET_{sel} strains, respectively. Of the five mutations in *P. xylostella* ryanodine receptor (PxRyR) that were investigated, I4790K and G4946E were detected in field populations, and only I4790K was found in both lab-selected strains. *P. xylostella* populations reared without exposure to insecticide resulted in a decline in RRs and mutation frequencies sharply. These results may indicate the potential correlation between diamide used history and target-site (PxRyR) mutations. These findings will be valuable for implementing effective diamide resistance management for *P. xylostella* and other insects in the field.

關鍵詞(Keywords)：*Plutella xylostella*, diamide insecticides, ryanodine receptor, target-site mutation

OA10

感染 SBV 的東方蜂幼蟲之發育與病毒複製相關的關鍵基因調控

Regulation of core developmental and virus-replication related genes of *A. cerana* larvae infected with SBVs

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背景/研究問題/材料方法

Virus infection causes significant damage to bees and bee industry, including sacbrood virus (SBV). Asian honey bees (*Apis cerana*) are sensitive to SBV and dying in large numbers when infected, while SBV rarely poses a fatal threat to European honey bees (*Apis mellifera*) colonies. SBV infect *A. mellifera* (a.k.a. AmSBV-AM) and *A. cerana* (a.k.a. AcSBV-AC), primarily affecting the brood of honey bees and resulting in larval death. Cross-infection of AcSBV-AC and AmSBV-AM between *A. cerana* and *A. mellifera* have been demonstrated. However, AcSBV-AC and AmSBV-AM are known to merely causing significant harm to *A. cerana*. To understand the difference between two honey bees after infected with AcSBV-AC and AmSBV-AM, artificial infection of honey bee larvae and transcriptome analysis was performed to identify the regulation of core genes of A. ceranaand A. mellifera.

結果/結論/應用啟示

The down-regulated differentially expressed genes (DEGs) of *A. cerana*/AcSBV-AC were mostly identified at 24 h.p.i. (1987), while *A. mellifera*/AmSBV-AM were mostly identified at 48 h.p.i. (1230). According to GO analysis, at 24 h.p.i., more developmental related genes were down-regulated in *A. cerana*/AcSBV-AC group than *A. mellifera*/AmSBV-AM group. qRT-PCR validation of DEGs showed that the high expression of RPA2gene in *A. cerana*/AcSBV-AC and *A. mellifera*/AmSBV-AM may be related to the replication of SBV and host-virus specificity, with high expression of RPA2 for a long time in the *A. cerana*/AcSBV-AC group. In addition, core genes that may cause *A. cerana* larvae to be sensitive to SBVs were found in the experiment, including, Dpp and yellow-f, which may affect wing morphogenesis, longevity, and development. After dsRNA treatment, *A. cerana*/AcSBV-AC group showed opposite regulatory trends. In summary, *A. cerana* larvae infected with SBVs regulate these core genes, leading to abnormalities in developmental systems, and increased viral replication, resulting in a large number deaths of *A. ceranalarvae*.

關鍵詞(Keywords)：sacbrood virus, *A. cerana*, *A. mellifera*, developmental related genes, virus replication

OA11

影響菸草粉蝨取食獲得 begomoviruses 的生物因子
Biological factors affecting the acquisition of begomoviruses by *Bemisia tabaci*

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背景/研究問題/材料方法

番茄黃化捲葉病毒是嚴重威脅全球番茄生產的病毒之一，在臺灣以 tomato yellow leaf curl Thailand virus (TYLCTHV) 與 tomato leaf curl Taiwan virus (ToLCTV) 兩種病毒最為普遍，田間約有 40% 之罹病植株為複合感染。由於 TYLCTHV 與 ToLCTV 均僅依賴菸草粉蝨 (*Bemisia tabaci*) 傳播，因此菸草粉蝨與病毒的交互作用在病毒的傳播與流行上有著重要的影響。本研究的目標為：(1) 比較菸草粉蝨取食獲得兩種病毒的效率；(2) 了解罹病植株病毒量對菸草粉蝨獲得病毒的影響；(3) 了解複合感染植株病毒量對菸草粉蝨獲得病毒的影響。

結果/結論/應用啟示

菸草粉蝨取食獲得 TYLCTHV 與 ToLCTV 病毒量皆隨時間增加而增加，粉蝨中腸的 TYLCTHV 病毒量於 9 小時達到平線區，ToLCTV 病毒量則於 24 小時達到平線區，表示菸草粉蝨取食獲得 TYLCTHV 的效率較高。這個差異可能與兩種病毒與中腸、主唾腺病毒受器之間的特定結合力有關。其次，菸草粉蝨中腸的 TYLCTHV 與 ToLCTV 病毒量皆隨罹病植株病毒量的增加而增加；而主唾腺中的病毒量也有同樣的增加趨勢。此外，菸草粉蝨於複合感染植株上取食後，不論植株內 TYLCTHV 與 ToLCTV 病毒量的比值高或低，中腸、主唾腺內 TYLCTHV 病毒量大多高於 ToLCTV，表示當菸草粉蝨取食複合感染植株，TYLCTHV 被粉蝨獲得、傳播的機會較高。綜合上述結果，我們認為 TYLCTHV 在粉蝨獲毒與傳播上較 ToLCTV 更有優勢，影響了兩種病毒在田間的佔比與流行。

關鍵詞(Keywords)：*Bemisia tabaci*, mixed infection, tomato, tomato yellow leaf curl virus, virus-vector interaction

OA12

Whole genomic sequencing and analysis of *Rhagastis binoculata* nucleopolyhedrovirus (NPV) in Taiwan

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背景/研究問題/材料方法

The diseased *Rhagastis binoculata* larva, showed a typical symptom of nucleopolyhedrovirus (NPV), was found in mountain area in New Taipei City. Based on the light microscope observation and PCR check we confirmed an NPV in the diseased *Rhagastis binoculata* larvae. Furthermore, using Kimura-2-parameter (K-2-P) distant analysis of the *Polh, Lef-8,* and *Lef-9* partial nucleotide sequences, this caution pathogen was confirmed as NPV and the virus had an ambiguous relationship with *Clanis bilineata* NPV (ClbiNPV). Therefore, this NPV was provisionally named “RhbiNPV”. To better understand the classification of this NPV, the whole genome sequencing was performed by using next-generation sequencing (NGS) technology and further validation by Sanger sequencing to complete the genome. The annotated using ORF finder on National Center for Biotechnology Information (NCBI) website to identify the ORFs in the genome. Besides, ORF identities were compared to other NPVs and phylogenetic analysis was also performed to evaluated the taxonomic position of RhbiNPV.

結果/結論/應用啟示

The genomic size of RhbiNPV is 128,901 bp in length with a total 136 putative ORFs. The GC content is 37.16%. A genome-wide analysis showed that RhbiNPV has 89.5 %, 39.3 %, 32.8 % and 26.4 % average ORF identities to ClbiNPV, Lymantria dispar nucleopolyhedrovirus (LdMNPV), Autographa californica nucleopolyhedrovirus (AcMNPV) and Cydia pomonella granulovirus (CpGV). There are some different features in its genome compared with other NPVs, i.e., RhbiNPV shares similar genomic features with ClbiNPV, including gene content and gene identity, but gene arrangement is opposite between Orf-36 to Orf-104. Blast searches revealed that a gene *GP37* from the RhbiNPV has 1 bp deletion when compared with *GP37* of other baculoviruses. This deletion disrupts the gene into 2 small *GP37* ORFs. A phylogenetic analysis based on the baculoviral genes *Polh, Lef-8,* and *lef-9* indicated that RhbiNPV is a Group II NPV that is closely related to ClbiNPV.

關鍵詞 (Keywords)：Kimura-2-parameter (K-2-P), *Rhagastis binoculata, Rhagastis binoculata* nucleopolyhedrovirus, RhbiNPV

OA13

麵包蟲幼蟲蟲糞的理化特性評估

Assessment of the physicochemical characteristics of mealworm (*Tenebrio molitor* L.) larvae frass

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背景/研究問題/材料方法

Integration of insect resources into the human food production system can serve as a partial replacement for traditional animal-based proteins. This strategy is a novel trend in the global food and feed industry, seen as an environmentally friendly and economically sustainable approach. However, the insect farming industry still faces the challenge of effectively managing insect frass. Among these, the mealworm (*Tenebrio molitor* L.) has been extensively studied and applied. This study aims to clarify the feasibility of using mealworm frass in agricultural production by analyzing its various physicochemical properties. The research includes measuring pH and electrical conductivity with a soil-to-water ratio of 1:5, elemental analysis of nutrient composition using an elemental analyzer, and measuring bulk density, particle density, total porosity, water content, and water-holding capacity. Furthermore, growing media were developed by mixing frass with materials such as spent mushroom substrates and rice hulls to preliminarily assess whether frass can enhance the water retention properties of growing media.

結果/結論/應用啟示

The pH of the frass ranged from 6.0 to 6.2, with electrical conductivity exceeding 7,100 μS/cm, and a carbon-to-nitrogen ratio below 14.45, categorizing it as a weakly acidic, highly conductive, and low carbon-to-nitrogen ratio resource material. Bulk density ranged from 0.548 to 0.792 Mg/m^3, water content from 416.9% to 446.0%, and water-holding capacity from 106.3% to 131.1%, indicating strong water retention properties. In different formulations of growing media, an increase in the content of frass led to an improvement in water retention capacity, showing a positive correlation. However, water retention capacity is only one of several indicators used to evaluate the quality of growing media. Without concerns of heavy metal contamination, the frass was dry and odorless, making it a suitable agricultural material. Further research should involve the cultivation of specific crops to understand their quality and yield when using growing media.

關鍵詞(Keywords)：昆蟲蛋白(insect-derived protein)、麵包蟲(*Tenebrio molitor* L.)、蟲糞(insect frass)、循環農業(circular agriculture)、作物栽培(crop cultivation)

OA14

麵包蟲幼蟲蟲糞添加廢菇包介質之設施栽培應用初探

Yellow mealworm added to spent shiitake substrates and rice husk to cultivate lettuce and seedling of strawberry in facilities

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背景/研究問題/材料方法

新社區香菇產業每年約產出近二億個廢棄的香菇太空包，又台灣每年產生約37萬噸的稻殼，本所已研發出回收香菇包經簡易處理後，加入稻殼混合後可種植草莓苗株、果實和夏季蔬菜，可提升廢棄香菇包之回收利用率，減低環境污染之衝擊。無脊椎動物糞便能化身成有機質肥料，補充栽培介質或作物養分管理所需的肥分，如國內已研究蚯蚓糞與黑水虻糞作為有機質肥料的可行性，結果表明兩者皆具有改善土壤性質與促進作物生長的功效。

結果/結論/應用啟示

試驗於本所半封閉式開頂溫室，以回收香菇包、稻殼和麵包蟲蟲糞等剩餘資材以不同比例調配作為草莓、紅烤肉萵苣之栽培介質，以市售泥炭土、香菇廢包+稻殼(V=1:1)、香稻(2:1)為對照組，香稻添加2.5和5.0%蟲糞為處理組。試驗結果顯示，紅烤肉萵苣以泥炭土產量最高，其次為香稻(2:1)+蟲糞5.0%，添加蟲糞可增加廢菇包介質種植紅烤肉萵苣的產量(顯著性差異)。豐香草莓走莖苗試驗結果，香稻(1:1)地上部鮮重顯著高於泥炭土，但地下部鮮重則較泥炭土低，添加蟲糞未明顯提高地上部或地下部鮮重的作用。香稻(2:1)地上部鮮重結果與(1:1)類似，地下部鮮重有高於泥炭土的趨勢，添加蟲糞仍無促進效果。草莓苗株(2.5吋軟盆)繁殖期需要30-45天，蟲糞在種植時加入廢菇介質內，肥分只在生長初期，故無法促進苗株營養生長

關鍵詞(Keywords)：廢香菇介質(spent shiitake substrates)、麵包蟲(yellow mealworm)、昆蟲糞(insect frass)、草莓(strawberry)、萵苣(lettuce)

OA15

原民部落作物害蟲調節服務功能調查及原民植物對有益天敵之助益
Investigation of pest regulation service function of aboriginal tribal crops and the benefit of aboriginal plants to beneficial natural enemies

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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。本研究主要探討原民部落農田中關鍵害蟲與其天敵之數量消長，評估其害蟲調節服務功能，並藉由開花特性原民植物的營造，提升有益天敵數量。本研究於 2022 年進行調查，地點和作物為花蓮縣瑞穗鄉屋拉力部落的文旦，以及玉里鎮織羅部落的水稻，分別於有機與慣行兩種耕作方式進行作物關鍵害蟲及天敵蟲相調查，此外，挑選十種開花性原民植物，測試其對於寄生性與捕食性天敵延長壽命之效果，評估後可將上述原民植物導入害蟲調節服務功能較薄弱之田區，作為後續評估其增加有益天敵數量與降低害蟲密度的效果。

結果/結論/應用啟示

水稻田方面，調查結果顯示在各生長時期有機田區的天敵數量皆高於慣行田區，其中以舞蛇數量最多，舞蛇為飛蝨和葉蟬之天敵，有機田區的舞蛇在水稻分櫱期至黃熟期間，平均數量均在 50 隻以上，而慣行田平均介於 3-24 隻之間，而在水稻孕穗開花期中飛蝨數量在慣行田區大於有機田區，其中一慣行區甚至多達 1500 隻，明顯高於有機田區數量；而在文旦園方面，慣行田區幼果期的薊馬數量總數最高達 1035 隻，薊馬數量為有機田區的 60 倍，但其天敵花椿象科數量僅較有機田區高出不到兩倍，天敵與食餌比例低；上述原因除了與殺蟲藥劑施用有關之外，田區植被組成亦為影響天敵族群之原因。另外在評估原民植物對天敵的生存效益試驗中，其中以穗花木藍、三葉埔姜與馬蘭的效果最好，寄生性天敵-格氏突闊小蜂(*Dirhinus giffardii* Silvestri)在這三種開花植物環境下，存活時間達 30 日，較對照組 5.4 日明顯延長，而對捕食性天敵-六條瓢蟲(*Cheilomenes sexmaculata*)亦能有效延長天敵壽命，其中成蟲在鴨舌癀、三葉埔姜及杜虹植物中可存活達 15 日，相較於對照組 5.8 日具明顯延長生存天數效果。後續將導入上述原民植物於田區進行營造，期望藉此增加地被植物的多樣性，提供豐富的棲地與食物來源，評估其增進害蟲調節功能之效果，以納入生態給付政策之參考。

關鍵詞(Keywords)：生態農業(ecoagriculture)、水稻(rice paddy)、文旦(pomelo)、棲地營造(habitat creation)、調節服務(regulating services)

OA16

運用本土天敵於有機田區成功控制稻黑椿象
Using native natural enemies to control rice black bugs in organic paddy rice

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背景/研究問題/材料方法

稻黑椿象為臺灣早期水稻五大害蟲之一，1970 年代化學農藥普遍使用後已鮮少發現。關山鎮水稻田區轉行有機操作 3 個期作後，於 2021 年第 2 期作收割時於部分田區出現大量稻黑椿象成蟲，當期作全區 100 公頃收成僅有機栽培正常收穫量之 7 成，損失慘重；至 2022 年第 1 期作結束時，田間稻黑椿象成蟲總數估計達上億隻，為害嚴重田區幾乎無收成；當時尚無有效的有機防治方法，同年第 2 期作蟲數更多，不僅造成減產，更衍生環境問題。

結果/結論/應用啟示

利用稻黑椿象成蟲偏好植株茂密稻欉之習性，於 2023 年第 1 期作宣導有機栽培區農友延後插秧，減少稻黑椿象成蟲遷入本田危害。針對成蟲族群較多的田區，以黑殭菌進行防治，另釋放人工培育之黑卵蜂降低稻黑椿象卵孵化率。殘存的若蟲再施用黑殭菌造成感染。綜合運用本土天敵已成功地將稻黑椿象族群數量減少為 2022 年同期之 8%，產量亦恢復正常水準，為蟲害管理中單純運用本土天敵防治成功的經典案例。

關鍵詞(Keywords)：稻黑椿象(black rice bug)、黑卵蜂(*Telenomus* sp.)、黑殭菌(*Metarhizium* sp.)、本土天敵(native natural enemies)

OA17

殺蟎劑對臺東地區鳳梨釋迦葉蟎類之抗藥性評估

Resistance evaluation of acaricides for controlling spider mite on atemoya in Taitung

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背景/研究問題/材料方法

葉蟎是番荔枝重要有害生物，為了解現行核准於番荔枝防治葉蟎之殺蟎劑效果，自臺東縣卑南鄉鳳梨釋迦田區採集神澤氏葉蟎及二點葉蟎，進行番荔枝核准登記 11 種殺蟎劑有效成分之藥效測試，以噴藥塔施藥後置於昆蟲培養室(28℃，12D:12L)，於 24 小時、48 小時進行觀察，計算死亡數並計算藥劑致死率，每處理 4 重複。藥劑敏感度試驗依不同藥劑濃度之抗藥性結果對葉蟎進行噴施，後續操作同藥效測試。

結果/結論/應用啟示

施藥後 48 小時，神澤氏葉蟎以 1%密滅汀乳劑及 30%賽派芬水懸劑處理者最佳，其死亡率分別達 83.8%及 100%；二點葉蟎以 30%賽派芬水懸劑處理者最佳，死亡率達 100%，其餘藥劑則未達 50%，推測臺東地區葉蟎對現行核准之大多數的殺蟎劑已產生抗藥性。藥劑敏感度試驗方面，施藥後 48 小時，神澤氏葉蟎以 4%畢汰芬水懸劑、10%得芬瑞可濕性粉劑、5%芬普蟎水懸劑處理者，其死亡率隨藥劑濃度增加線性提升；而二點葉蟎以 20%畢達本水懸劑、5%芬普蟎水懸劑、50%馬拉松水基乳劑處理者，其死亡率隨藥劑濃度增加線性提升，其他處理則無此現象。本試驗結果將應用於宣導番荔枝農民慎選效果較佳之殺蟎劑，以有效防治葉蟎。

關鍵詞(Keywords)：鳳梨釋迦(atemoya)、殺蟎劑(acaricides)、神澤氏葉蟎(*Tetranychus kanzawai* (Kishida))、二點葉蟎(*Tetranychus urticae* (Koch))、抗藥性(resistance)

OA18

黑水虻與魚粉胺基酸組成之變異程度比較

Comparison of variation of amino acid profiles of black soldier fly and fishmeal

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背景/研究問題/材料方法

Recently, scientists have been studying the possibility of replacing fishmeal (FM) with black soldier fly (*Hermetia illucens*; BSF) meal, and many positive effects of BSF meal as a feed ingredient have been demonstrated. However, there are evidences that the nutritional value of BSF varies with the feeding substrate. To investigate the feasibility of replacement of FM with BSF, the present study focused on the consistency of amino acid (AA) profile of BSF reared with different substrates (guava pomace, GP; restaurant wastes, RW) and FM produced in different countries and seasons. The analyses of BSF samples were conducted by certified third party inspection bodies, and the data of FM was collected from published literatures. The coefficient of variation (CV) of each AA was then calculated.

結果/結論/應用啟示

The highest average CV was shown in RW (0.23), followed by FM produced in different countries (0.13) and seasons (0.1 for *G. potassou*, and 0.07 for *B. boops*). It was lowest in GP (0.06), indicating GP was the most consistent in terms of AA profile. For BSF reared with GP, the most variable AA was proline, while it is histidine or tyrosine for FM. Arginine was generally the most consistent AA in BSF and FM. Lysine, which is often regarded as the limiting AA for many farmed species, was found to be rather stable in individual fish species, but slightly higher in BSF. However, lysine content in FM became more variable when considering different origins.

Although FM is a great source for essential AAs, the locational and seasonal variations are its drawback. Conversely, BSF has a more consistent AA profile if nutritionally stable substrates are used. The findings can increase the feasibility of FM replacement with BSF meal, as BSF is found to exhibit an advantage of amino acid consistency over fishmeal.

關鍵詞(Keywords)：黑水虻(black soldier fly)、胺基酸組成(amino acid profile)、魚粉(fishmeal)、季節性變化(seasonal variation)

OA19

國高中生對食用昆蟲的態度及可能影響因素之探討-以臺中市區為例

The attitude of secondary school students towards edible insects and possible influential factors- take Taichung city for example

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背景/研究問題/材料方法

近年來環境保護意識興起，過去數十年傳統畜牧行為造成環境破壞也逐漸受到重視，尋找穩定且非常見家畜飼養以提供蛋白質成為了重要議題。在眾多替代肉品中，昆蟲食品不僅在許多國家是傳統飲食文化的一部分，更是環境友善的優質蛋白質來源。然而，在臺灣，食用昆蟲的文化正在逐漸消逝，民眾對於食用昆蟲的認識已不如以往，新的世代甚至可能不認為昆蟲是可以食用的。本研究希望透過態度 A-B-C 模式探討臺中市中學生對於食用昆蟲的態度。

結果/結論/應用啟示

研究結果顯示，高中生對於食用昆蟲的情感上並無太多負面的想法。然而，在認知方面，即使學生了解昆蟲食品的營養價值，以及食用昆蟲對環境帶來的正面效益，對於昆蟲食品的處理方式、來源的認識仍有所不足。在行為方面，則是發現無論昆蟲以何種料理方式呈現，都無法得到較佳的行為偏好分數。綜合研究結果，未來若需要推廣食用昆蟲，學校方面可以多讓學子接觸昆蟲食品並教育食用昆蟲的價值及食用方式，例如在學校多提供學生接觸昆蟲食品的機會，激發學生的興趣之餘，亦讓他們更熟悉和接受這種替代蛋白質的來源。

關鍵詞(Keywords)：糧食系統(food systems)、食用昆蟲(edible insect)、食蟲(entomophagy)、替代蛋白質(alternative proteins)、A-B-C 模式(A-B-C model)

OA20

環境降溫對於青蔥甜菜夜蛾防治效果研究
The effect of environment cooling on the control of beet armyworm (*Spodoptera exigua*)

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背景/研究問題/材料方法

甜菜夜蛾(*Spodoptera exigua*)為青蔥之重要害蟲，其初齡幼蟲群聚於蔥葉表面，隨齡期增長，轉為潛入蔥管內取食。其近年於青蔥重要產區──宜蘭縣三星鄉為害甚鉅。尤其夏季持續高溫且乾旱之氣候，以及殺蟲劑頻繁使用產生抗藥性，使甜菜夜蛾防治作業難度遽增。據初步觀察，甜菜夜蛾之發生與氣溫呈正相關，與降雨量則呈負相關。本研究旨在開發藉由田間降溫，以減少甜菜夜蛾危害率之技術。利用搭設黑網或明涼網降低蔥田白天溫度，或夜間灑水模擬降雨，干擾成蟲交配產卵，於青蔥生長期持續調查危害率，以評估對於甜菜夜蛾之防治效果。

結果/結論/應用啟示

根據試驗結果，夜間灑水、搭設黑網與明涼網之操作組，其甜菜夜蛾危害率均有所降低，為對照組之六至三成不等，尤以黑網組之甜菜夜蛾危害率於試驗期間均維持 10%以下(為對照組之三成)，最為有效。遮蔭網可有效降低田間白天氣溫，日高溫相較對照組之差達 10°C，但對夜間氣溫影響不明顯，整體而言可降低日均溫 3°C，夜間灑水則可些略降低夜溫約 0.4°C。未來若能針對成蟲飛行、交配或產卵的活動高峰灑水，則可節約用水量，減少水份逆境對蔥株健康之影響。經實地調查發現，夜間成蟲於遮蔭網下植株停棲數量亦明顯少於無遮蔭區。此發現顯示除影響日間氣溫之外，遮蔭網對成蟲活動可能亦具物理阻攔或驅避效果，為甜菜夜蛾的綜合管理提供一個新的可用選項。

關鍵詞(Keywords)：甜菜夜蛾(*Spodoptera exigua*)、遮蔭網(shade net)、噴水(water spray)、綜合害物管理(integrated pest management (IPM))

OA21

應用無人植保機噴施淡紫菌 TNZZS6 發酵產物之田間防治試驗

Field trials of spraying fermentation products of *Purpureocillium takamizusanense* TNZZS6 for controlling *Tessaratoma papillosa* Drury with unmanned aerial vehicle

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背景/研究問題/材料方法

淡紫菌 *Purpureocillium takamizusanense* TNZZS6 菌株為自荔枝椿象分離純化之蟲生真菌，室內接種試驗證實該菌株對荔枝椿象成蟲及若蟲皆具感染能力，展現其應用於荔枝椿象生物防治之發展潛力。目前可透過液態發酵及固態發酵技術，建立淡紫菌 TNZZS6 初步量產作業流程，以穩定供給田間防治試驗之接種源。為評估無人植保機噴施淡紫菌 TNZZS6 對荔枝椿象之田間防治成效，本試驗應用臺製無人植保機 JPL1 以飛行速度 3 m/s、飛行高度距離 2-4 m 等飛行參數自動化執行農噴路徑，隔週防治 1 次，連續 3 次。田間防治期間，隔週調查各區荔枝椿象族群密度變化，計算田間防治率，藉此評估應用無人植保機噴施淡紫菌 TNZZS6 防治荔枝椿象之可行性。

結果/結論/應用啟示

田間防治試驗結果顯示，對照區之荔枝椿象族群密度防治前為 11.71 隻/棵，3 次淡紫菌防治後，族群密度增加至 36.86 隻/棵。淡紫菌液態發酵處理區之荔枝椿象族群密度防治前為 5.57 隻/棵，3 次淡紫菌防治後，族群密度下降至 4.86 隻/棵。淡紫菌 TNZZS6 液態發酵液對荔枝椿象族群防治率為 72.29%。而淡紫菌固態發酵區之荔枝椿象族群密度防治前為 10.29 隻/棵，3 次淡紫菌防治後，族群密度下降至 4.15 隻/棵。淡紫菌 TNZZS6 固態發酵產物對荔枝椿象族群防治率為 87.2%。綜合上述結果，淡紫菌 TNZZS6 液態發酵及固態發酵產物對荔枝椿象族群之田間防治率達 72% 以上。應用無人植保機噴施淡紫菌發酵產物可展現一定的田間防治成效，未來淡紫菌 TNZZS6 發酵產物之劑型需考量添加抗乾燥劑、防曬劑等賦形物，增進淡紫菌 TNZZS6 商品之抗逆境能力及致病力。

關鍵詞 (Keywords)：荔枝椿象 (*Tessaratoma papillosa* Drury)、淡紫菌 (*Purpureocillium takamizusanense*)、液態發酵(liquid fermentation)、固態發酵(solid state fermentation)、無人植保機 (unmanned aerial vehicle (UAV))

OA22

落花生土壤害蟲調查與草螟蛾 *Sufetula* sp.發生概述
Survey of the soil pests affecting peanuts and the occurrence of *Sufetula* sp.

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背景/研究問題/材料方法

雲林縣落花生栽培區常年發生莢果上出現不明孔洞，造成品質與產量損失。關於害蟲種類，除曾採獲文獻紀錄之金針蟲(叩頭蟲幼蟲之俗名)外，另發現一種草螟蛾幼蟲蛀食莢果。農業試驗所於2014 年進行調查，確認草螟蛾為 *Sufetula* sp.，並觀察其偏好取食幼嫩莢果。但由於土壤害蟲採樣不易，長久以來都無法進一步了解田間發生狀況。2022 年起以餌站誘集法於雲林地區普查，確認害蟲危害狀況，並進行田間發生調查與藥劑試驗。

結果/結論/應用啟示

田間普查 2022 年秋作草螟蛾 *Sufetula* sp.發生率 58.3%、金針蟲 8.3%，2023 年春作為 70.6%及11.8%。採得之金針蟲經形態鑑定為 *Aeolus* spp.，密度低也未有明顯危害，推測草螟蛾為莢果孔洞主因。草螟蛾幼蟲於落花生種植後 2 至 3 個月始被採獲，依各期作而異。當期若發生時間早，整體危害程度較高。此外晚植田受害程度普遍高於早植田。於落花生開始結莢時施用系統性殺蟲劑硫敵克及剋安勃，收穫時莢果受害率為 3.4%及 3.7%，對照藥劑得芬諾為 6.2%。草螟蛾可以玉米根部為寄主，鄰田為玉米之落花生田，採獲草螟蛾之機率顯著較高。後續除了防治研究外，由於文獻紀錄 *Sufetula* 屬已知寄主皆為單子葉植物，*Sufetula* sp.的生物特性、寄主範圍，與其對落花生之取食利用，值得深入探討。

關鍵詞(Keywords)：落花生(peanuts)、土壤害蟲(soil pests, *Sufetula*)、金針蟲(wireworm)

OA23

稻黑椿象 (半翅目：蝽科) 卵寄生蜂-黑卵蜂 (膜翅目：緣腹細蜂科) 於不同溫度下之寄生表現

Parasitic preference under different tempertures in an egg parasitoid wasp (Hymenoptera: Scelionidae) of *Scotinophara lurida*

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背景/研究問題/材料方法

稻黑椿象 *Scotinophara lurida* (Burmeister) 為民國 60 年以前臺灣水稻五大害蟲之一，後因殺蟲劑普及轉為潛在害蟲；然而自 110 年起，臺東縣關山鎮面積 100 公頃之有機水稻專區遭此蟲危害蒙受嚴重損失。臺東區農業改良場從稻黑椿象卵中發現臺灣本土寄生蜂黑卵蜂 (*Telenomus* sp.)，田間寄生率高，具應用之潛能。本研究探討黑卵蜂於 3 種不同溫度下寄生表現，試驗在 26、28 及 30±1°C 恆溫生長箱下連續寄生 2 週，以替代寄主卵製成之卵片供 1 日齡黑卵蜂雌蜂寄生，並每日更換卵片，記錄其產下之子代數、雌蜂數及雌蜂比。

結果/結論/應用啟示

黑卵蜂 (*Telenomus* sp.) 在 26、28 及 30°C 下 2 週內每隻雌蜂平均子代數分別為 54.5、52.6、44.4 隻，三種溫度間沒有顯著差異；子代雌蜂數為 34.4、29.3、22.9 隻，26°C 與 30°C 之間有顯著差異，28°C 與 26、30°C 之間則無顯著差異；雌蜂比則分別為 63%、59%及 54%，三種溫度間沒有顯著差異，子代雌蜂數與雌蜂比會隨著寄生日數增加而遞減。由試驗結果得知，黑卵蜂在 26°C 的環境下平均子代數和雌蜂數最高，寄生可達最高繁殖效益，未來可應用於量產流程中。

關鍵詞(Keywords)：稻黑椿象(*Scotinophara lurida*)、黑卵蜂(*Telenomus* sp.)、溫度(temperature)、寄生表現(parasitic preference)、生物防治(biological control)

OA24

葫蘆科作物主要產區菸草粉蝨 (Bemisia tabaci)對 16 種國內登記殺蟲劑之感受性監測研究

Monitoring on the field sensitivity of whiteflies against registered insecticides in Taiwan

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背景/研究問題/材料方法

菸草粉蝨是世界著名的廣食性害蟲，已知的寄主植物範圍超過 900 種，在臺灣的寄主紀錄亦達145 種以上，常見者包括葫蘆科、茄科、十字花科、豆科等重要經濟作物。除了直接為害寄主作物之外，亦可傳播 110 種以上植物病毒病害。國內外防治菸草粉蝨均以殺蟲劑為主，經連續施用造成選汰壓力，導致抗藥性族群發展。依據 Sparks et al. (2020) 分析結果，菸草粉蝨在『易產生抗藥性的農業害蟲』中名列第 4，僅次於小菜蛾 (*Plutella xylostella*)、二點葉蟎 (*Tetranychus urticae*)與桃蚜 (*Myzus persicae*)，故已造成害蟲管理上的壓力。為監測地區粉蝨對國內登記殺蟲劑之感受性差異，以利農友調整輪替用藥種類，本研究規劃以葫蘆科作物主要產區(雲林、嘉義、臺南、高雄、屏東等)為監測點，供試藥劑為國內登記於葫蘆科作物之 10 種作用機制殺蟲劑，包括畢芬寧、可尼丁、速殺氟、阿巴汀、百利普芬、派滅淨、賽安勃、氟尼胺等 16 種成品農藥。利用葉片浸漬法(leaf-dipping method)進行第 1 子代粉蝨成蟲之生物檢定，以檢視田間菸草粉蝨對目前登記藥劑之感受性現況。

結果/結論/應用啟示

本年度完成雲林縣崙背鄉洋香瓜、莿桐鄉胡瓜、台南縣歸仁鄉南瓜等品系粉蝨對前述 16 種成品農藥之感受性檢測。結果顯示，各品系粉蝨以阿巴汀 2% EC 致死效果最佳，於登記濃度之死亡率可大於 90%，賽安勃 10.26% OD、速殺氟 21.8% SC 次之，其餘供試藥劑則各有不同的表現。另一方面，從作用機制類別觀之，以 IRAC 3A 與 IRAC 4A 之死亡率最低，因 IRAC 4A 為國內外防治菸草粉蝨的主要用藥，後續擬就 4A 類殺蟲劑進行抗藥性探討。

關鍵詞(Keywords)：菸草粉蝨 (*Bemisia tabaci*)、感受性(sensitivity)、監測(monitor)、國內登記殺蟲劑(registered insecticides in Taiwan)

OA25

農業長期生態樣區指標生物族群與環境因子之關聯性探討：以六條瓢蟲為例

Exploring the correlation between indicator organism populations and environmental factors in an agricultural long-term ecological station: A case study of *Cheilomenes sexmaculata*

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背景/研究問題/材料方法

瓢蟲為農業生態系中的生態指標，可反應生態環境變化。本研究以瓢蟲作為指標生物，於農業試驗所溪口農場及台南區農業改良場雲林分場試驗區進行長期調查，調查期間為水稻每期作之分蘗初期起，每二星期置換黃色黏板，進行5-6次調查，並以2014-2022年水稻兩個期作樣區所調查的優勢瓢蟲-六條瓢蟲為研究對象，利用農業氣象觀測網監測系統網站資料，進行溫度、相對濕度、日照時數及累積雨量等環境氣候因子之相關分析。

結果/結論/應用啟示

分析結果有助於瞭解六條瓢蟲在特定環境條件下的生態行為和適應能力，以及氣候變遷下氣候因子對天敵昆蟲族群之影響，作為農業病蟲害管理策略參考資料，助於制定更具適應性的生態管理策略。除氣候因子外，瓢蟲的數量與其食餌族群之間的動態密切相關，未來可納入瓢蟲食餌的探討，以更全面瞭解氣候因子對農業生態系中害蟲及天敵的影響。

關鍵詞(Keywords)：瓢蟲(ladybug)、環境因子(environmental Factors)、農業長期生態研究(agricultural long-term ecological research)、指標生物(indicator species)

OA26

Establishment of high potential entomopathogenic fungi selection markers by aligning phenotype and gene expression levels

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背景/研究問題/材料方法

Entomopathogenic fungi are facultative pathogens of insects and widely used for pest control. In application, it is crucial to select the high conidia production, stress tolerance (i.e., thermotolerance, osmotic stress, and oxidative stress etc.) and virulence strains. In this study, we aligned the above phenotypes with relative genes to establish a platform for fungal selection. Therefore, 4 *Beauveria bassiana*isolates (Bb-NCHU-141, 143, 153, 157) and 2 *Metarhizium pemphig*isolates (Mp-NCHU-2 and 125), 1 *Metarhizium lepidiotae*isolate (Ml-NCHU-9) and 1 *Metarhizium anisopliae*isolate (Ma-NCHU-69) were selected to evaluate the thermotolerance assay, conidia productivity assay and osmotic tolerance. Moreover, the EPF isolates (Bb-NCHU-141, 157, Ma-NCHU-69, Mp-NCHU-125) will subject to RT-qPCR to measure expression levels of relative genes for investigating the correlation between gene expression levels and tolerance to environmental stress.

結果/結論/應用啟示

Based on the observations of phenotype differences, Bb-NCHU-141 and 157 showed the largest differences in thermotolerance, conidia productivity and osmotic tolerance. Ma-NCHU-69 and Mp-NCHU-125 revealed the largest differences in above phenotypes. The expression of the relative genes, including *hog1*, *rgs1* and *cag8*, which associated with conidial production, thermotolerance and osmotic stress, were subjected to RT-qPCR. The gene expression levels of *hog1* and *rgs1*in Bb-NCHU-157 were higher than those of Bb-NCHU-141 on the 14 days-culture. The gene expression levels of*hog1* and *cag8* in Mp-NCHU-125 were higher than those of Ma-NCHU-69 on the 14 days-culture. The gene expression level is positive correlated with conidia productivity in *Beauveria* isolates (r=0.543 and 0.714) and *Metarhizium* isolates (r=0.600 and 0.543). For osmotic tolerance, the gene expression level is positive correlated in *Beauveria* isolates (r=0.334) and *Metarhizium* isolates (r=0.943). For thermotolerance, the gene expression level is positive correlated in *Beauveria* isolates (r=0.711). In conclusion, the gene expression could be associated with fungal phenotypes and thus provide insights into fungal selection and screening process.

關鍵詞(Keywords)：*Beauveria*, Metarhizium, environmental stress

OA27

新式蜂球應用於施放赤眼卵蜂防治玉米秋行軍蟲

Application of the new wasp ball for releasing Trichogramma wasps to control the fall armyworm in the corn field

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背景/研究問題/材料方法

赤眼卵蜂為卵寄生性天敵廣泛用於生物防治，尤其應用於防治重要害蟲，秋行軍蟲(*Spodoptera frugiperda*)、亞洲玉米螟(*Ostrinia furnacalis*)和甘蔗條螟(*Proceras venosatus*)。赤眼卵蜂田間防治施放目前主要依賴人力，傳統釘書機釘放方式較費工，農民採用意願低，需要開發新式施放技術，改善操作便利性助於提高農民使用意願。本研究開發新式蜂球施放赤眼卵蜂，並研發機械自動化化生產裝置。本研究亦應用蜂球於玉米秋行軍蟲田間防治試驗，採用農藥減量結合施放赤眼卵蜂防治，並與傳統蜂片防治進行比較，評估蜂球防治效力。

結果/結論/應用啟示

本研究以生態友善為基礎進行開發，新式蜂球為純紙漿製作，材質可分解無汙染，應用雷射精準切割出蜂口，使赤眼卵蜂可飛出並防止螞蟻進入取食。蜂球生產採用機械化自動量產，設備由原料供給系統及自動化封裝系統組成，蜂球自動化封裝設備採用圓盤加工機技術，有效提高天敵產品產量。玉米田間防治試驗，採用農藥減量結合施放赤眼卵蜂防治秋行軍蟲，結果顯示新式蜂球與傳統蜂片防治效率相似皆可降低秋行軍蟲受害率，證實新式蜂球可實際應用於田間防治。新式蜂球便利施放，助於提高農民使用意願與增加田間防治應用面積。

關鍵詞(Keywords)：生物防治(biological control)、天敵(natural enemy)、蟲害綜合管理(integrated pest management)、玉米(maize)

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

以誘引巢體進行南投濁水溪流域蜂類調查之測試
Using trap nests for bee/wasp survey at Zhuoshui River, Nantou

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背景/研究問題/材料方法

蜂類在生態系服務中扮演重要的角色：花蜂類作為授粉者與植物的繁殖息息相關，寄生性蜂類與捕食性蜂類則可以控制其他昆蟲的數量；蜂類作為授粉與生物防治的工具在國內與國際上都有實際的應用。部分獨居性蜂類 (solitary bee/wasp) 有在細長管道或坑洞內築巢並產卵的習性，因此可以使用誘引巢體 (trap nest) 使其築巢作為蜂類調查的方法。誘引巢體會因為當地物種、氣候、設計等差異而有不同的引誘結果，在國外已有諸多研究，但在台灣則鮮少作為調查工具。本研究自 2021 年 8 月於埔里至梅峰沿路設置了 10 處誘引巢體，每個月進行一次採樣，將有被築巢的板片帶回研究室進行後續觀察與記錄。

結果/結論/應用啟示

使用誘引巢體做調查除了能長時間記錄當地蜂種類外，也有助於了解蜂類的築巢形式、獵物、幼蟲分類、生活史，同時能採集到以蜂類為宿主的寄生性蜂類、蠅類與鞘翅目昆蟲。其結果與掃網及黃水盤誘引所得到的蜂種類有明顯的差異，部分在誘引巢體採集到的物種未出現在掃網及黃水盤。根據目前的結果，我們確認誘引巢體確實有助於蜂類調查的完整性，並有機會用於分類學、行為學、生態學等研究。

關鍵詞(Keywords)：獨居性蜂類(solitary bee/wasp)、誘引巢體(trap nest)、生物多樣性(biodiversity)

OB02

全球暖化對台灣家白蟻和格斯特家白蟻食物資源競爭的影響

Impact of global warming on food resource competition between Formosan and Asian subterranean termites (Blattodea: Rhinotermitidae)

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背景/研究問題/材料方法

Coptotermes formosanus and *Coptotermes gestroi* are the main pest species, responsible for > 95% of termite infestations in Taiwan. The objective of this study conducted experiments on temperature-mediated food resource competition between the two species. The bioassay was conducted at 17, 19, 20, 21, 22, 24, 29, and 31°C using 21-by-16-cm plastic arenas connect to two-year-old colonies of respective species from the two side. These arenas were filled with agar and contained 20 inserted wooden pieces. The occupied wooden pieces and excavating tunnel distance were utilized as indicators of competition. 17°C and 29°C represent the monthly mean minimum and maximum temperatures in Taichung over the past 30 years. 19°C and 31°C projected for the next 50 years as comparative controls against current conditions. This study aims to investigate the impacts of extreme climate changes on the tunnel excavated distance and wood pile occupation of the two termite species.

結果/結論/應用啟示

The results indicate the tunnel excavated distance and wood pile occupation in this bioassay were significant different. No significant difference in the excavated tunnel length of *C. formosanus* across different temperatures (P=0.43). However, for *C. gestroi*, there is a significant difference in tunnel length across different temperatures (P=0.02). Comparing two species, a significant difference (P<0.001) of excavating distance is observed for temperatures exceeding 24°C. Specifically, *C. formosanus*only dominates at 21°C, with both the wood pile occupation (13.3/20, 66.5%) and the excavated distance (61.91±54.80). On the other hand, *C. gestroi* occupied significantly more wood pile than *C. formosanus* when the temperature was > 24°C. In our study, as the temperature increased, *C. gestroi* exhibited a gradual increase in the mean length of excavation. These results suggest that under the scenario of future global warming, the competition for food resources between the two termite species may be influenced, particularly at higher temperatures, where *C. gestroi* could potentially display greater competitiveness.

關鍵詞(Keywords)：台灣家白蟻(*Coptotermes formosanus*)、格斯特家白蟻(*Coptotermes gestroi*)、氣候變遷(climate change)、食物資源競爭(food resource competition)

OB03

A taxonomic review of Japanese *Aprostocetus* Westwood, 1833 (Hymenoptera: Eulophidae), with notes of potential significance of *Aprostocetus* in evolutionary research

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背景/研究問題/材料方法

Aprostocetus contains at least 813 species in the world. Among them, six species, *A. doronokianus*, *A. doutti*, *A. minutus*, *A. hagenowii*, *A. pallipes*, and *A. pallidipes* have been recorded from Japan. The former three species parasitize Hemiptera.*A. hagenowii* and *A. pallipes* parasitize Blattidae and Cecidomyiidae, respectively. Host information of *A. pallidipes* has not been provided. Clarifying ecological traits of parasitoids, such as host and annual life history is essential toward sustainable development of basic and applied research. In this context, we are constructing comprehensive identification system of Japanese *Aprostocetus* species by combining characters of morphology, DNA, and host. In this presentation, we provide results of our research focusing on Japanese *Aprostocetus* species that parasitize gall midges. Galls induced by Cecidomyiidae were collected from various localities in Japan. Reared parasitoids were used for morphological comparisons. We also examined specimens kept in the Natural History Museum, London, Hokkaido University, Japan, and Kyushu University, Japan. We analyzed partial mtDNA sequence of an *Aprostocetus* species that has more than two host species.

結果/結論/應用啟示

We reared six *Aprostocetus* species from ten sorts of cecidomyiid galls. Morphological observation revealed that all these six species were undescribed. *Aprostocetus* sp. 1 was reared from five *Rhopalomyia*gall midges, *R. cinerarius*, *R. giraldii*, *R. iwatensis*, *R. struma*, and *R. yomogicola*. *Aprostocetus* sp. 2, *Aprostocetus* sp. 3, *Aprostocetus* sp. 4, *Aprostocetus* sp. 5, and *Aprostocetus* sp. 6 were reared from *Lasioptera achyranthii*, *L. rubi*, *Lasioptera* sp., *Oligotrophus betheli*, and *Illiciomyia yukawai*, respectively. Our analysis of partial mtDNA of *Aprostocetus* sp. 1 detected existence of five intraspecific groups that corresponded to their hosts. Our results suggested existence of high species diversity of *Aprostocetus*on gall midge and potential significance of *Aprostocetus* in evolutionary research.

關鍵詞(Keywords)：taxonomy, Chalcidoidea, parasitoid, host associated diversification, gall midge

OB04

利用 CLIMEX 預測長足捷蟻 *Anoplolepis gracilipes* 在台灣的物種分布模型–以土壤溫度建立預測模型

Predicting the species distribution model of the yellow crazy ant Anoplolepis gracilipes in Taiwan using CLIMEX – a predictive model base on soil temperature

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背景/研究問題/材料方法

長足捷蟻 *Anoplolepis gracilipes* 被視為世界百大入侵種之一。其入侵性強，具有良好的環境適應性。在南台灣該物種已被記錄，會攻擊本土陸蟹，佔領原生蟻種的棲地。近期研究指出，全球的土壤溫度與氣溫間存在著明顯的差異。另外，使用土壤溫度模型，能有效預測長足捷蟻的潛在分布區域，其中以深度 30 公分的土壤溫度預測時表現最佳。利用土壤溫度模型，臺灣的相關資訊與應用仍相當缺乏，因此本研究欲建構一適用於 CLIMEX 物種分布模型的台灣土壤溫度模組，並且與 Maxent 模型的預測結果交叉比較，以探討其應用於預測台灣長足捷蟻及其他新興害蟲潛在分布的可行性，同時評估模型的不確定性。最後嘗試判斷影響長足捷蟻分布的主要環境因素。

結果/結論/應用啟示

建立完成的土壤深度 5、10、20、50 公分的最高與最低溫度線性回歸模型平均回歸係數 R2 為 0.88、標準誤差 1.34℃，能夠穩定預測土壤溫度。在預測長足捷蟻方面適存區與深度呈正比，深度 50 公分的土壤溫度預測表現最佳，高於氣溫圖層 15%，若僅用氣溫預測，很可能導致低估。CLIMEX 與 Maxent 兩模型均顯示台灣多數平地都適合長足捷蟻，且分布變化易受到極端高溫與極降雨影響。本研究完成土壤的模組，可提供其他土棲生物預測的現況和未來一個新的調整方向。

關鍵詞(Keywords)：長足捷蟻(*Anoplolepis gracilipes*)、土壤溫度模型(soil temperature model, CLIMEX, Maxent)

OB05

以幼蟲期發育表現探討瓜實蠅(*Zeugodacus cucurbitae*) (Diptera: Tephritidae)白蛹品系的大量飼養條件

Studies on the mass rearing requirements for the larval stage of white pupa melon fly strain (*Zeugodacus cucurbitae*) (Diptera: Tephritidae)

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背景/研究問題/材料方法

果實蠅科(Tephritidae)害蟲管理技術中，不孕性蟲技術(Sterile insect technique (SIT))為達到區域性撲滅害蟲族群的重要方法。SIT 計畫發展中，最重要的材料為具有白蛹基因的族群。該性狀能夠作為性聯遺傳育種的材料，篩選出單一雄蟲進行釋放。也能用於分子生物研究上的追蹤標記，方便人員或機器進行辨識。然而，儘管白蛹基因的族群已被應用許久，對其基本的生物學了解有限。本研究記錄了第一筆白蛹品系與野生型褐蛹品系的瓜實蠅(*Zeugodacus cucurbitae*)比較資料，針對幼蟲期在 20℃、25℃、30℃下的發育時間差異，以及 25℃下生命表的族群介量。

結果/結論/應用啟示

發現白蛹品系的幼蟲期在 20℃為 24.7 ± 0.13 天、25℃為 17.3 ± 0.13 天、30℃為 12.7 ± 0.12 天；褐蛹品系在 20℃為 25.8 ± 0.25 天、25℃為 17.7 ± 0.20 天、30℃為 12.3 ± 0.08 天；兩者間有顯著差異。白蛹品系 25℃下的生命表：淨增值率(R_0)為 333.1204 子代/♀、平均繁殖率(F)為 1265.585 子代/♀、內在增值率(r)為 0.1742 /天、無限增值率(λ)為 1.1903 /天、平均世代時間(T)為 33.25 /天。褐蛹品系為：淨增值率(R_0)為 366.9717 子代/♀、平均繁殖率(F)為 1167.364 子代/♀、內在增值率(r)為 0.1621 /天、無限增值率(λ)為 1.1760 /天、平均世代時間(T)為 36.33 /天。綜上所述，白蛹品系在 25℃下的平均繁殖率較高，平均世代時間較短，在大量飼養技術上具有優勢。

關鍵詞(Keywords)：瓜實蠅(*Zeugodacus cucurbitae*)、不孕性蟲技術(sterile insect technique)、生命表(life table)、發育時間(developmental time)、大量飼養(mass rearing)

OB06

人類世的生物加速反應

Acceleration of biological responses in Anthropocene

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背景/研究問題/材料方法

地球系統已進入劇烈加速度時代。逾半數無冰棲地遭開發、氣候加速變遷。生物很可能產生相應的加速反應，然而生物多樣性的時間與空間變化資訊仍相當零散。本研究首次調查生物分布位移(公里/年)以及群聚重組(%/年)在過去逾一世紀的速度變化，使用生物時序反應資料庫—BioShifts與 BioTIME，探索不同生態域(陸域與海域)、氣候區(溫帶與熱帶)、生理特性(植物、內溫及外溫動物)以及山地對上平地的反應速度如何隨時間改變。

結果/結論/應用啟示

過去兩世紀內，陸域生物加速朝山頂遷移，但沿緯度的位移並未增快，海洋生物也無加速移動。山區外溫動物，又以鱗翅目為主，以高於平均 3 倍的加速度(0.00003 公里/年)爬升、超前等溫線位移速度，卻也暗示了山頂空間急遽縮減的隱憂，尤其在熱帶，生物上移更為迅速。但整體生物群聚的重組速度在過去一世紀先加速後趨緩，唯生物類群間存在明顯差異。如山區與溫帶群聚的初始重組速度快，但減速幅度也大；相對地，陸域外溫及海洋內溫動物仍持續加快重組速度。我們的結果揭示，不同類群、氣候區或海陸域的生物面對人類世大規模環境變遷各有其反應特徵，探索背後機制為預測及管理劇烈加速度時代下的生物多樣性變化提供重要資訊。

關鍵詞(Keywords)：劇烈加速度時代(the Great Acceleration)、生態系統驟變(abrupt ecological change)、生態系統潰堤點(ecosystem tipping point)、生物多樣性重新分布(biodiversity redistribution)、群聚重組(community reshuffling)

OB07

A study on the effects of organic acids and probiotics supplements on insecticide toxicity in honeybees (*Apis mellifera*)

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背景/研究問題/材料方法

Honeybee (*Apis mellifera*) colonies have been declining due to stressors, like insecticides. The adverse effect of insecticides on honeybees’ immune system can be improved by supplementing probiotics and organic acids. Therefore, this study examined the toxicity of insecticides (Carbaryl, Chlorpyrifos, Deltamethrin, Dimethoate, and Imidacloprid) on worker honeybees as well as the effects of organic acids (citric acid and malic acid) and probiotics (TS6, EM) on the toxicity of the above-mentioned insecticides.

結果/結論/應用啟示

The results of the experiment demonstrated that worker honeybee mortality was significantly higher at 96 HAT when exposed to organophosphates (Chlorpyrifos and Dimethoate) and carbamate (Carbaryl) at all five concentrations. In addition, organophosphates showed 100% mortality between six and 24 hours at all concentrations. While neonicotinoids (Imidacloprid) and pyrethroids (Deltamethrin) exhibited significantly lower mortality in compare to other insecticides. The supplementation of organic acids (malic acid and citric acid) reduced the toxicity of Deltamethrin and Imidacloprid. A significant reduction in worker honeybee mortality has been observed in the Deltamethrin and Imidacloprid treated groups which received the probiotic feed supplements EM and TS6. Despite the addition of feed additives, Chlorpyrifos toxicity could not be reduced. In conclusion, this study confirmed that the use of feed additives such as citric acid and malic acid, TS6 and EM probiotics could reduce the toxicity caused by many insecticides.

關鍵詞(Keywords)：mortality, pesticides, probiotics, organic acids, toxic chemical

OB08

授粉者之性別對共花植物間的競爭和共存有其重要性
Pollinator sex matters in competition and coexistence of co-flowering plants

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背景/研究問題/材料方法

Male and female pollinators often exhibit sex-specific preferences for visiting different flowers. Recent studies have shown that these preferences play an important role in shaping the network structure of pollination mutualism, but little is known about how they can mediate plant-plant interactions and coexistence of competing plants. The ecological consequences of sex-specific pollination can be complex. Suppose that a plant is favoured by female pollinators. They produce male pollinators, who may prefer visiting other competing plants and intensify the negative effects of inter-plant competition. Here, we analysed a simple two plant-one pollinator model with the sex structure of the pollinator.

結果/結論/應用啟示

We observed that (i) sex-specific pollination can have complex consequences for inter-plant competition and coexistence (e.g. the occurrence of non-trivial alternative stable states in which one plant excludes or coexists with the other depending on the initial conditions), (ii) male and female pollinators have distinct ecological consequences because female pollinators have a demographic impact owing to reproduction, and (iii) plants are likely to coexist when male and female pollinators prefer different plants. These results suggest that sex-specific pollination is crucial for competition and coexistence of co-flowering plants. Future, pollination research should more explicitly consider the sex-specific behaviour of pollinating animals.

關鍵詞(Keywords)：替代穩定狀態(alternative stable states)、植物與植物之間的競爭(plant-plant competition)、授粉互利共生(pollination mutualism)、性別差異(sex difference)、物種共存(species coexistence)

OB09

台灣東方蜜蜂高度適應性之分子層次研究:基因表現與單核苷酸多態性的關聯

Molecular insights into the altitude adaptation of the Asian honey bee: Correlations between gene expression and SNPs

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背景/研究問題/材料方法

Individuals exhibit various adaptations such as physiological responses, life history adaptation, and behavioral adaptation to improve their fitness and survival rates. These adaptations are determined by their genetic makeup. Our research involves collecting Asian honey bees from elevations ranging from 500 to 2000 meters, analyzing their transcriptomes and single nucleotide polymorphisms (SNPs) to identify genes that may be linked to their ability to adapt to different elevations.

結果/結論/應用啟示

We analyzed the transcriptome of Asian honey bees collected from various elevations and found that there were between 121 and 559 differentially expressed genes (DEGs). There appeared to be a correlation between the number of DEGs and the differences in elevation, indicating that gene expression profiles may adapt to changes in elevation. We also conducted Gene Ontology (GO) analysis to identify potential molecular mechanisms involved in elevation adaptation. Our analysis revealed several GO terms, such as “oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen,” “structural constituent of cuticle,” and “iron ion binding,” which were present in at least four comparisons. We identified a total of 401131 heterozygous sites in four different samples from the SNP results. Additionally, all DEGs were associated with SNPs, which could potentially alter protein sequences and, therefore, individual fitness. While our findings suggest that molecular adaptation may explain how Asian honey bees adapt to climate change, further analysis is required to confirm our hypothesis.

關鍵詞(Keywords)：Asian honey bee, *Apis cerana*, elevation adaptation, differentially expressed genes, single nucleotide polymorphisms

OB10

台北植物園與中和四號公園授粉網絡與其時間動態

The pollination network and its temporal dynamic in Taipei Botanical Garden and Zhonghe No. 4 Park

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背景/研究問題/材料方法

訪花為昆蟲與植物常見交互作用，昆蟲的生活史需求及植物的繁殖策略，影響兩者的形態適應以及配對關係之演化。本研究自 2022 年 2 月至 2023 年 8 月，調查台北植物園與中和公園昆蟲-植物訪花配對與次數。每月各樣區進行兩次 20mins 目視調查，記錄當月開花植物與訪花昆蟲組成，及各配對事件隻次。比較植物與昆蟲物候資料，及與開花植物交互動態，探討訪花昆蟲多樣性與授粉網絡之時間分佈。

結果/結論/應用啟示

共記錄訪花昆蟲 110 種，膜翅目 56 種、鱗翅目 39 種、雙翅目 15 種。訪花事件 500 次以上植物 6 種；100-500 共 17 種；1-100 共 74 種；無訪花紀錄 63 種，其中蜜蜂科訪花次數最高。兩公園在 5-6 月及 11 月為訪花高峰，1-3 月為低峰，中和公園 8-10 月另有一低峰，訪花事件時間分佈受植物多樣性與開花數量共同影響。花期集中的植物在開花期間，較全年開花植物之被訪花次數多，兩者全年加總的訪花次數接近。授粉網絡顯示膜翅目雙翅目訪花涵蓋廣泛類群且全年活動，膜翅目的訪花頻度遠高於雙翅目，推測膜翅目與開花植物配對連結性更強。鱗翅目傾向利用提供花蜜為獎勵的植物，主要活動於 4-8 月，這些物種花期與授粉者生活史呈現一致性。提高都市植物多樣性，滿足不同功能群昆蟲所需資源，可使群落授粉功能更為穩定，並有機會外溢至較不優勢的開花植物。

關鍵詞(Keywords)：pollinator, pollination network, urban ecology

OB11

獨角仙、外米擬步行蟲及長角象鼻蟲之幼蟲腸道菌分離、鑑定及菌相差異。

Comparison of larval gut microbiota in Japanese rhinoceros beetle (*Trypoxylus dichotomus*), lesser mealworm (*Alphitobius diaperinus*) and coffee bean weevil (*Araecerus fasciculatus*) larva.

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背景/研究問題/材料方法

昆蟲腸道內具豐富的共生菌生態，不同的昆蟲種類及取食環境，其協助分解食物的腸道菌亦不同。為探討未來昆蟲腸道菌對腐植酸的轉換能力，及增加土壤碳匯潛力，故擬針對三種常見腐食性甲蟲獨角仙 (*Trypoxylus dichotomus*)、外米擬步行蟲 (*Alphitobius diaperinus*) 及長角象鼻蟲 (*Araecerus fasciculatus*) 進行研究。

分離上述三種甲蟲腸道內共生菌，培養於 LB 培養基，進行 16S rDNA 定序，並將序列於 NCBI 資料庫進行菌種比對。另進行甲蟲腸道之總基因體學分析，增幅腸道共生菌的 16S v3-v4 區域的核酸片段，大規模分析序列、建立其序列資料，進行不同甲蟲腸道內細菌的種類多樣性分析。

結果/結論/應用啟示

由上述三種甲蟲幼蟲腸道分離出 118 株菌，其中以 *Bacillus* 屬的細菌最多，且大多分離自獨角仙幼蟲。經總基因體學分析發現三種昆蟲腸道菌相差異大，相同的菌種僅有一株，為 *Corynebacterium* 屬；獨角仙腸道中的菌種豐富度最高，且菌種數量遠大於另外兩種甲蟲，推測可能原因為獨角仙幼蟲生活於土壤中造成的差異。外米擬步行蟲幼蟲腸道的優勢菌群為鏈球菌科 (Streptococcaceae) 佔比約 59%；長角象鼻蟲的優勢菌群為乳酸菌科 (Lactobacillaceae) 佔比約 58%；而獨角仙的的優勢菌群為瘤胃菌科 (Ruminococcaceae)、毛螺菌科 (Lachnospiraceae)，二者佔比相當。已知 *Bacillus* 屬菌種可促進農業資源物稻草分解成腐植質，具增加土壤碳匯潛力。本研究分離之 *Bacillus* 屬細菌種類豐富，將可提供未來昆蟲腸道共生菌進一步應用及碳匯研究參考。

關鍵詞(Keywords)：獨角仙(Japanese rhinoceros beetle)、外米擬步行蟲(lesser mealworm)、長角象鼻蟲(coffee bean weevil)、腸道微生物(gut microbiota)

OB12

台灣青蔥甜菜夜蛾的抗藥性調查

Investigation of insecticide resistance in *Spodoptera exigua* on green onion in Taiwan.

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背景/研究問題/材料方法

甜菜夜蛾為廣食性蔬菜害蟲，為青蔥上的重要害蟲。青蔥栽培者在甜菜夜蛾高峰期為減低危害損失，常以高頻度化學藥劑進行殺蟲防治，對田間甜菜夜蛾造成極高的選汰壓力。進行殺蟲劑的抗藥性研究有助於在蟲害管理上提供精準的用藥防治。本研究於青蔥主要產地包括彰化、雲林、宜蘭等地區採集甜菜夜蛾檢測其對多種殺蟲劑的感受性，探討抗藥性發生情形。

結果/結論/應用啟示

由檢測 22 種殺蟲劑結果得知，在宜蘭、彰化、雲林採集的甜菜夜蛾皆對佈飛松、畢芬寧、芬化利、賽滅寧、培丹等殺蟲劑之感受性低，建議暫停推薦使用。不同地區之藥劑感受性結果顯現不同區域及用藥習慣所呈現藥劑感受性發展情形確實有所不同,擬定用藥策略也需因地制宜。此外,宜蘭三星、彰化芳苑、雲林元長採集的甜菜夜蛾分別對因得克與剋安勃為 4.79-2487.71 倍與 264.96-1951.96 倍的抗藥性。進一步以小菜蛾抗剋安勃的魚尼丁受體 I4743M 點突變來檢測抗剋安勃的台灣甜菜夜蛾族群發現宜蘭三星、彰化芳苑、雲林元長 3 個田間抗性族群均具有 100%同型合子抗性點突變，顯現此點突變確實與甜菜夜蛾對剋安勃抗性機制有高度相關。

關鍵詞(Keywords)：甜菜夜蛾(beet armyworm (*Spodoptera exigua*))、抗藥性(insecticide resistance)、剋安勃(chlorantraniliprole)、因得克(indoxacarb)、魚尼丁受體(ryanodine receptor)

OB13

嬌小、大量且多樣：臺灣落葉層甲蟲計劃啟動！

Tiny, numerous and diverse: Taiwanese Leaf Litter Beetles Project has started!

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背景/研究問題/材料方法

Tiny in body size, numerous in specimens and diverse in species is the 'toxic mix' making studies of leaf litter beetles difficult and time-consuming. Consequently, nearly nothing is known about this important group of beetles in Taiwan. They are supposed to be decomposers affecting soil formation and forest ecology and recovery, yet we know nothing about the biology and evolution of individual species: are some of them crucial for forest ecology, vulneralble to alien species or climate change, or can some of them help with forest recovery? Our projects aims at (1) initiating an extensive study of Taiwanese leaf litter beetles across taxonomic groups, (2) documenting their diversity and distribution with special focus on endemic and alien species, and (3) providing a reliable tool for a quick identification for further studies on biology and ecology.

結果/結論/應用啟示

We DNA-barcode all morphotypes from each sample using ONT sequencing, and established a team of experts (more than 30 researchers worldwide at the moment) providing reliable identifications. We have already released the first dataset from Huisun to BOLD database, and we are processing the next set (1454 barcodes in total, ca. 460 species). We also collect new samples from across Taiwan to be analyzed in the near future. The first results include numerous first records of families, tribes, genera and species for Taiwan, e.g., the widespread seed-boring bark beetle *Coccotrypes advena*, rediscovery of the Taiwan endemic *Sivacrypticus taiwanus* (Archeocrypticidae) and a description of a new *Gyrelon*species (Cerylonidae). DNA barcodes also allow the first insights in diversity of some lineages, indicating the unexpected species diversity in *Panelus* (Scarabaeidae), altitude-limited lineages of *Lederina* (Melandryidae) or a separate lineage for east Asian populations of *Coccotrypes advena*. We believe this project will build a solid base for ecology and forestry research, for training a new generation of beetle systematists in Taiwan, and for understanding the unique biodiversity of Taiwanese forests.

關鍵詞(Keywords)：Coleoptera, forests, biodiversity, DNA barcoding, Taiwan

OB14

台灣鋏蠓 (*Forcipomyia taiwana*) 幼蟲棲地偏好與環境因子研究
Habitat preference and environmental factors of the biting midge, *Forcipomyia taiwana*

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背景/研究問題/材料方法

台灣鋏蠓為重要騷擾性害蟲，其幼蟲主要棲息於陰暗、裸露且濕潤的地面，主要以土壤表面之微藻類與藍綠菌等為食，然而目前尚未能清楚掌握其幼蟲生態與棲所，使得防治成效有限，也在化學藥劑防治上耗費用量與成本。本研究以國立自然科學博物館為試驗場域，發展標定都市綠地幼蟲孳生地點及土壤特性之方法，使用陸用羽化網收集地面羽化的成蟲，藉此找出台灣鋏蠓熱區，並以土壤採集法調查土壤幼蟲以確認棲所環境，記錄該處的土壤濕度、植被覆蓋，瞭解台灣鋏蠓與其他蠓科幼蟲及環境因子的相關性。

結果/結論/應用啟示

利用羽化網共進行 129 個樣站 136 次調查，採集到台灣鋏蠓的陽性率為 0.404；而 85 個土壤採集樣本中陽性率則為 0.45，若不考慮部份測試性的調查，陽性率將分別達 0.44 及 0.65，顯示基於前人研究基礎，利用羽化網與土壤採集能更有效且精準找到 幼蟲棲地。棲地環境因子分析結果顯示，都市綠地易成為台灣鋏蠓棲地的土壤包括保水性佳的花壇、人為澆灌區域及有建築物或樹林提供遮蔭的裸露地面，其土壤濕度介於 6-12%。在防治策略的建議上可透過種植地被植物、覆蓋落葉或增加陽光曝曬等方式改變該處環境減少幼蟲數量。本研究對於台灣鋏蠓幼蟲棲地的特性之瞭解，預期可作為制定環境友善防治台灣鋏蠓策略之參考。

關鍵詞(Keywords)：台灣鋏蠓(*Forcipomyia taiwana*)、幼蟲棲地(larva habitat)、羽化網(emergence trap)、蠓科幼蟲採集(collection of Ceratopogonidae larvae)、環境友善(environmental friendly)

OB15

國立自然科學博物館園區蠓科物種多樣性

Diversity of Ceratopogonidae in the green space of National Museum of Natural Science

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背景/研究問題/材料方法

台灣鋏蠓(*Forcipomyia taiwana*)(雙翅目：蠓科)為國立自然科學博物館園區重要吸血性昆蟲，希望能透過棲地改變與重點施藥來有效抑制台灣鋏蠓族群數量，以期作為都市防治策略之參考。但在防治過程中發現除小腿調查外，其他調查方法皆可能採到台灣鋏蠓或他種蠓科昆蟲，如未解決鑑定問題將無法確認各項防治方法之成效。故本研究於科博館園區設置捕蚊燈進行蠓科昆蟲誘集，使用形態及分子特徵鑑定物種，瞭解都市綠地中蠓科昆蟲多樣性，以利後續台灣鋏蠓防治評估與策略制定。

結果/結論/應用啟示

本研究配合科博館園區台灣鋏蠓小腿誘集調查，於2021年8月起至2023年7月進行40次燈光誘集調查，共採得75,738節肢動物樣本，其中蠓科昆蟲佔總數之7%，台灣鋏蠓佔總數之1.4%。使用形態及DNA條碼鑑定，於科博館採到之蠓科昆蟲包括22種鋏蠓(*Forcipomyia*)、5種毛蠓(*Dasyhelea*)、2種庫蠓(*Culicoides*)、5種裸蠓(*Atrichopogon*)共34個形態種，經序列上傳至NCBI序列比對，僅比到蘭花鋏蠓 (*F. pulcherrima*)，其餘物種則有待進一步確認。透過燈光誘集樣本的形態與分子鑑定結果，有助於連結幼蟲與成蟲形態，確認羽化網調查及土壤採集之樣本物種。同時，分子鑑定亦可協助連結外形相異之蠓科物種雌雄蟲，冀望透過蠓科鑑定做為後續調查與防治基礎，以避免因鑑定錯誤導致防治相關試驗誤差。

關鍵詞(Keywords)：台灣鋏蠓(*Forcipomyia taiwana*)、蠓科鑑定(Ceratopogonidae identification)、DNA條碼(DNA barcode)、形態(morphology)

論文宣讀：行為、生理、個體生物學

Oral Session: Ethology, Physiology and Organismic Biology

OE01

以幾丁質為基質純化大腸桿菌表現系統中的 Galectin1-melittin 融合蛋白

Chitin as a matrix for the purification of Galectin1-Melittin fusion protein expressed in *Escherichia coli.*

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背景/研究問題/材料方法

The application of recombinant protein is a mature technology, however, the cost of protein purification remains high. There is a growing demand to develop cost effective and rapid purification method. Galectin-1 (Gal1) is a mammalian exocytotic extracellular protein containing carbohydrate recognition domain (CRD) specific for β-galactoside, a structural similar to that of chitin. Our previous studies showed that Gal1 could bind with chitin to enhance 3T3 cells and chondrocyte growth efficiency on the Gal1-coated chitosan membranes and disrupt insect peritrophic matrix, an anatomical structure composed of chitin and proteins lined the insect midgut. In view of the availability and binding properties with Gal1, we aim to develop chitin as an affinity matrix for the purification of Gal1 fusion proteins by using melittin (MLT, an important bee venom with high therapeutic value) as an example.

結果/結論/應用啟示

The results showed that Gal1-MLT fusion protein overexpressed in Escherichia coliwas successfully pulled down by chitin power. Moreover, the chitin bound Gal1-MLT fusion protein could effectively eluted with SDS-solution. After removal of SDS, the purified fusion protein was further subjected to MLT biological activity assay. The results showed that the recombinant MLT exhibit antibacterial activity comparable to that of commercial product.

關鍵詞(Keywords)：蛋白質純化(purification)、半乳糖凝集素-1(Galectin-1)、蜂毒肽(melittin)、幾丁質(chitin)、大腸桿菌表現系統(*Escherichia coli*. expression system)

OE02

亞致死劑量益達胺誘發工蜂早熟之生理機制探究

Investigating physiological mechanisms of sublethal imidacloprid-induced precocious foraging in honey bee workers

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背景/研究問題/材料方法

西洋蜂為真社會性昆蟲，工蜂之日齡分工機制受諸多因子所調控。前人研究指出，工蜂體內之青春激素含量為影響其內外勤務轉換之關鍵，轉變為外勤蜂的過程中，必會伴隨青春激素含量急遽上升之現象，而以外力促使內勤蜂體內青春激素含量增加，則會誘使其提早成為外勤蜂。此外，暴露於環境逆境源 (如益達胺) 中，會使工蜂提早離巢，並影響其飛行與返巢能力。此些負面影響，極可能與蜂群衰竭失調症候群的重要特徵，即工蜂於短時間內大量離巢消失之現象密切相關。我們近期之研究發現，幼蟲期時暴露於 10 ppb 益達胺的環境中會促使內勤蜂青春激素生合成相關之基因表現量上升。為進一步釐清環境逆境源誘發工蜂早熟離巢現象之成因，本研究使用氣相色譜質譜儀，建立檢測青春激素之程序，並監測其於工蜂體內之含量變化，以探討幼蟲期暴露於亞致死劑量益達胺中，對工蜂生理層面之影響。

結果/結論/應用啟示

本研究現已建立最佳之青春激素檢測流程，並用以檢測幼蟲期暴露於亞致死劑量益達胺之工蜂，其生理數據變化資訊。實驗結果顯示，從第 15 日齡開始，工蜂體內之青春激素含量已高於未餵藥組，表示暴露於極低劑量益達胺下，便會使工蜂體內的青春激素含量於較低日齡時就顯著增加，並可能誘使工蜂提早離巢之現象發生。

關鍵詞(Keywords)：蜂群崩解失調症候群(colony collapse disorder (CCD))、亞致死劑量益達胺(sublethal imidacloprid)、青春激素(juvenile hormone III)、西洋蜂(*Apis mellifera*)

OE03

黃原鼻白蟻的生殖階級發育途徑

Reproductive castes development of Prorhinotermes flavus (Blattodea: Rhinotermitidae)

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背景/研究問題/材料方法

所有白蟻物種皆為真社會性昆蟲，主要仰賴一對有翅生殖型 (alate) 建立新的巢群，蟻王蟻后長期共存，稱為主要繁殖型 (primary reproductives)，然而，我們在恆春半島、蘭嶼及綠島發現的黃原鼻白蟻 (*Prorhinotermes flavus* (Bugnion & Popoff, 1910)) 常被觀察到大量補充生殖型 (neotenic castes, secondary reproductives)，其發育途徑仍屬未知。透過顯微鏡觀察標本與測量形質，再利用顯微斷層掃描 (micro-CT) 與電子顯微鏡 (SEM) 觀察性腺與腹部表皮皺褶，歸納出各階級兩性的辨識方法，再利用實驗室內飼養各種階級組成的群體，誘導產生各類生殖型，確認黃原鼻白蟻各類生殖型的發育途徑。

結果/結論/應用啟示

黃原鼻白蟻的生殖型分成 4 種：有翅生殖型、無翅補充生殖型 (apterous neotenic caste)與 2 種短翅補充生殖型(brachypterous neotenic castes)。有翅生殖型的發育途徑經由幼蟲 (larva) 蛻皮 2-3 次轉變為擬工蟻 (pseudergate)，再蛻皮 3-6 次成為若蟲 (nymph)，而後僅蛻皮 1 次成為有翅生殖型；無翅補充生殖型則由擬工蟻蛻皮而成；第一型的短翅補充生殖型經由若蟲蛻皮直接轉變而成；第二型的短翅補充生殖型則是經由若蟲退階蛻皮 (regressive molt) 轉變為短翅擬工蟻後，再蛻皮而成。生殖階級的腹部背板表皮有些微隆起，而非生殖階級的腹部背板表皮平坦。黃原鼻白蟻各階級雄性腹板皆未被蓋住，有尾針 (styli)；而雌性生殖型的第 7 腹板完全蓋住第 8 和第 9 腹板，無尾針；雌性非生殖階級的第 7 腹板則部分蓋住第 8 和第 9 腹板，並帶有尾針。建構黃原鼻白蟻各類生殖型發育途徑將為研究白蟻生殖與婚配機制提供重要的基礎資訊。

關鍵詞(Keywords)：黃原鼻白蟻(*Prorhinotermes flavus*)、生殖階級 (reproductive castes)、發育途徑 (development pathway)

OE04

消除 PI-*Wolbachia* 誘導漿黑卵蜂 *Telenomus remus* 之雌性功能性童貞突變 (female functional virginity mutation)

Induction of female functional virginity mutations in the wasp *Telenomus remus* by eliminating PI -*Wolbachia*.

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背景/研究問題/材料方法

漿黑卵蜂 *Telenomus remus* Nixon (Scelionidae) 是一種繁殖率高且易於大規模飼養生物防治秋行軍蟲的優秀天敵，其受到 PI-*Wolbachia* 感染後生殖模式會由產雄孤雌生殖 (arrhenotoky) 轉變為產雌孤雌生殖 (thelytoky)，對生物防治應用更具優勢，然而研究發現以外在方式移除漿黑卵蜂體內 PI-*Wolbachia*，會誘發生殖能力異常的雌性功能性童貞突變 (female functional virginity mutation)，筆者團隊探討屏東地區之漿黑卵蜂族群是否也會產生此突變或是其他生殖能力上的異常以評估 PI-*Wolbachia* 感染族群施放於田間的適性。為評估筆者團隊建立之感染 PI-*Wolbachia* (*w*Rem)族群生殖異常情形的發生，成功移除了 *w*Rem，並利用移除品系與無感染品系 (wild type, wt) 進行雜交及自交試驗，以子代雄性比作為是否成功受精，評估生殖能力是否異常。

結果/結論/應用啟示

移除 *w*Rem 後 *T. remus* 雄性比顯著的提升，且無論雌雄個體在與 wt 雜交處理中，均幾乎無法產生任何雌性，由此可知此異常與雌性功能性童貞突變不同，尚有其他的因素導致。本研究證實筆者團隊採集之 *w*Rem 菌株，確實會令 *T. remus* 族群產生生殖力異常，但與僅影響雌性的功能性童貞突變不同。可能是透過專一性演化 (obligate evolution) 所積累之突變所導致。且試驗中發現此性狀無法透過有性生殖摻入 wt 族群，此結果可在未來生物防治之安全性評估中做為重要參考。

關鍵詞(Keywords)：寄主專一性(host specificity)、生物防治(biological control)、wRem 共生菌(wRem Symbiotic bacteria)、生殖障礙(reproductive disorders)、秋行軍蟲(*Spodoptera* frugiperda)

OE05

東方果實蠅對甲基丁香油反應之關鍵氣味結合蛋白特性分析

Study of key odorant-binding proteins associated with methyl eugenol responsiveness in *Bactrocera dorsalis*

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背景/研究問題/材料方法

Long-term screening from use of intoxicated methyl eugenol (ME) attractants has been shown to increase the number of ME-unresponsive male oriental fruit flies (*Bactrocera dorsalis* (Hendel)), creating a potential control gap. This study aims to analyze differential gene expressions and in vitro protein characteristics of target odorant-binding proteins (OBPs) associated with ME responsiveness in male flies. We reared cumulative generations from wild fly populations with and without ME responsiveness in our laboratory and carried out whole-transcriptome gene analysis to screen out candidate OBPs with differential expressions related to ME responsiveness. The differential expressions of candidate OBPs were verified by real-time polymerase chain reaction through ME-induced reaction-related experiments. Differentially expressed target OBPs were expressed in vitro with *E. coli*for subsequent analysis of protein properties.

結果/結論/應用啟示

Following repeated screening through cumulative generations, ME non-responsiveness was maintained at 10-20% of the entire population. Whole-transcriptome analysis and verification of differential gene expressions in candidate OBPs revealed an OBP that has not yet been published in functional studies. The OBP showed low expression in non-responsive fly populations following ME treatment, so we speculate that it may be a key target associated with ME non-responsiveness in oriental fruit flies. This study analyzed the characteristics of candidate OBPs and successfully expressed and purified candidate OBPs in vitro. We also plan to analyze the affinity of OBPs to ME molecules using fluorescence competition binding assays.

關鍵詞(Keywords)：甲基丁香油(methyl eugenol)、東方果實蠅(*Bactrocera dorsalis*)、氣味結合蛋白(odorant-binding protein)、蛋白質體外表現(protein expression in vitro)

OE06

共生蟎透過比例辨識法選擇埋葬蟲宿主

Proportional processing of burying beetle host selection in the phoretic mite

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背景/研究問題/材料方法

Phoretic animals, by attaching to other species with greater mobility, can access resources otherwise unobtainable. Choosing a proper host could be vital for their survival and reproduction, yet its underlying mechanism remains to be tested empirically. Although proportional processing is a recognized cognitive strategy in psychophysics, most research on this topic focuses on vertebrates - whether such sensory methods apply in invertebrates remain understudied. We investigate whether the phoretic mites (*Poecilochirus carabi*) show a preference for larger burying beetle hosts (*Nicrophorus nepalensis*) and whether such behaviour aligns with proportional processing. We introduced mites onto adult beetle and confined them with a mite-free beetle, allowing interaction for ten minutes. Each beetle pair was exposed to a gradient of mite densities: 1, 5, 10, 20, up to 40 mites. After the experiment, we determined the number of mites on each beetle, and analysed the relationship between mites' preference for beetle size and 1) absolute body size difference, 2) proportional size difference, and 3) mean size of each pair of the beetles.

結果/結論/應用啟示

When the densities of introduced mites are high, they show a stronger preference for larger beetles, especially when both options are of smaller size. This preference declines when both hosts are larger beetles. However, the proximate and ultimate causes of this behaviour require further investigation. These findings reveal that proportional processing might be more prevalent in invertebrates, and plays an essential role in the host selection of phoretic animals than previously thought.

關鍵詞(Keywords)：宿主選擇(host selection)、比例辨識法(proportional processing)、行為生態(behavioural ecology)、埋葬蟲(burying beetle)、共生蟎(phoretic mite)

OE07

Comparative genomics of *Purpureocillium lilacinum* NCHU-NPUST-175 and Molecular Marker Development

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背景/研究問題/材料方法

The *Purpureocillium lilacinum* NCHU-NPUST-175 (Pl-NCHU-NPUST-175) is an entomopathogenic fungus with the potential to control *Forcipomyia taiwana*. During EPF field application, molecular markers play a key role in fungal surveillance to identify fungal species or verify the presence of applied fungi. This study completed the whole-genome sequencing of Pl-NCHU-NPUST-175 by using Oxford Nanopore Technologies (ONT) and performed comparative genomics approaches for the development of Pl-NCHU-NPUST-175 strain and species-specific molecular markers. For comparative genomics analysis, the genome of Pl-NCHU-NPUST-175 was compared with two other strains *Purpureocillium* spp. to identify the distinctive genomic regions (DGRs). The candidate DGRs were confirmed by PCR to validate the specificity.

結果/結論/應用啟示

The whole genomic size of Pl-NCHU-NPUST-175 was 36.76 Mbp, with 27 contigs. Among these contigs, the largest contig was 6.78 Mbp, and the N50 contig size was 4.08 Mbp. The GC% was 58.51%. There were 13,157 putative open reading frames (ORFs) in the genome with a gene density of 63.36%. The number of exons was 44,886, with an average of 3 exons per gene. Through a comparative genomic analysis, 1154 fragments with low similarity which lengths are greater than 5000 bp were identified between Pl-NCHU-NPUST-175 and *P. takamizusanense* (ID: 111624), *P. lilacinum* (ID: 42115). Subsequently, ten specific primers (pl_1-pl_10) were designed and tested. Among these primer sets, 8 molecular markers, including 7, were identified as species- specific among *Purpureocillium* spp., whole only one molecular marker, pl_6, was identified as strain-specific among different strains of *P. lilacinum*. This study underscores the feasibility of developing molecular markers using a comparative genomics approach.

關鍵詞(Keywords)：淡紫擬青黴菌(*Purpureocillium lilacinum*)、分子標記(molecular markers)、比較基因體學(comparative genomics)、全基因體定序(whole genome sequencing)

OE08

Transcriptome analysis of entomopathogenic fungi, *Beauveria bassiana* infected coffee berry borer *Hypothenemus hampei* (Ferrari)

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背景/研究問題/材料方法

Hypothenemus hampei (Ferrari), commonly known as the coffee berry borer (CBB), poses a significant threat to coffee production, resulting economic losses within the coffee industry. Given the growing concerns associated with chemical control methods, the need for an eco-friendly management strategy, such as microbial control has become increasingly apparent. Beauveria bassiana (Bb) is widely utilized as a biological control agent to manage coffee berry borers effectively. However, there remains a scarcity of data regarding the molecular factors that contribute to the virulence of *B. bassiana* against CBB, as well as the mechanisms underlying CBB responses to fungal infection. In this study, we performed the RNA-seq and conducted de novo assembly of the transcriptomes of both CBB and a fungal isolate Bb-NCHU-271, followed by differential gene expression (DEG) and gene ontology analysis to uncover the interaction between CBB and *B. bassiana*.

結果/結論/應用啟示

Based on RNA-seq data from CBB infected with Bb-NCHU-271 compared with non-infected CBB, a total of 274 differentially expressed genes (DEGs) were identified, comprising 120 were up-regulated genes and 154 were down-regulated genes. The Gene Ontology indicated that most up-regulated GO terms included "membrane" (GO:0016020), "plasma membrane" (GO:0005886), and "nucleus" (GO:0005634). Conversely, down-regulated GO terms encompassed "membrane", "nucleus", and "regulation of transcription by RNA polymerase II" (GO:0006357). As for the fungal response, we detected 1609 DEGs by comparing the infected CBB with Bb-NCHU-271 cultured on the medium. Among these DEGs, 1308 genes were up-regulated, while 301 were down-regulated. The Gene Ontology indicated that the major up-regulated GO terms were "membrane" (GO:0016020), "nucleus" (GO:0005634), and "ATP binding" (GO:0005524). However, most down-regulated GO terms included "membrane", "ATP binding", and "metal ion binding" (GO:0046872). Our future research endeavors, we plan to employ qRT-PCR to validate the outcomes of the DEGs analysis. This approach will allow us to obtain a better insight into the mechanisms of Bb infection and shed light on the defensive strategies employed by CBB to counter fungal infection.

關鍵詞(Keywords)：蟲生真菌(entomopathogenic fungi)、白殭菌(*Beauveria bassiana*)、咖啡果小蠹(coffee berry borer, *Hypothenemus hampei*)、轉錄體(transcriptome)、差異表現基因(differentially expressed genes)

OE09

白蟻不對稱彈性大顎最佳幾何比例：二維模型探究

Optimal shapes for termite’s asymmetric elastic mandibles: 2D geometric models

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背景/研究問題/材料方法

兵蟻是白蟻巢中用於防禦的階級，在天敵與環境的選汰壓力下，演化出多樣的大顎型態；其中的彈性大顎是透過左右大顎相互擠壓產生形變，所儲存的彈性位能在釋放瞬間可使大顎達到遠超於肌肉收縮可及的速度。彈性大顎依形態可分為對稱與不對稱，前人發現巴拿馬小白蟻(*Termes panamaensis*)的對稱型大顎的可產生 67 m/s 的高速彈擊，而新渡戶歪白蟻(*Pericapritermes nitobei*)的不對稱型大顎更能產生 132 m/s 的超高彈擊速度。為探討不對稱大顎的形狀變異如何影響攻擊表現，我們提出簡化的二維幾何模型，將複雜的大顎形態簡化、並對右大顎長度標準化為三個參數：R_L(左大顎相對長度)、R_M(大顎間距相對長度)、R_B(左大顎基部佔總長之比例)，來評估在不同運動範圍條件下，不同參數如何互相影響並決定最終按壓角度，從而影響能量儲存及彈擊表現。

結果/結論/應用啟示

研究顯示，在不對稱彈性大顎系統中，左大顎長度與大顎間距緊密相關：拓寬大顎間距方能延伸左大顎長度，卻又會降低能量儲存潛力；而左大顎基部比例則可用以調節此性能損失。此外，加入新的運動範圍條件可改善模型對左大顎自然角度的預測，按壓角度的峰值位置也更接近現生物種，解決過去模型部分預測不符真實的問題。透過對照現生物種，我們得以探究不對稱彈性大顎的最佳幾何比例。

關鍵詞(Keywords)：白蟻(termite)、彈性大顎(elastic mandibles)、幾何模擬(geometric simulation)、彈性位能(elastic potential energy)、形態空間(morphospace)

OE10

Wolbachia 感染對漿黑卵蜂適應高溫的影響
The effects of Wolbachia infection on thermal adaptation in *Telenomus remus*

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背景/研究問題/材料方法

近年來氣候變遷造成溫度升高，極端高溫頻繁發生。溫度變化除了對昆蟲及其體內共生物有直接影響，亦可能干擾兩者間隨著長期的互動而演化出的共生關係。本研究透過一小時的高溫 (40°C) 處理漿黑卵蜂 (*Telenomus remus*) 與其內共生菌 *Wolbachia*, *w*Rem，利用轉錄組分析 (RNA-seq) 探討高溫和 *w*Rem 不同處理間，*T. remus* 基因表現差異的影響。同時藉由成蟲期所經歷的高溫處理，測試各處理之族群親代 1) 存活率、2) 繁殖力等生活史影響。

結果/結論/應用啟示

RNA-seq 分析比較高溫和室溫下有無 *w*Rem 感染的差異表現基因，分別有 2401 個和 1689 個，且高溫處理族群之上下調基因數量皆高於室溫組別，於轉錄組基因中與存活相關之 Hsp 70、90 等基因，在不同環境下有無 *w*Rem 感染的 *T. remus* 皆有表現量差異。一小時 40°C 高溫處理後，不論有無 *w*Rem 感染，成蟲存活率皆顯著的降低，但對雌蟲繁殖力的影響則不顯著。此外漿黑卵蜂體內的 *w*Rem 並沒有改變 *T. remus* 面臨高溫後的死亡率。本研究利用 RNA-seq 技術對極端高溫環境下的漿黑卵蜂提供轉錄組資訊，有助於為寄生蜂適應極端高溫提供新見解，並持續尋找影響漿黑卵蜂耐熱性相關基因，可在未來進行生物防治作為篩選品系的參考。

關鍵詞(Keywords)：轉錄組分析(RNA-seq)、適存值(fitness)、極端氣候事件(extreme climate events)、次世代定序(next generation sequencing, NGS)

OE11

一種喜白蟻性隱翅蟲的擬寄生性隱翅蟲
A staphylinid parasitoid of a staphylinid termitophile

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背景/研究問題/材料方法

隱翅蟲科的 Lomechusini 族共約 2,500 種，包含許多喜螞蟻性或喜白蟻性的物種，從專性捕食者到巢內共生物，與社會性昆蟲之間具有十分多樣的共生關係，然而大部分物種的生活史及幼生期資訊卻十分稀少，尤其是物種數高達 900 多種的 *Zyras* 屬，已知約 60 個物種被記錄與螞蟻或白蟻有關，然而整個屬卻僅有一筆幼生期資訊。本研究即針對臺灣土白蟻 (*Odontotermes formosanus*) 覓食區域附近活動的兩種 *Zyras* 屬物種進行生活史研究。

結果/結論/應用啟示

透過野外觀察、室內行為實驗與食性偏好分析，本研究確認了隱翅蟲科中尚未紀錄的生活史策略。其中一個物種，*Zyras sauteri*，為臺灣土白蟻的專性捕食者，雌蟲產下巨大卵並具有不取食的幼生期。另一個尚未描述的物種，*Zyras* sp.，其幼蟲被證實為 *Z. sauteri* 幼生期的專性擬寄生者。本研究針對此特殊的生活史及交互關係，提出可能的起源情境假說。

關鍵詞(Keywords)：前角隱翅蟲亞科(Aleocharinae)、喜白蟻性(termitophily)、擬寄生生物(parasitoid)、共生生物(symbiont)

OE12

顯微斷層掃描 (Micro CT) 在昆蟲學研究的應用
Micro computed tomography in entomological research

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背景/研究問題/材料方法

顯微斷層掃描是近年來一項針對小型動物的造影技術。藉由 X 光的穿透性及三維影像的建立，保持樣本完整性的同時提供生物內部的構造。目前台灣研究單位所提供機型的解析度為 0.35 至 9 微米，可依照使用者的需求選擇。但事前的樣本製備及染色，以及事後的影像合成及分析上需要許多繁雜的技術。為了讓更多的使用者在使用顯微斷層掃描之前，能夠理解並活用此項服務於研究上，本次以現有的成果及過往研究整理以供參考。

結果/結論/應用啟示

目前斷層掃描在觀察上，可以忽略光學上的遮蔽問題以取得完整的外部形態，但針對密度較低的軟組織，根據觀察目標仍需經過不同濃度及時間的染色處理才能清楚成像。透過昆蟲外部形態的特徵和內部組織的變化，可以推斷棲地環境和食性，進一步深入研究物種的分類和特徵演化。三維影像除了作為力學研究中模擬肌骨組織的運動，製作實際立體模型和仿生機器，也在收藏和展示方面提供便利性，增加研究者之間的信息交流。除了昆蟲本身，這項技術也適用於觀察非生物體，包括巢腔內部的挖掘情況和周圍棲息地的變化，進一步了解昆蟲的行為和防治研究。因此近年來，微型斷層掃描已經成為防檢疫、法醫昆蟲學和考古學等領域不可或缺的技術。

關鍵詞(Keywords)：斷層掃描(computed tomography)、昆蟲(insect)、形態(morphology)、顯影劑(radiocontrast agent)、化石(fossil)

OE13

利用桿狀病毒表面展示技術建立呼吸道病毒感染血清檢測系統

Establishment of serological detection systems for respiratory virus infections using baculovirus surface display technology

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背景/研究問題/材料方法

Respiratory tract infections are among the most devastating infectious diseases, accounting for more than 138 million new cases and nearly 1 million deaths each year. Serological assays that identify antibodies elicited by virus infection are needed to support the distinction of causative pathogens to implement effective treatment and disease control. However, it is of great challenge and danger to collect sufficient representative viruses for the assay. In this study, we demonstrated that baculovirus surface display technology, which consists of baculovirus AcMNPV and insect cell line Sf21 derived from *Spodoptera frugiperda*, can be used to establish a serological detection system for respiratory virus infection. We generated recombinant baculoviruses to display the surface antigens of important respiratory viruses, such as influenza viruses, respiratory syncytial viruses, and human coronaviruses. Sf21 cells infected with the viruses will be used to develop a cell-based enzyme-linked immunosorbent assay (ELISA) system to detect antibodies in patients’ serum.

結果/結論/應用啟示

After generating the recombinant baculoviruses and infecting Sf21 cells with the viruses, we found that all the antigens were expressed in the infected cells and most of the antigens adequately displayed on the plasma membrane of Sf21. We seeded the infected cells into microwell plates to be the antigens of ELISA and applied serum samples from pediatric patients with known infections to the system. ELISA signals of the samples were found to occur at corresponding viral antigens, indicating that the antigens displayed on the Sf21 cell surface interacted specifically with antibodies in the serum samples. Our results demonstrate that the cell-based ELISA can be used to detect antibodies elicited by respiratory virus infections. As the system avoids the use of dangerous human-infectious viruses, it can become an important new tool for epidemiological research of increasingly severe respiratory infections and contribute significantly to the control of respiratory diseases.

關鍵詞(Keywords)：桿狀病毒(baculovirus)、酵素結合免疫吸附分析法(enzyme-linked immunosorbent assay (ELISA))、呼吸道病毒感染(respiratory virus infection)、血清學檢測(serological analysis)、秋行軍蟲(*Spodoptera frugiperda*)

OE14

解析 *vasa* 基因在孤雌胎生豌豆蚜的發育表現以及演化意涵

Dissecting the developmental expression and evolutionary significance of *vasa* genes in the parthenogenetic and viviparous pea aphid *Acyrthosiphon pisum*

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背景/研究問題/材料方法

Aphids, notorious agricultural pests with a vast host plant repertoire, notably exhibit a highly prolific asexual phase, resulting in rapid population growth and detrimental effects on their host plants. Unlike most insects, aphids possess multiple copies of the essential germline gene, *vasa*, a feature we explored in our study, focusing on the pea aphid (*Acyrthosiphon pisum*) as a model organism in developmental biology. This species boasts four *vasa* homologs collectively referred to as *Ap-vasa*. Our primary objective was to investigate the expression patterns of these four Ap-Vasa proteins in the asexual and viviparous phase of the pea aphid's life cycle, shedding light on the evolutionary consequences of *vasa* gene duplication. Additionally, we conducted experiments, including drug treatments, to unveil the intricate cellular mechanisms governing the precise anchoring of the germline-specific Ap-Vasa1 protein at the posterior region of oocytes and embryos.

結果/結論/應用啟示

Our research involved genetic data collection from eleven aphid species, revealing a range of three to six *vasa* paralogs. We discerned that aphids typically maintain four *vasa* paralogs, with instances of three likely due to gene loss and those with six attributed to further gene duplication events. Examining gene expression patterns, we found that only Ap-Vasa1 exhibited germ cell and presumptive germ plasm-specific expression, while the other three paralogs were exclusively expressed in somatic tissues. Surprisingly, our experimental drug treatments unveiled that actin, not tubulin as previously assumed, plays a pivotal role in the cytoskeletal system, facilitating the germ plasm-driven mechanism. In summary, our study delved into the intricate evolutionary aspects of *vasa* gene duplication in aphids. We discovered that only one *vasa* paralog retained its specialized germline function and provided compelling evidence highlighting actin's role in supporting the Vasa-based assembly of maternal germ plasm, particularly in hemimetabolans, with a specific focus on aphids.

關鍵詞(Keywords)：蚜蟲(aphids)、無性生殖胚胎發育(asexual embryogenesis)、生殖漿(germ plasm)、生殖細胞(germ cells)、生殖基因(germline genes)

OE15

多樣寡家蟻探索行為與集體覓食行為之初探

Preliminary study of exploration behavior and collective foraging behavior by the marauder ant *Carebara diversa*

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背景/研究問題/材料方法

樣寡家蟻 (*Carebara diversa*) 因集體覓食方式，而被稱「亞洲掠奪蟻」 (Asian marauder ant)。在社會性昆蟲中，工蟻個體行為差異對群體行為深具影響。過往研究多描述多樣寡家蟻的集體覓食行為，對於工蟻個體與群體在陌生環境下的探索行為知之甚少。本研究分兩大試驗，一為探索部分，設計四個覓食區，各放置大蠟蛾 (*Galleria mellonella*) 幼蟲、蜂蜜水、洋芋片與雀榕 (*Ficus wightiana*) 種子，分別探討個體與群體工蟻的探索行為。另一集體覓食部分，蟻巢連接單一覓食區，覓食區中放置上述四種食物，以觀察蟻巢內工蟻集體覓食的行為。

結果/結論/應用啟示

個體探索試驗結果顯示，多數工蟻先接觸洋芋片，其次是種子與蜂蜜。值得注意的是，有 33.8% 工蟻在測試時間內並未探索到任何食物。在試驗中 60.8% 工蟻僅接觸一種食物，且以洋芋片居多；5.4% 工蟻接觸了兩種食物。工蟻從探索至找到食物，平均所花費的時間並無顯著差異。群體探索試驗分為兩群，一群為未具探索經驗的工蟻，多數先接觸大蠟蛾幼蟲，其次為蜂蜜水；另一群為有探索經驗的工蟻，則以接觸洋芋片居多，其次是大蠟蛾幼蟲，此結果顯示有探索經驗的工蟻似乎影響了群體探索行為。集體覓食試驗中，小型工蟻最先離巢覓食，當小型工蟻接觸到大蠟蛾幼蟲後，便會出現中型兵蟻前來協助搬運幼蟲。集體覓食過程中，工蟻以含蛋白質與脂質食物為優先選擇對象。

關鍵詞(Keywords)：多樣寡家蟻(*Carebara diversa*)、工蟻(worker)、探索行為(exploration behavior)、集體覓食(collective foraging)

論文宣讀：醫學昆蟲學
Oral Session: Medical Entomology

OM01

Detection of *Anaplasma*, *Babesia*, *Ehrlichia*, and *Neoehrlichia* in ticks from small mammals in Kinmen, Taiwan

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背景/研究問題/材料方法

Ticks are obligatory hematophagous ectoparasite and some pathogens can be transmitted through transstadial or transovarial transmission making it a vector for human and zoonotic diseases. However, the symptoms of tick-borne infections are mostly non-specific and are difficult to be diagnosed correctly. Moreover, the reason of the increasing cases of fever origin are unknown and of interest. In recent years, studies on the prevalence of *Rickettsia* in Kinmen have been addressed but other pathogens are not included. To better understand the existence and prevalence of tick-borne agents in Kinmen, a long-term and systematic survey was conducted from August 2018 to June 2022. Ticks were morphologically identified and total genomic DNA was extracted from an individual tick from captured small mammals. PCR with primers of *p44*, 16S, and 18S genes were used for the detection of *Anaplasma*, *Babesia*, *Ehrlichia*, and *Neoehrlichia* spp. Positive samples were sequenced for further phylogenetic analysis.

結果/結論/應用啟示

In this study, 692 small mammals were trapped from Kinning, Kincheng, and Kinhu around Kinmen. Five species of rodents (*Callosciurus erythraeus*, *Mus musculus*, *Rattus losea*, *Rattus norvegicus*, and *Rattus tanezum*) and one species of *Suncus murinus*were identified. A total of 926 ticks were collected, and the major tick species was *lxodes granulatus*. The positivity rate of *Anaplasma phagocytophilum*, *Candidatus* Neoehrlichia mikurensis, *Ehrlichia*, and *Babesia* spp. in *lxodes granulatus* was 2.0% (4/200), 8.5% (17/200), 42.5% (85/200), and 0% (0/11) respectively. The sequences of *Anaplasma phagocytophilum* (n=4), *Candidatus* Neoehrlichia mikurensis (n=17) and *Ehrlichia* spp. (n=85) shared similarity of 100%, 100%, and 100% to reference sequence on NCBI, respectively. The study provides basic information and proposes the potential relationship between tick-borne pathogens and the origin of unknown fever in Kinmen.

關鍵詞(Keywords)：zoonotic diseases, *Anaplasma*, *Babesia*, *Ehrlichia*, *Candidatus* Neoehrlichia mikurensis

OM02

臺北市立動物園廄刺蠅對白犀牛之危害調查

The survey of infestation of *Stomoxys calcitrans* (Diptera: Muscidae) on *Ceratotherium simum* in Taipei Zoo

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背景/研究問題/材料方法

廄刺蠅不只造成畜牧業的損失，也對動物園的動物造成危害，包含血液流失、使動物緊迫、傳播病源等，但在動物園內危害程度受環境因子的影響瞭解尚不充分。本研究旨在開發評估廄刺蠅對園內白犀牛的危害程度之方法，並探討影響動物受廄刺蠅危害程度高低之因子。本實驗以臺北市立動物園內白犀牛個體為觀察對象，先使用 Image J 軟體計算傷口面積作為分母、廄刺蠅覆蓋傷口的面積作為分子，依比例分出 5 級以評估危害程度，再根據不同傷口上廄刺蠅的聚集情況，記錄廄刺蠅在不同天氣和動物所在位置條件下的危害程度，以及不同環境測量因子(溫度、濕度、風速、光強度和紫外線指數)，最後使用無母數統計法分析危害程度和不同因子間的關係。

結果/結論/應用啟示

天氣因子方面，雨天和多雲、雨天和晴天兩組之間具顯著差異，其餘組別無顯著差異；位置條件方面，室內和門前、樹蔭下和太陽直射處之間均具顯著差異，其餘組別間則無顯著差異。對不同環境測量因子進行相關性分析與迴歸，結果顯示環境測量因子和危害程度之間的相關性有限，且迴歸模型的適合度低。未來需累積更多數據以提升模型的可信度，並進一步研究其他環境因子對廄刺蠅危害的影響。建議適當提供動物室內環境，以降低廄刺蠅的危害。

關鍵詞(Keywords)：廄刺蠅(Stable fly)、白犀牛(white rhinoceros)、危害程度(infestation level)、環境因子(environmental factors)、蟲害管理(pest management)

OM03

Progress of proposing ecology-based control measure against the stable fly in Japan

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背景/研究問題/材料方法

The stable fly, *Stomoxys calcitrans* (Diptera: Muscidae), has been known as a serious pest of livestock, such as cattle, swine, and equine, in the world. Its frequent and painful blood-sucking behavior induces intensive evasive behaviors by livestock, resulting in reduced productivity. Moreover, the stable fly mechanically transmits various pathogens, including bovine leukemia virus that causes enzootic bovine leukosis (EBL). In Japan, the number of cattle developing EBL in 2022 was 4334, which was a 44-fold increase since the nationwide survey conducted in 1998. At present, the pest management system largely depends on chemical insecticides as well as insect-proof net, a kind of physical control. In other words, ecological traits of the stable fly have not been paid attention in constructing the management system in Japan.

結果/結論/應用啟示

Our field survey suggested that blue sticky trap was suitable for monitoring the stable fly because of high trapping ability and relative specificity as compared to other colors, red, yellow, black, white, and black and white stripe. By using blue sticky trap, we monitored seasonal abundance of the stable fly that performed in wide range of Japan. Current data suggested the northern populations have one peak in summer, while the southern populations have two peaks, spring peak and autumn peak. In this presentation, we provide a series of results and discuss ecology-based control measure against the stable fly in Japan.

關鍵詞(Keywords)：*Stomoxys calcitrans*, *Spalangia cameroni,* integrated pest management

OM04

Survey of the sand fly population in the urban city of Taipei Botanical Garden

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背景/研究問題/材料方法

Phlebotomine sand flies are natural vectors of leishmaniasis, bartonellosis, and sand fly fever. In Taiwan, four species of sand flies were reported based on morphological charactersin 1970. Leishmaniasis is a neglected tropical zoonosis, and six cases of indigenous cutaneous leishmaniasis had been recorded in Taiwan from 1985 to 2009. Understanding sand flies’ species and distribution is vital for species diversity and disease risk assessment in Taiwan. This study aimed to elucidate the establishment of sand flies in urban city in northern Taiwan. The Taipei Botanical Garden was chosen as the sampling area with intense human activities. The UV light traps (360~400nm) with dry ice were set up at eight sampling locations from eve (18:00) to the next morning (08:00) twice a month. The morphological characters were applied to species identification, including wing venation, Newstead’s spines, cibarium, and pharynx. Molecular identification of species was based on the mitochondrial cytochrome c oxidase subunit I (*COI)* gene by PCR. The NCBI BLAST algorithm calculated *COI* sequence similarity, and the phylogenetic relationship was constructed by MEGA 11.0.13 software.

結果/結論/應用啟示

From April 2021 to December 2022, 38 sand flies were successfully collected from eight sampling locations in the Taipei Botanical Garden. Morphological identification of 38 collected specimens demonstrated 37 *Sergentomyia barraudi* and 1 *Se. iyengari*. However, the *COI* sequences showed that 37 samples were similar to *Se. schwetzi* (Similarity: 88%, KJ481123) and one similar to *Se. iyengari*(Similarity: 95%, MF966734). The discrepancy between morphological and molecular identification results infers that novel species of sand fly population that appeared in urban city in northern Taiwan could be discriminated by examining the internal character and *COI* sequence. Our research indicates that at least one population of sand fly exists in the Taipei Botanical Garden. Evidence will help us to realize the sand fly population, the risk of sand fly-borne disease, and an efficient prevention strategy.

關鍵詞(Keywords)：*Sergentomyia*, leishmaniasis, *COI*, cibarial teeth, pharynx

OM05

台灣病媒蚊感染沃爾巴克氏菌調查與其對節肢病毒之效果評估

Investigation of Wolbachia infection in vector mosquitoes in Taiwan and assessment of its impact on arthropod viruses

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背景/研究問題/材料方法

蚊蟲媒介諸多疾病，如登革熱、日本腦炎、屈公病與瘧疾等。對病媒蚊的控制，平時以病媒蚊監測，高密度時進行孳生源清除與與幼蟲防治，當病例發生時，多以化學噴藥立即壓制環境中的病媒蚊數量與環境孳生源清消。綜觀國際，在蚊蟲傳播傳染病的防治上，亦多是以化學藥劑控制病媒蚊散播病原，但因蚊蟲對化學藥劑產生抗藥性的情況日趨嚴重，因此多方開發新穎防治技術有其必要，其中包含利用沃爾巴克氏體(*Wolbachia*)作為微生物防治。本研究調查 *Wolbachia* 於臺灣各縣市病媒蚊間的感染情形，並嘗試於評估帶有 *Wolbachia* 之蚊蟲對節肢病毒之抑制效果，做為將來欲採取 *Wolbachia* 病媒防治時之參考。

結果/結論/應用啟示

臺灣野外病媒蚊自然感染 *Wolbachia* 的比例分別為白線斑蚊 97%最高，熱帶家蚊 95%次之，中華瘧蚊 32.5%，白頭家蚊的感染率則為 22.2%，而在本次的調查中矮小瘧蚊無 *Wolbachia* 感染現象。另野外埃及斑蚊自然感染 *Wolbachia* 的比例為 22%，且經 *Wolbachia* 種類分析發現包含 supergroup A 及 supergroup B。實驗室先前研究亦顯示帶有 *Wolbachia* 之白線斑蚊對登革一型病毒需要較長的 EIP 時間。綜合本研究與其它文獻之結果均顯示埃及斑蚊確實有感染 supergroup A 及 supergroup B 的 *Wolbachia*，若未來欲採取 *Wolbachia* 作為病媒防治的策略，無論是採取族群取代策略(replacement strategy)或族群抑制策略(reduction strategy)，皆需進一步評估野外埃及斑蚊自然感染 *Wolbachia* 可能造成的影響。

關鍵詞(Keywords)：沃爾巴克氏菌(*Wolbachia*)、病媒防治(vector control)、埃及斑蚊(*Aedes aegypti*)

論文宣讀：系統分類、族群遺傳、演化

Oral Session: Systematics, Population Genetics and Evolution

OS01

臺灣產黑殭菌屬 12 菌株之系統學研究

The systematic study of 12 strains of *Metarhizium* (Ascomycota: Sordariomycetes) in Taiwan

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背景/研究問題/材料方法

黑殭菌屬 (*Metarhizium*) 為子囊菌門 (Ascomycota)、糞殼菌綱 (Sordariomycetes)、肉座菌目 (Hypocreales)、麥角菌科 (Clavicipitaceae) 之蟲生真菌 (Entomopathogenic fungi)，為常被研究及利用的昆蟲病原微生物類群。目前本屬之種級分類因專家間意見紛呈，並不穩定，造成此現象之原因主要有二：1) 因存在隱蔽種 (Cryptic species)，故外觀形態特徵常無法作為鑑定依據與 2) 諸多往昔研究僅以單一基因序列 (如：*ITS*) 作為物種界定標準，失之偏頗。故本研究使用包含核醣體基因 (Ribosomal gene, rDNA)、管家基因 (Housekeeping genes) 及毒力基因 (Virulence genes) 等 3 類共 9 個不同進化速度之基因部分序列，並以操作邏輯相異之最大概似法 (Maximum likelihood) 及最簡約法則 (Maximum parsimony) 建構實驗室所保存之 12 黑殭菌屬菌株間親緣關係 (Phylogeny)，再輔以形態、寄主昆蟲種類與多個生理、生化特徵進行物種判定。

結果/結論/應用啟示

初步結果顯示此 12 菌株確可形成數個單系群 (Clade)，且至少有 1 菌株在 DNA 序列和形態上皆與本屬模式種黑殭菌 (*Metarhizium anisopliae* (Metsch.) Sorokin) 差異頗大，故判定其為另一同屬物種應無疑慮。其餘各菌株雖所處之單系群具高支持度，同源性 (Monophyly) 無爭議，但形態與生態等其他特徵則尚未足以支持他們與模式種確實為不同物種。故未來仍需持續累積更多資訊，以獲取足夠證據來釐清這些菌株的分類地位。

關鍵詞(Keywords)：黑殭菌(*Metarhizium anisoplia*)、蟲生真菌(entomopathogenic fungi)、隱蔽種(cryptic species)、親緣關係(phylogeny)

OS02

穿山甲木鼻白蟻 (蜚蠊目: 木鼻白蟻科) 的生態棲位與階級發育
Ecological niches and caste development of *Stylotermes halumicus* (Blattodea: Stylotermitidae)

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背景/研究問題/材料方法

木鼻白蟻科是一類僅分布於東亞且稀有的白蟻類群，是新等翅類群 (Neoisoptera) 的基群，在演化上是介於木白蟻與鼻白蟻科兩個迥異科別的關鍵角色，但目前僅有分類學研究，缺少基礎生物學資訊，而台灣分布有穿山甲木鼻白蟻 (*Stylotermes halumicus*)，是探索木鼻白蟻生態資訊的絕佳對象。我們藉由調查整棵樹木的方式，分層檢查木鼻白蟻的巢體結構，並取得完整巢群。透過形質測量，藉以推測木鼻白蟻的階級發育路徑。此外，由於白蟻巢群大部分個體皆沒有明顯性徵，卻可能存在單一性別的階級分化，本研究利用 micro-CT 觀察內部生殖器官以驗證性別分化情形。本研究完整呈現木鼻白蟻的生態棲位與階級組成的重要資訊。

結果/結論/應用啟示

目前所有的 *S. halumicus* 都在活樹上發現，3 棵分段檢查的樹木內，都不具接地通道與地下隧道，白蟻分布於樹高 2 公尺以下，活動範圍約在垂直 1 公尺內，3 個巢群分別有 952、2381 與 7178 隻個體，兵蟻比例介於 1-3%內，在階級發育的部分，*S. halumicus* 具有 3 個幼蟲 (larva) 齡期，蛻皮為擬工蟻後，最終都會轉變為前兵蟻 (presoldier) 或有翅芽若蟲 (nymph)，且有翅芽若蟲只經 1 次蛻皮成為有翅繁殖型 (alate)，不具有特化的真工蟻，屬於線性發育模式；在性別分化方面，各階級雌雄比例相同，不具備單一性別的分化。本研究揭示稀有木鼻白蟻的生態棲位與階級發育路徑，對新等翅類群的演化過程提供關鍵性的證據。

關鍵詞(Keywords)：個體發育學(ontogeny)、發育路徑(developmental pathway)、性別比(sex ratio)、樹內昆蟲相(insect fauna in tree)、顯微斷層掃描(micro computed tomography)

OS03

利用粒線體基因體探討臺灣產竹節蟲的親緣關係
Using mitogenome reconstructing phylogeny of Taiwan stick insects

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背景/研究問題/材料方法

Stick insects (Phasmatodea) is an insect order famous for its habit of camouflage. However, the evolution and systematic issue has been debated for decades due to morphological convergence and rapid evolution. In recent years, molecular phylogenetic approaches have been employed to recover phasmatodean evolutionary history. Nevertheless, stick insects in Taiwan were rarely sampled or sequenced in phylogenetic research. To clarify the relationships and systematic positions of stick Taiwan insects, we newly assembled mitogenome sequence from 16 Taiwan phasmatodean species (including 10/11 genera in Taiwan) and 32 additionally downloaded sequence read archives (SRAs) from GenBank using genome-skimming methods and analyzed along with published 42 mitogenomes (including 41 phasmatodean species and one ebiopteran outgroup). Maximum likelihood and Bayes inference phylogenetic trees were inferred using IQ tree and Mrbayes respectively.

結果/結論/應用啟示

Sixteen mitogenome of Taiwan phasmatodean species were successfully assembled. Results of phylogenetic analysis suggest that nearly half of genera in Taiwan were polyphyletic, need for further systematic revision. Furthermore, our sequence data with high assembly quality provided a solid, robust base for phylogenetic study of stick insects in Taiwan. On the other hand, our results also indicated that mitogenomes of stick insects underwent a different evolutionary history with nuclear genes, require more comprehensive taxon sampling and sequence data to clarify the high-level evolution among stick insects.

關鍵詞(Keywords)：竹節蟲目(Phasmatodea)、基因體略讀法(genome-skimming)、粒線體(mitochondria)、粒線體基因體(mitogenome)

OS04

Pseudalomya 屬(膜翅目：姬蜂科：姬蜂亞科)於臺灣之首次發現及其族級分類地位探討

Discovery of the genus Pseudalomya (Hymenoptera: Ichneumonidae: Ichneumoninae) from Taiwan and the implication on its tribal placement

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背景/研究問題/材料方法

Pseudalomya Telenga, 1930 is a rare genus that comprises two species and is restricted to the Eastern Palaearctic and high mountains of the Oriental region. Presenting intermediate morphological characters between two ichneumonine tribes, Alomyini and Phaeogenini, the tribal placement of *Pseudalomya* remains controversial. While previous *28S*-based molecular phylogenies suggested *Pseudalomya* belongs to Phaeogenini, subsequent comprehensive studies lacked its sampling. As a result, the current phylogenetic position of this genus is considered *incertae sedis*. Upon discovering three unique *Pseudalomya* specimens from a project surveying insect fauna in the Dasyueshan area of Shei-Pa National Park, this study aims to identify the Taiwanese specimens by morphological evidence and re-evaluate the tribal placement of *Pseudalomya* by a multigene molecular phylogeny based on one mitochondrial marker (*COI*) and two nuclear markers (*28S* and *18S*).

結果/結論/應用啟示

Following a morphological comparison, the Taiwanese *Pseudalomya*was considered a new species. It can be diagnosed from other congeners by the combination of its body coloration, shape of frontal horn, punctures of face, sculptures of metasomal tergites, and wing venation. A multigene molecular phylogeny also suggests that the genus *Pseudalomya* belongs to the tribe Phaeogenini and is distanced from Alomyini. This is the first record of *Pseudalomya* from Taiwan, and further studies are needed to understand the comprehensive distribution, biology, and diversity of this genus.

關鍵詞(Keywords)：分類學(taxonomy)、分子親緣關係(molecular phylogeny)、新物種(new species)、姬蜂科(Ichneumonidae)、臺灣(Taiwan)

OS05

臺灣跳蟲 (彈尾綱) 之多樣性
Diversity of Collembola in Taiwan

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背景/研究問題/材料方法

跳蟲屬於彈尾綱 (Collembola) ，是廣泛分布全球的小型節肢動物，全球已知的物種有約 9400 種，預估多樣性則高達 50,000-500,000 種。牠們的棲地類型十分廣泛，包括土壤、植被、沙漠、冰河和洞穴等。跳蟲在土壤生態系中扮演十分重要的角色，參與枯落物分解、養分循環、和微生物的交互作用，同時是掠食性節肢動物的食物資源。儘管跳蟲有驚人的多樣性並提供許多生態功能，我們對於臺灣跳蟲的了解卻十分有限。因此，本研究透過敲擊植被、柏氏漏斗、馬氏網和目標搜索的方式，在臺灣各種不同的棲地採集跳蟲樣本，並進行形態和分子的分析，以增進我們對臺灣跳蟲多樣性的了解。

結果/結論/應用啟示

本研究將臺灣跳蟲的物種名錄從 1981 年 26 種新增至 2022 年 58 個物種，同時修訂 2022 年正式發表的名錄，做為未來跳蟲多樣性與生態學研究的基礎；我們進一步探討偽圓跳蟲科 (Dicyrtomidae) 的親緣關係和系統分類，提出有關種內形態變異、隱蔽種多樣性以及新種等議題，以及未來臺灣跳蟲研究的展望。

關鍵詞(Keywords)：彈尾綱(Collembola)、物種名錄(checklist)、偽圓跳蟲科(Dicyrtomidae)、系統分類(systematics)、新種(new species)

OS06

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

Family Tephritidae (the true fruit flies) is one of the most economically important dipteran families, with larvae of most species developed in plant tissues. Subfamily Dacinae is an ecologically diverse group, with species predominantly native to South-East Asia. Most of the dacine species recorded from Taiwan belong to two major tribes, Dacini and Gastrozonini. Tribe Dacini is frugivorous, causing damage to the host plant through ovipositor punctures and larval growth. While non-pest species are associated with a narrow range of known hosts, particular pest species are polyphagous with a broad host range. Severe infestation on commercially produced fruits can lead to fruit rot or premature drop, leading to considerable crop loss. Thus, the taxonomy of Dacini may pave the way to improve pest management and quarantine. However, a current taxonomic system of Dacini relies on the color pattern as the primary diagnostic character for species delimitation, regardless of its high intraspecific variation. Tribe Gastrozonini is Poaceae-breeding. Taxonomic study of the group is relatively scarce and limited compared to other tephritids. This study aimed to revise the Dacinae species of Taiwan and search for a more stable set of traits for their taxonomic system.

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 once-declined record of *Zeugodacus yayeyamana* (Matsumura, 1916) from Taiwan has been verified, with a description of the species’ biology. 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

OS07

系統分類成果與在地知識流通的距離－分類群地方名稱的關鍵橋樑角色與推動策略

The gap between systematics achievements and local knowledge dissemination - the important bridging role of taxon vernacular names and promotion strategies

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背景/研究問題/材料方法

系統分類在生物研究領域扮演著關鍵角色，有助於理解分類群間的關係及多樣性，以及作爲學名變動的依據。然而，以學名作為具高多樣性的分類群的名稱來貫串生物資訊的文本或資料庫，相對來說不若分類群的「地方名稱，在華語使用地區即中文名稱」能取得較高的知識傳遞效益；再者，若中文地方名的使用未能直接隨研究(包含組合名變動與誤鑑定觀點)發表而修訂，並作中文名稱變動的建議，則「約定成俗」的地方名將隨時間與變動的學名在演進的知識上逐漸產生差距。此外，當代臺灣具有生物多樣性資訊、公民科學、網路社群與學術團體間對知識流通的正向循環，對於以領導臺灣昆蟲議題與社群為自詡的團體來說，就既有期待「議題的主導」、「社群的推展」與「教育的推廣」等效應的產生，則分類群地方中文名稱的推動勢必當屬著力的領域範疇。

結果/結論/應用啟示

考慮此議題在當代臺灣昆蟲範疇的進展時，以下幾點值得注意，即(1)大多數分類群中文名稱均由其高階分類階層之名稱衍生，且存在「假借尾音的規律」；(2)在高多樣性昆蟲中仍有相當高比例的物種缺乏中文名稱，以及(3)對於過去的學名變動或誤鑑定分類群，尚未形成中文名稱變動方面的共識。在此，我們首次倡議在宏觀考量世界昆蟲物種皆有中文名稱，並對其他華語使用區系產出之中文名稱作案例參考的情境下，提出應規劃「臺灣昆蟲物種建議中文名稱命名原則」，並建議成立「臺灣昆蟲中文名稱諮議暨推動小組」等實踐細項的規劃，以促進系統分類知識的在地流通。

關鍵詞(Keywords)：博物學(natural history)、命名學(nomenclature)、分類處理(taxonomic treatment)、教育推廣(educational promotion)、在地認同(local Identity)

OS08

An undescribed species of Australian gall-inducing soft scale (Hemiptera: Coccidae)

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背景/研究問題/材料方法

There are just a very few species of soft scales (Coccidae) which induce galls on their host plants. These galling coccids only occur in South Africa and New Zealand. Several specimens of soft scales were found in conical galls on the leaves of *Cryptocarya vulgaris* B. Hyland and *Beilschmiedia recurva* B. Hyland (Lauraceae) in rainforest in northeast Queensland. Here, we show the morphologies of the first-instar nymph and the adult female of this coccid, which is the first record of a gall-inducing soft scale for Australia, and compare these with some supposedly closely-related endemic species such as *Austrolecanium* spp. and also non-Australian gall-inducing soft scales. Five gene regions (*18S*, *28S*, *COI*, *EF1α* and *wg*) of four independent loci including mitochondrial and nuclear genome were sequenced from one specimen (LGC02790) of the galling coccid to determine the relationships and thus the generic status of the new galling species. Maximum Parsimony (MP) and Maximum Likelihood (ML) were used to estimate phylogenies.

結果/結論/應用啟示

Considering (i) a series of morphological differences from other gall-inducing soft scales, and (ii) the topology of the phylogenetic trees estimated by two methods with different underlying assumptions, we conclude that the LGC02790 is an undescribed species and strongly supported as sister to *Austrolecanium*.

關鍵詞(Keywords)：Coccomorpha, taxonomy, phylogeny, gall, Coccid

OS09

20 年未解之謎—台灣的半板竹節蟲(Phasmatodea: Lonchodidae: Necrosciinae: Hemiplasta)的分類地位?

A two-decade mystery of stick insects – What is the identity of the genus Hemiplasta (Phasmatodea: Lonchodidae: Necrosciinae) in Taiwan?

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背景/研究問題/材料方法

長角枝竹節蟲亞科(Necrosciinae)是竹節蟲目中物種多樣性最高的亞科，目前約有 113 屬、840 種，而在台灣此亞科的物種大部分為樹棲性，不論是在野外觀察記錄或採集上均較為困難，因此分類與生態研究均尚未完整。台灣的半板竹節蟲屬(*Hemiplasta*)首次被提及於 2002 年黃世富的圖鑑中，而近年研究卻顯示該屬可能僅分布於蘇拉威西島(Sulawesi)一帶，與台灣地理位置相隔甚遠，因此過去在台灣被認為是半板竹節蟲的物種身分值得被重新探討。本研究自全台各地的殼斗科原始林進行採集，紀錄寄主植物、飼養以收集卵的形態資料，同時前往各大博物館檢視標本，以形態和分子證據釐清台灣產半板竹節蟲屬之分類地位以及物種多樣性。

結果/結論/應用啟示

在台灣往昔的紀錄中，半板竹節蟲僅被提及一種，並以 *Hemiplasta* sp.表示。但在目前的採集結果中，我們發現了 3 個形態種，能以翅的長度與卵的形態等特徵將其明顯區別，並且在比對 *COI* 及 *28S* 序列後也支持其為不同物種。此外，透過與 Genbank 資料庫上長角枝竹節蟲亞科的序列重建分子親緣關係，初步結果顯示台灣的物種與真正的半板竹節蟲為不同支系，並且兩者在形態上也有差異。未來希望能檢視更多相關類群的標本，以釐清分子與形態上所有近緣屬的特徵差異，並找到台灣物種合適的屬級地位。

關鍵詞(Keywords)：生物多樣性(biodiversity)、半板竹節蟲屬(*Hemiplasta*)、整合分類學(integrative taxonomy)、長角枝竹節蟲亞科(Necrosciinae)、臺灣(Taiwan)

論文宣讀：都市昆蟲學
Oral Session: Urban Entomology

OU01

Contact toxicity and repellent effects of clove powder, clove oil, and its major bio-active compounds against destroyer ants, *Trichomyrmex destructor* (Hymenoptera: Formicidae), under laboratory conditions

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背景/研究問題/材料方法

Destroyer ants are widely distributed urban pests that are generally controlled with synthetic insecticides. However, rapid development of insecticide resistance and their extensive use have raised concerns about their detrimental impacts on both human health and the environment. Therefore, numerous botanical essential oils and their individual components have been extensively tested against this urban pest. Nevertheless, no research has been conducted to assess the effectiveness of clove-based products against destroyer ants. Therefore, in this study clove powder, clove oil, and its three major bio-active compounds (eugenol, β-caryophyllene, and eugenol acetate) were evaluated for their contact toxicity and repellency against destroyer ants under laboratory conditions.

結果/結論/應用啟示

Contact toxicity bioassay results showed that clove powder applied at 7 and 10 mg/cm2 caused 100% ant mortality within 6 hours after treatment (HAT), respectively. At highest concentration of clove oil (2.5 µL/cm2), the highest percentage of ants (94%) died within 6 HAT. Eugenol applied at 2 and 2.5 µL/cm2 resulted in 100% ant mortality within 6 HAT, respectively. Furthermore, β -caryophyllene and eugenol acetate applied at 2.5 µL/cm2 exhibited 100% ant mortality within 6 HAT. Similarly, repellency results showed that the clove powder applied at 2.5 mg/cm2 repelled 93% of ants within 3 HAT. Clove oil, eugenol, β-caryophyllene, and eugenol acetate applied at 2.5 µL/cm2 induced highest ant repellency (94, 95, 86, and 89%) within 3 HAT, respectively. This study determined that all the clove-based test items-controlled destroyer ants reasonably well by exhibiting concentration dependent effects in both contact toxicity and repellency bioassays conducted under laboratory conditions.

關鍵詞(Keywords)：bio-active compounds, clove oil, contact toxicity, destroyer ants, repellency

OU02

A field study on the effects of EM probiotic supplements on honeybee, *Apis mellifera* (Hymenoptera: Apidae), productivity

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背景/研究問題/材料方法

European honeybees (*Apis mellifera*) are the most intensively managed honeybee species in the world. They are crucial for commercial beekeeping due to their high economic value. However, global honeybee populations are declining due to various environmental factors, including antibiotic use in apiculture leading to antimicrobial resistance. Hence, probiotics containing beneficial bacteria have been recognized as a favorable alternative to antibiotics. Therefore, the main objective of this study was to investigate the effects of different concentrations of Effective Microorganisms (EM) probiotics as a feed additive on the European honeybee's productivity, by analyzing honey production, pollen collection, and royal jelly production.

結果/結論/應用啟示

EM Probiotics at different amounts (medium EM = EM 25 mL/hive, high EM = EM 50 mL/hive) mixed with sugar water solution were fed to honeybees, and their productivity was compared with a commercial product. Treatment groups were fed directly by inoculating the probiotic with 500 ml of sugar water solution. The duration of the experiment, the number of hives, and the frequency of treatment supplementation varied according to the experiment (honey, pollen, and royal jelly). Results indicate, hives supplemented with high EM, produced more honey, pollen, and royal jelly as compared to other concentration of EM, suggesting that this is the beneficial dosage of EM. This study underscores the potential of EM probiotics, particularly at dose high EM, to enhance the productivity of European honeybee colonies. Sustainable and cost-effective EM probiotics offers a promising alternative to antibiotics in beekeeping practices. Such approaches are vital in maintaining their role in agriculture and ecosystem.

關鍵詞(Keywords)：effective microorganism probiotics, feed supplement, honey, honeybee, sugar water solution

壁報展示：農業昆蟲學
Posters: Agricultural Entomology

PA01

The role of new invasive plants as alternative hosts for *Phthorimaea absoluta* (Lepidoptera: Gelechiidae) and the implication for tomato pest management

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背景/研究問題/材料方法

Tomato leaf miner *Phthorimaea absoluta* (Lepidoptera: Gelechiidae) is one of the most destructive insect pests on tomatoes and allied plants. This specialized feeder forms galleries in fruits & stems and “mines” within leaves. Records show that this disastrous effect has had a huge impact on global tomato production, which could cause 100% damage to the plants. The significance of tomatoes as the primary host has been highlighted by previous studies based on oviposition preference and larval performance. Many experts have recently expressed concern about the host shift from tomato to other host plants, and this may explain how this lepidopteran pest persists while the tomato resource is not available in summer. In the present study, we evaluated the feeding performance of *Phthorimaea absoluta* by inoculating 20 neonate larvae to each of 16 Solanaceae plant species (Five replicates for each plant species). This allowed us to explore the susceptibility and the capacity to act as alternative hosts. During this assay, the larval period, larval mortality, and pupation success were examined. We also used the Euclidian distance method to perform a cluster analysis.

結果/結論/應用啟示

One-way ANOVA test showed that there were significant differences across plant species in the larval period ($p = 0.000$), larval mortality ($p = 0.011$), and pupation success ($p = 0.011$). *Solanum tuberosum*, which was identified as a potential alternative host for this pest in earlier investigations, and *Nicotiana plumbaginifolia* shared a 90.35% identical susceptibility, according to the cluster analysis. In addition to *Solanum lycopersicum, Solanum tuberosum, Solanum nigrum*, and *Nicotiana plumbaginifolia* were grouped, demonstrating their appropriateness as alternative hosts. This finding suggests that the new invasive plant can serve as a refugium for the moth when tomatoes are not available, and the management plan needs to consider the diversity and abundance of Solanaceae plants in the tomato production area.

關鍵詞(Keywords)：larval performance, host shift, herbivory, solanaceae species, susceptibility

PA02

利用機器模擬熊蜂振動評估番茄授粉效能

Assessment of tomato pollination efficiency through machine-mimicked bumblebee vibrations

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背景/研究問題/材料方法

糧食作物的生產是重要的議題。尤其以果實為主的作物都需要昆蟲進行授粉。但花藥型態為孔裂的作物，主要依賴振動授粉結果。目前台灣溫室栽培的有機番茄，主要仰賴熊蜂協助番茄授粉。然而因為氣候變遷及成本的考量，有必要尋找替代方案。本研究目的為透過機械產生特定頻率的振動，應用於溫室中種植的番茄作物(*Solanum lycopersicum*cv.” Matt’s Wild Cherry”)，評估機械授粉的效能。首先利用可攜式校正振動機(Portable calibrating vibrator Model 8100)產生振動，透過波形產生器(Arbitary waveform generator AG051)產生正弦波並調整振幅和頻率，比較不同頻率後，以 500 Hz 作為最佳振動頻率並進行田間試驗，並與熊蜂授粉進行比較。

結果/結論/應用啟示

機械振動授粉分為 4 組：振動時間 5 秒於單朵花及花序基部，另外兩組為振動時間 10 秒於單朵花及花序基部。結果顯示，機械授粉的著果率較熊蜂低(53.2%－59.31% vs. 72.8%)，且番茄重量較輕(4.38g－7.09g vs. 9.03g)、種子數量較少(21.57－33 vs. 47.02)，但甜度與酸度和熊蜂授粉組有類似的效果。果實內部型質(橫切面高度、橫切面果皮面積、橫切面果皮厚度等)與熊蜂授粉後的番茄果實並無明顯差異。本研究顯示機械振動授粉在番茄果實品質上的優勢和不足。未來的研究可以進一步探討如何改進機器模擬授粉技術，以提升果實產量和品質。

關鍵詞(Keywords)：振動授粉(buzz pollination)、氣候變遷(climate change, green house, machine pollination)

PA03

馬尼拉小繭蜂病毒中 microRNA 調節影響斜紋夜蛾胰島素脂肪代謝途徑

Snellenius manila bracovirus microRNAs regulate insulin lipid metabolism pathways in *Spodoptera litura*

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背景/研究問題/材料方法

台灣重要的農業害蟲斜紋夜蛾(*Spodoptera litura*)，危害玉米、葉菜類及毛豆等作物，啃食植株葉肉組織造成嚴重經濟損失。馬尼拉小繭蜂 (*Snellenius manila*)為斜紋夜蛾的寄生性天敵，產卵至斜紋夜蛾幼蟲體內並注入病毒 *S. manila* bracovirus (SmBV)產生 microRNA。

結果/結論/應用啟示

miRNA 不僅會抑制斜紋夜蛾幼蟲的免疫反應、還會使蟲體生長速度變慢。miRNA 影響了寄主體內分泌系統造成蟲體生長速率下降。胰島素信號途徑(insulin signaling pathway)會影響昆蟲生長發育。而脂質是昆蟲體內重要的能量儲存形式，因此聚焦在脂質途徑上。欲了解胰島素是否會影響斜紋夜蛾幼蟲體內脂質代謝，再以 miRNA 抑制斜紋夜蛾幼蟲的脂肪生成。觀察以寄生、注射方式在斜紋夜蛾幼蟲體內注入 miRNA 後，幼蟲體型以及胰島素影響脂肪生成途徑中關鍵基因變化量。期望後續開發環境生物友善之基因農藥以替代化學農藥，以達成害蟲防治效果。

關鍵詞(Keywords)：馬尼拉小繭蜂(*Snellenius manilae*)、斜紋夜蛾(*Spodoptera litura*)、脂肪代謝(lipid metabolism)、SmBV(*S. manilae* bracovirus)、miRNA(microRNA)

PA04

研製海藻酸鈉凝膠餌劑應用於長腳捷蟻防治

Development of alginate hydrogel baits for management of Anoplolepis gracilipes

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背景/研究問題/材料方法

長腳捷蟻 (*Anoplolepis gracilipes*) 是世界上最具入侵性的蟻種之一，對於被入侵地區生態與經濟造成危害。防治長腳捷蟻大多使用液態餌劑，使用時須備餌站台，增加防治成本，為此研製成本低且適合大規模應用的海藻酸鈉凝膠載體。海藻酸鈉凝膠餌劑其成本低、可生物降解，將其作為載體吸收液態餌劑可省去餌站台成本，在無法到達的區域，亦可使用無人機噴灑。體積小的凝膠餌劑或許可促使螞蟻將其搬運回巢提高防治成效。本實驗所使用的毒劑為硼砂，並針對凝膠餌劑進行(1)失水量；(2)長腳捷蟻對失水凝膠餌劑的取食偏好；(3)硼砂與凝膠珠的水合作用；(4)凝膠餌劑對硼砂的吸收；(5)實驗室內致死功效；(6)野外長腳捷蟻是否搬運凝膠餌劑。

結果/結論/應用啟示

凝膠餌劑在底材與相對濕度較高的環境下可維持較長時間。長腳捷蟻對於失水量 0 - 75% 凝膠珠取食意願並無明顯偏好。硼砂濃度對於凝膠珠的水合有負面影響，硼砂濃度與凝膠珠的重量成反比。利用硼砂快速檢測試劑進行檢測，得知 2-6%濃度硼砂的糖水均可被凝膠珠吸收。實驗室內致死率結果得知浸泡含 6%硼砂濃度的凝膠餌劑效果尤佳，浸泡含 4%的硼砂的凝膠餌劑次之，浸泡含 2%硼砂的凝膠餌劑則需花費最多時間。於高美濕地實測發現，野外的長腳捷蟻會取食與搬運直徑約 2mm 的糖水凝膠餌劑，含有三種不同硼砂濃度凝膠餌劑同樣也會取食與搬運。未來應用上若想延長凝膠餌劑在野外的效用，或許可再施用前預先在該場域灑水，降低凝膠餌劑的失水數率，並添加其他誘引物質在凝膠珠內，如:味精或追蹤費洛蒙，提高長腳捷蟻的發現與搬運率，提高餌劑對於長腳捷蟻群落的覆蓋度。

關鍵詞(Keywords)：長腳捷蟻(*Anoplolepis gracilipes*)、海藻酸鈉(sodium alginate)、凝膠餌劑(hydrogel baits)、硼砂(borax)、外來種防治(management of alien species)

PA05

11 種殺蟎劑對鳳梨釋迦二點葉蟎毒性測試

Toxicity of 11 acaricides for *Tetranychus urticae* on atemoya

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背景/研究問題/材料方法

近年來葉蟎已成為鳳梨釋迦重要有害生物之一，尤以二點葉蟎(*Tetranychus urticae* (Koch))為甚。然而殺蟎劑對葉蟎防治效果不佳之案例時有所聞，為了解現行核准登記於防治番荔枝葉蟎之 11 有效成分殺蟎劑之殺蟎效果，針對鳳梨釋迦二點葉蟎進行殺蟎劑藥效測試，做為未來擬定田間防治策略之參考。選用之殺蟎劑以相對安全劑型水懸劑或水基乳劑進行室內藥效測試，供試二點葉蟎於 2022 年採自臺東縣卑南鄉鳳 4 處鳳梨釋迦果園，於室內飼育繁殖後，以浮葉法使用噴藥塔進行藥效測試，計算施藥後 24 小時及 48 小時之死亡蟎數，計算藥劑致死率。

結果/結論/應用啟示

室內測試 11 種核准登記於防治番荔枝葉蟎類之殺蟎劑，其推薦濃度對 4 處鳳梨釋迦園採得之二點葉蟎防治效果，僅亞醌蟎、賽派芬於 2 處果園採得之二點葉蟎 48 小時後致死率達 50%以上，前者致死率平均 50.8± 6.8%，後者則平均 44.2± 40.8%，不同果園採得之二點葉蟎存在高度族群差異。整體而言，番荔枝核准使用的殺蟎劑對二點葉蟎的致死率，IRAC 3A 之芬普寧 24.9%、IRAC 21A 之畢達本、畢汰芬、得芬瑞及芬普蟎最高 32.7%；IRAC 23 之賜派芬及賜滅芬 9.5%，IRAC 6 之密滅汀 12.1%；IRAC 1B 馬拉松 6.2%，致死率均低於 50%。推測臺東縣卑南鄉鳳梨釋迦果園之二點葉蟎對多數的核准使用殺蟎劑已有產生抗/耐藥劑的趨勢。

關鍵詞(Keywords)：鳳梨釋迦(*Annona cherimola* x *Annona squamosa*)、二點葉蟎(*Tetranychus urticae*(Koch))、殺蟎劑(acaricides)

PA06

實驗室飼育顯示紫背草為秋行軍蟲的潛在替代性寄主植物(鱗翅目：夜蛾科)

Laboratory rearing reveals red tasselflowers as a potential alternative host plant of fall armyworms (Lepidoptera: Noctuidae)

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背景/研究問題/材料方法

The fall armyworm (FAW), *Spodoptera frugiperda*, is a highly destructive agricultural pest that invaded Taiwan in June 2019. Studies have documented many cash crops and ornamental plants as FAW’s host plants in invaded habitats. While weeds are ubiquitous, little is known about their potential as FAW’s host plants. Tasselflowers (*Emilia*) are common Asteraceae weeds in Taiwan, and there have been occasional observations of FAW feeding on tasselflowers in our laboratory settings. In this study, we aimed to investigate whether FAW can complete its life cycle by feeding on two common tasselflowers species, namely *E. praetermissa* and *E. sonchifolia* var. *javanica*. Additionally, a plant-host shift experiment was conducted to examine the potential transition of FAW from its primary host, maize, to tasselflowers. Upon confirming any of the tested species as potential hosts, we would subsequently compare their distributions with that of FAW and the total planted maize area to assess their co-existence within the natural/agricultural habitat.

結果/結論/應用啟示

Our results revealed that FAW can successfully complete their life cycle on the leaves of *E. sonchifolia* var. *javanica* but cannot survive on *E. praetermissa*. Furthermore, FAW larvae feeding on a maize plant can switch to *E. sonchifolia* var. *javanica* when their primary host plant (maize) is unavailable. A spatial comparison of the distributions of FAW, the range of *E. sonchifolia* var. *javanica*, and the cultivated maize areas in Taiwan reveals their co-existence, thus reinforcing the hypothesis of tasselflowers as alternative hosts. These findings contribute to the understanding of potential alternative hosts for this significant pest and provide implications for pest management strategies of FAW.

關鍵詞(Keywords)：人工飼育(artificial rearing)、菊科(Asteraceae)、秋行軍蟲(fall armyworms)、替代性寄主植物(alternative host plants)、雜草(weeds)

PA07

台灣野生與栽培種大豆對啃食性害蟲之轉錄體分析與相關化學防禦代謝物分析

Transcriptome and metabolome analyses to study the defense mechanisms of Taiwan soybean plants against chewing herbivore

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背景/研究問題/材料方法

大豆目前為世界性的糧食作物，因全球氣候變遷，環境年高溫期拉長及暖冬現象不斷發生(IPCC 2021)，進而導致害蟲大發生期拉長。這使得台灣多種蟲害在全球氣候變遷影響下日益嚴重。基於現階段台灣本土大豆品種缺乏蟲害抗性之相關研究，本研究團隊利用斜紋夜盜蛾(*Spodoptera litura*)為標的害蟲，選出具抗蟲性與感蟲性之台灣現有栽培大豆品種，並與台灣野生大豆進行蟲害誘導轉錄體分析，以及受害蟲啃咬後其代謝產物差異分析，進而探討大豆對啃食性蟲害之防禦機制及代謝物變化，並期望從野生與抗蟲栽培種大豆中找出具有抗蟲害能力之基因與相關代謝物成分。研究結果除了將找出未來育種高抗蟲性大豆之分子標誌加速育種進程，其找出之指標代謝物亦可應用在生物防治製劑的開發，進而降低栽培大豆之農藥使用量並提高大豆產量。

結果/結論/應用啟示

本研究團隊篩選出台灣本土之抗蟲(金珠)與感蟲大豆(高雄 11 號)栽培種，並納入台灣本土野生大豆進行轉錄體定序。轉錄體分析結果中，我們發現野生種、抗蟲栽培種與感蟲栽培大豆其防禦基因表達模式迥然不同，並找到與防禦相關卻於三個品種大豆中具有不同表達的六個基因，其中包括許多抗病蟲害相關代謝物的調控基因。另外，不同大豆間蟲咬誘導的代謝物明顯分群且防禦相關植物荷爾蒙表現模式也不同，這些都值得我們繼續深入研究大豆的防禦代謝物與機制。

關鍵詞(Keywords)：大豆(soybean)、轉錄體學(transcriptomics)、代謝體學(metabolomics)、斜紋夜盜蛾(*Spodoptera litura*)、環境友善(environmentally friendly)

PA08

免耕與耕犁下玉米田地表節肢動物相差異

Differences in arthropod assemblages and insect pest occurrence between no-tillage and Plowed corn fields

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背景/研究問題/材料方法

免耕農業是一種使用於種植農作物而不會因耕作而影響土壤的農業技術。免耕耕作減少了土壤中水土流失的耕作原因，特別是在傾斜地形的沙質和乾燥土壤中。免耕的可能的益處包括滲入土壤的水量增加，土壤對有機物的保留以及養分循環。上述這些方法可以增加土壤中和土壤上的生命數量和多樣性。農業部農試驗所研發玉米部整地栽培技術，藉由減少整地頻率，增加表土層有機質含量及土壤微生物多樣性，提高土壤生產力，有助玉米維持平均水準以上的產量。但對於土壤節肢動物及重要蟲害發生影響尚未由詳細調查評估資料。因此，本研究以地面陷阱法及目視調查法，於 112 年農業試驗所 1 期作玉米田，調查不整地及整地下，玉米田土壤表面節肢動物種類及數量，及重要害蟲秋行軍蟲平均危害率。

結果/結論/應用啟示

試驗結果顯示，整地及不整地方式下，玉米田秋行軍蟲 *Spodoptera frugiperda* (Smith) 1797 等害蟲發生及平均危害率並無顯著差異。於地面調查到節肢動物相以蜘蛛及昆蟲為主，其中以螞蟻及跳蟲是調查到數量最多。剛整地後，玉米田區螞蟻及跳蟲數量與生物多樣性較為整地玉米田低，但後續調查中則便無差異，此因玉米田種植初期雖有整地與不整地之差異，但後續生產管理則採用香果操作模式。本試驗初步調查結果顯示，不整地對後續玉米田害蟲發生並無影響，但若要提高田區生物多樣性，後續生產管理應採用環境友善模式。

關鍵詞(Keywords)：免耕農耕(no-tillage farming)、玉米田(maize field)、生物多樣性(biodiversity)

PA09

豆科雜糧小型害蟲相初步調查
Preliminary surveillance of small pests in upland legume crops

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背景/研究問題/材料方法

近期農業政策注重提高國內雜糧糧食自給率，田間病蟲害管理為重要輔導策略之一。本研究為了解目前雜糧作物小型害蟲管理缺口，在 112 年針對重要豆類雜糧落花生 (*Arachis hypogaea*) 及大豆 (*Glycine max*) 進行初步蟲害發生調查，於台中霧峰地區分別以隨機取樣目視植株及餌站誘集方式調查其地上部及地下部害蟲相。

結果/結論/應用啟示

調查結果顯示春季栽培(3-6 月)落花生地上部常見刺吸式害蟲為小綠葉蟬 (*Empoasca* spp.)及以台灣花薊馬 (*Frankliniella intonsa* (Trybom))為主之數種薊馬，全期受蛾類幼蟲啃食葉片危害；大豆地上部常見害蟲為豆花薊馬 (*Megaluropthrips usitatus* Bagnall) 及蛾類幼蟲，調查期間適時防治可有效減緩地上部之小型害蟲發生；在大豆及落花生田周圍使用餌站誘集所得害蟲為金針蟲(叩頭蟲幼蟲)，也誘得長角黃山蟻、蠼螋、跳蟲、隱翅蟲及根蟎類等土棲昆蟲，我國少有害蟲對於落花生地下部果莢發育的影響紀錄，有關地下部害蟲及相關雜糧作物害蟲天敵研究值得更多的注意。

關鍵詞(Keywords)：落花生(peanut)、大豆(soybean)、蟲害調查(pest surveillance)

PA10

東方蜂微粒子於精選熊蜂腸道的滯留與取食反應

The retention of Nosema ceranae in the intestines and feeding response on Bombus eximius

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背景/研究問題/材料方法

政府近年開放檢疫溫室有條件使用西洋熊蜂 (*Bombus terrestris*) 為作物授粉昆蟲，其成本效益迅速獲得廣大農民歡迎；有鑑於國外使用西洋熊蜂的溢散，造成外來種的衝擊、蜜蜂疾病擴散、生物多樣性失衡等問題，因此如何讓農民使用安全的授粉昆蟲，是值得探討的議題。精選熊蜂 (*B. eximius*) 是台灣最早以人工飼養研究的本土物種，現階段已商業化；然而精選熊蜂不易馴化飼養，在溫室內授粉行為與效率亦與西洋熊蜂有差別，因而暫難以替代進口熊蜂。由於熊蜂飼養需依賴西洋蜜蜂 (*Apis mellifera*) 所採集的新鮮花粉，因此針對蜜蜂共通性疾病探究精選熊蜂飼養的瓶頸問題，其中之一為東方蜂微粒子 (*Nosema ceranae*) 的真菌病原，欲探討精選熊蜂感染該病原後在其腸道的滯留期與取食反應。東方蜂微粒子研究材料取自嘉義大學養蜂場之西洋蜜蜂，以人工接種繼代培養並定量；精選熊蜂為商業化群體，配置以誘導工蜂形成的偽蜂后 (psuedoqueen) 真社會蜂群 (eusocial colonies)，以獲得足夠蜂群樣本 (n = 8 colonies) 進行餵食試驗 (feeding test)，感染檢測則透過 PCR。

結果/結論/應用啟示

人工餵食 50000 (spore/10μl) 東方蜂微粒子對於精選熊蜂成蜂存活無顯著影響，在日齡別與花粉處理皆表現低感染率 (1.9%, n = 54)；以 100000 (spore/10μl) 東方蜂微粒子處理在消化道的滯留時間為 3–48 hours，較已報導的西洋熊蜂紀錄 (1–6 hours) 長；然而在蜂群試驗中以含 125000 (spore/g) 微粒子之花粉處理組別，其糖水消耗量增加了 14.6%，且幼雛數量與對照組相比顯著下降了 47.5%，顯示東方蜂微粒子在消化道的滯留增加蜂群的能量消耗，可能會削減其對抗疾病及增加致死壓力，後續有待釐清精選熊蜂對於東方蜂微粒子的滯留期是種特異性 (species-specific) 或是來自於馴化的品種差異。本應用程序優化後可發展成為精選熊蜂行為觀察的外部表徵指標模型，有助於熊蜂疾病發生檢測及篩選馴化，節省及減少繁瑣冗長的飼養消耗與基因檢測的生產成本。

關鍵詞(Keywords)：熊蜂(bumble bee)、微粒子病(Nosema disease)、餵食試驗(feeding test)、真社會蜂群 (eusocial colony)

PA11

無人植保機噴灑不同劑型農藥之霧滴分布情形
Droplets distribution of different pesticide formulations by unmanned aerial vehicle

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背景/研究問題/材料方法

近年來無人植保機應用於病蟲害防治日益廣泛，其省工且可減少藥液使用量之優點逐漸受到農業重視。本試驗於蓮花田應用無人植保機噴灑不同劑型之農藥，分析藥液霧滴飄散分布情形，以作為後續適用於無人植保機農藥劑型之選擇。試驗將水試紙固定於無人植保機飛行路徑之左右 1 m、3 m、5 m、7 m、10 m、15 m、20 m、30 m 及 50 m 處之蓮葉葉面和葉背，無人植保機 DX10 搭配空心圓錐噴頭 TR8001 噴灑不同劑型農藥，分別為賽洛寧 2.8%乳劑、賽洛寧 2.46%膠囊懸著劑、馬拉松 50%水基乳劑、馬拉松 25%可濕性粉劑、覆滅蟎 20%水溶性粉劑及益達胺 9.6%溶液等 6 種登記於蓮花上之藥劑。藥劑噴灑後回收水試紙，以軟體 Image J (National Institutes of Health) 分析藥劑噴灑至水試紙上之霧滴覆蓋面積(% area)及霧滴數量。

結果/結論/應用啟示

相同飛行參數下，六種農藥劑型的飄散距離於上風處均可達到 5 m，其中益達胺溶液及覆滅蟎水溶性粉劑飄散距離較遠，可達上風處 7 m；而下風處六種劑型飄散距離均可達到 15 m，其中賽洛寧膠囊懸著劑飄散距離達下風處 30 m 仍有藥液附著情形。以相同飄散距離比較，上風處 1 m 葉面以益達胺溶液之霧滴沉積覆蓋率及霧滴數量高於其他劑型，葉背則以馬拉松水基乳劑及馬拉松可濕性粉劑之霧滴沉積覆蓋率及霧滴數量高於其他劑型；於下風處 1 m，以賽洛寧乳劑於葉面及葉背之霧滴沉積覆蓋率及霧滴數量顯著高於其他劑型。另外不論上風處或下風處 1 m，僅有馬拉松可濕性粉劑霧滴沉積覆蓋率及霧滴數量皆為葉背大於葉面。另外比較於相近風速條件下的兩種農藥劑型之霧滴飄散結果，馬拉松水基乳劑於上風處 1 m 及下風處 5-15 m 不論葉面和葉背霧滴沉積覆蓋率和霧滴數量皆高於賽洛寧膠囊懸著劑，表示此劑型應用於無人植保機防治時可達到較高的覆蓋面積，進而提高蓮花害蟲接觸農藥的機會。由上述結果顯示，無人植保機噴灑農藥時，霧滴分布確實受到農藥劑型之影響，不同的作物特性及防治的害蟲種類，都應有其合適的農藥劑型。以蓮花重要害蟲小黃薊馬為例，以無人植保機防治時，應選用藥劑粒徑小、飄散較遠的農藥劑型如水基乳劑，可增加藥液與蟲體接觸機會，但仍應注意藥液飄散對環境的影響。

關鍵詞(Keywords)：無人植保機(unmanned aerial vehicle)、霧滴飄散(droplets drift)、農藥劑型(pesticide formulations)

PA12

評估殺蟲劑與蟲生真菌對檬果褐葉蟬藥效試驗初探

Evaluation of efficacies of insecticides and entomogenous fungi against mango leafhoppers (*Idioscopus nitidulus* (Walker))

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背景/研究問題/材料方法

檬果葉蟬類害蟲主要好發於檬果花期，可透過取食檬果組織液直接造成檬果樹勢衰弱或花器凋落，另外也可間接引發煤煙病，造成檬果產量與品質的經濟損失。田間主要發生葉蟬種類為檬果褐葉蟬及檬果綠葉蟬。目前防治葉蟬的主要手段為化學防治，在正確的防治時機，輪流使用不同殺蟲機制的農藥可有效抑制葉蟬的發生密度。本試驗欲探討檬果登記藥劑對檬果褐葉蟬的藥效反應，同時針對白殭菌、淡紫菌等蟲生真菌比較其致死效果。本試驗將檬果褐葉蟬置於 50ml 之離心管內，利用滾瓶法讓藥劑均勻接觸蟲體，於處理後 24 及 48 小時計算死蟲數，每一處理 3 重複。測試藥劑計有(A)21.8%速殺氟水懸劑 3,600 倍，(B)20%達特南水溶性粒劑，(C)20%亞滅培水溶性粉劑，(D)18.2%益達胺水懸劑，(E)2.8%畢芬寧乳劑，(F)2.46%賽洛寧膠囊懸著液，(G)白殭菌孢子懸浮液(10^7conidia/ml)及(H)淡紫菌孢子懸浮液(TNZZS6) (10^7conidia/ml)。

結果/結論/應用啟示

結果顯示速殺氟、達特南、益達胺及亞滅培 4 種藥劑效果甚佳，於處理後 48 小時即可造成芒果葉蟬 84~100%死亡率。但合成除蟲菊類藥劑(畢芬寧、賽洛寧)藥效較差，其中以賽洛寧效果較好，但 48 小時校正死亡率也僅達 65.3%。目前初步試驗結果顯示作用機制屬尼古丁乙醯膽鹼受體競爭性調節劑之化學藥劑效果均佳，這類藥劑具有系統移行性，可有效防治刺吸式口器害蟲。蟲生真菌則以白殭菌效果較佳，48 小時校正死亡率約 22.0%，但與化學藥劑相比，藥效相對較差。由於蟲生真菌在施用後需和昆蟲接觸、感染才能造成害蟲死亡，成效自然較為緩慢。田間調查結果顯示芒果葉蟬族群主要發生高峰為檬果花期及檬果採收期後。為降低葉蟬族群密度，可於檬果花期施用尼古丁類藥劑進行防治。由於此次試驗中蟲生真菌藥效均不佳，若針對有機農友建議葉蟬防治方式，尚須進一步測試其他非化學農藥防治資材或嘗試將其與蟲生真菌進行混和處理，觀察是否能提高殺蟲效力，將是未來的研究方向。

關鍵詞(Keywords)：檬果褐葉蟬(*Idioscopus nitidulus* (Walker))、化學防治(chemical control)、蟲生真菌(entomogenous fungi)

PA13

檳榔蟲害安全用藥暨農藥減量示範

Demonstration of safe use of pesticides for Areca nut pests and pesticides reduction

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背景/研究問題/材料方法

檳榔栽培歷史悠久，主要產區於屏東、南投、嘉義、花蓮及臺東等地，但因非政府推薦或鼓勵的作物，一直無較詳細的疫病蟲害生態與防治資料，導致檳榔病蟲害發生時，農民無法確認原因也無適當的防治方法，使得部分農民使用非檳榔的防治用藥。緣此，本試驗於嘉義梅山地區應用檳榔登記用藥進行病蟲害防治，觀察檳榔結果狀態及病蟲害發生情形，提供農民用藥選擇，進而維護用藥安全。試驗處理共分為兩組，分別為農民慣行組(H)：以農民習慣用藥(3 種殺蟲劑)。處理組(T)：庫斯蘇力菌 SA-12 可濕性粉劑 600 倍、福化利乳劑 3000 倍。分別自花期開始施藥，共施藥 4 次，於盛花期調查花苞數量，再於檳榔採收期調查果實數量、重量及病蟲害發生情形。

結果/結論/應用啟示

本次試驗調查結果顯示田間主要病蟲害以蚜蟲、粉介殼蟲、盾介殼蟲及椰子綴蛾為主。經由調查檳榔花苞受損情形，花苞受損率處理組為 4.9%，而農民慣行組則為 41.1%。採收期調查結果顯示檳榔果實上鱗翅目害蟲的危害比例處理組為 0.4%，農民慣行組則為 1.0%。每花序平均結果數處理組為 156 顆，農民慣行組為 105 顆。平均每顆果實重處理組為 4.7 克，農民慣行組為 4.3 克。處理組與農民慣行組的化學農藥減量比例為 67%。透過以上試驗結果，檳榔蟲害經由登記用藥防治後，不僅能大幅降低化學農藥使用，田間椰子綴蛾危害率降低，使檳榔花苞良率高，亦讓結果數量明顯提升，同時收成的檳榔品質也較佳，建議農民可依照上述施藥種類及方法，於檳榔花期進行檳榔蟲害防治，以達到有效用藥、農藥減量之目標。

關鍵詞(Keywords)：檳榔(*Areca catechu*)、椰子綴蛾(*Tirathaba mundella* Walker)、農藥安全(pesticide safety)

PA14

Molecular identification of a microsporidia from cucumber moth, *Diaphania indica* (Saunders)

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背景/研究問題/材料方法

Microsporidia are obligate intracellular fungi with a wide range of hosts, including vertebrate and invertebrate animals. For invertebrate microsporidia, the reports are mostly found in insects. In this study, the diseased larvae of the cucumber moth, *Diaphania indica* (Saunders) were found in the fields of Taichung Taiwan Agricultural Chemicals Research Institute and Tainan Taiwan Agricultural Chemicals Research Institute. These diseased larvae were homogenized and observed under the light microscope. The mature spore of microsporidia was observed and therefore, it was confirmed as microsporidiosis in cucumber moth. To better understand this microsporidium, the whole ribosomal RNA (rRNA) was cloned and sequenced. Moreover, the phylogenetic analysis based on the rRNA sequence was also performed to evaluate the taxonomic position.

結果/結論/應用啟示

It is the first report of microsporidiosis in the cucumber moth larvae in Taiwan. The fresh spores were oval in shape. Fresh spores were measured 3.737 ± 0.290 × 2.079 ± 0.140 μm (length × width, n = 200). The complete rRNA genome is 4292 bp. The length of the large subunit rRNA (LSUrRNA), internal transcribed spacer (ITS), small subunit gene (SSUrRNA), intergenic spacer (IGS) and 5S region are 2498 bp, 183 bp, 1224 bp, and 277 bp, and 116 bp, respectively. The orientation of the microsporidia rRNA genome is LSUrRNA-ITS-SSUrRNA-IGS-5S, which showed a typical *Nosema* genus feature. The phylogenetic analysis respectively based on the sequences of LSUrRNA, SSUrRNA, and partial LSUrRNA-ITS-partial SSUrRNA, showed that the microsporidia belong to the genus *Nosema*, however, it still needs more evidence, such as ultrastructure, life cycle observation and whole genomic sequence to clarify the classification of this microsporidium.

關鍵字(Keywords): Microsporidia, *Nosema*, ribosomal RNA, cucumber moth, *Diaphania indica*

PA15

Oviposition preferences of the fall armyworm (*Spodoptera frugiperda*) in response to various potential push and pull plants, in Taiwan

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背景/研究問題/材料方法

Fall armyworm (FAW), *Spodoptera frugiperda*, is a major polyphagous pest that mainly feeds on maize and other cash crops. Oviposition preference performance on various hosts may help to predict which plants will be targeted when the favorable hosts are not present and facilitate the development of effective integrated pest management (IPM) strategies to mitigate the potential damages caused by FAW. By assessing the egg-laying preferences of this destructive pest, we aimed to provide insights into selected plants that might be susceptible to infestation and also to identify potential alternative hosts that could serve as trap or repellent crops.

結果/結論/應用啟示

The results showed that FAW females laid eggs on all tested host plants, but significant differences were observed in the number of egg masses and eggs among the different plants. In no-choice bioassays, maize *(Zea mays)*, napier grass *(Pennisetum purpureum)*, and para grass *(Urochloa mutica)* were found to be the most preferred host plants, with significantly higher number of eggs and egg masses compared to the cage wall. On the other hand, sunhemp *(Crotalaria juncea)*, desmodium *(Desmodium uncinatum)*, molasses grass *(Melinis minutiflora)*, egyptian clover *(Trifolium alexandrinum)*, sweet sorghum *(Sorghum dochna)*, natal grass *(Creeping rhynchelytrum)*, and mung bean *(Vigna radiata)* were the least preferred host plants, with significantly lower number of eggs and egg masses compared to the cage wall. In two-choice bioassays, significant differences in terms of number of eggs and egg masses, were found among various combinations of host plants, except for napier and nill grass. In positional three-choice bioassays, differences in number of eggs and egg masses were observed for certain combinations involving C:S:D:W (maize, sunhemp, desmodium, cage wall) and D:C:S:W (desmodium, maize, sunhemp, cage wall). However, S:D:C:W (sunhemp, desmodium, maize, cage wall), interestingly, only showed significant differences for maize. Overall, this study provides insights into the egg-laying preferences of FAW females among different host plants, which can be valuable for pest management strategies and understanding the ecology of FAW infestations. Ultimately, the implementation of push-pull strategies in managing agricultural pests serves to enhance sustainable food production while ensuring minimal impact on other organisms, aligning with the goals of Sustainable Development Goal 2 (zero hunger) and Sustainable Development Goal 12 (responsible consumption and production).

關鍵字(Keywords): integrated pest management, host plants, oviposition preference, pest ecology, polyphagous pest, repellent crops, sustainable development goals, trap crops

壁報展示：生物多樣性、族群與群聚生態學

Posters: Biodiversity, Population and Community Ecology

PB01

臺灣櫻花鉤吻鮭大型水棲昆蟲食餌攝入塑膠微粒

Microplastic ingestion in large aquatic insect prey of Taiwan salmon *Oncorhynchus masou formosanus*

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背景/研究問題/材料方法

塑膠微粒(microplastic)為全世界目前所關注的議題之一，台灣在這方面的研究並不多，然而淡水生態系統中塑膠微粒的研究又相對海洋來的少。雪霸國家公園境內多條溪流為臺灣櫻花鉤吻鮭(*Oncorhynchus masou formosanus*)重要棲息地，本研究分別在武陵地區三溪流以舒伯氏水網採集，以塑膠微粒的豐度及濃度來描述此魚種食餌體內塑膠微粒的發生情況。瞭解是否經由生物累積放大效應對高食性階層生物造成影響？

結果/結論/應用啟示

參考臺灣櫻花鉤吻鮭的食性分析(Liao et al., 2012)，將大型鮭魚偏好取食水棲昆蟲 4 目 8 科 10 分類群定義為大型食餌，本研究共得 737 隻水棲昆蟲、105 個塑膠微粒。顯示武陵地區溪流水棲昆蟲體內有塑膠微粒汙染，微纖維(microfiber)占比最高(99%)。從 One-way ANOVA 和 Kruskal-Wallis test 分析塑膠微粒的豐度與各目水蟲、溪流、取食功能群之間沒有顯著性，但是與季節有顯著性。以塑膠微粒濃度來看 One-way ANOVA 顯示與取食功能群間有顯著性，Kruskal-Wallis test 顯示與季節間有顯著性。這些發現提供了武陵地區溪流塑膠微粒污染的證據，未來的工作應尋求更大的樣本量，檢查來源、運輸和對溪流環境影響來監測該地區的塑膠微粒，同時為管理策略提供信息。

關鍵詞(Keywords)：塑膠微粒(microplastic)、水棲昆蟲(aquatic insect)、武陵地區溪流(Wuling area stream)、臺灣櫻花鉤吻鮭(*Oncorhynchus masou formosanus*)

PB03

白足扁琉璃蟻族群結構與環境降雨量之關係

The relationship between the *Technomyrmex albipes* colony and the environmental precipitation

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背景/研究問題/材料方法

目前台灣已發現約 300 多種螞蟻，其中有 24 種為外來種螞蟻。近年因便利的運輸系統及過度土地開發，加速外來種螞蟻擴展領地，其強侵略性及高繁殖力對原生生態造成威脅，同時也影響人為活動，因此也被視為入侵物種(invasive ant)，其中包括白足扁琉璃蟻(*Technomyrmex albipes*)等。自 1912 年，台灣即有白足扁琉璃蟻存在記錄。該物種以枯枝竹條為巢，主要以液態蜜源為食。目前白足扁琉璃蟻已擴散至高雄市六龜區及美濃區，形成超級群落，因為婚飛期有翅型個體夜間受路燈與居所光源吸引，大量飛入居民生活環境中，造成騷擾性的危害。自 2020 年起針對白足扁琉璃蟻進行調查，發現覓食工蟻、有翅型及工蟻型雄蟻個體數量會受環境降雨量影響。當降雨量增加時，族群個體數量顯著下降，推測多雨量會破壞蟻群巢穴，且影響族群穩定性。而當隔年降雨量降低，工蟻數量則會提高，其中有翅型個體顯著增加，推測是為了擴大群族範圍，增加族群數量。為了追蹤該物種擴散程度以及了解族群量，於路燈下設立自製陷阱，誘集婚飛個體。另外也會固定每個月於該地進行個體採集及族群數量統計，並與月降雨量及氣溫資訊進行比對，探討各階級存在比例與環境變化之關係。

結果/結論/應用啟示

根據數量統計可知，各月份降雨量與在工蟻及蟻后數量間具有相關性，能以 300 毫米及 900 毫米雨量作為數量級距。當降雨量低於 300 毫米時，工蟻數量可達 6000 隻，隨著降雨量增加，數量逐漸減少。蟻后方面，當降雨量高達 900 毫米時，婚飛個體出現時間將延後 1~2 個月，且數量較少，隔年數量則徒增，推測降雨量是影響該物種族群量的主要因素。此外，白足扁琉璃蟻族群有特殊的工蟻型雄蟻，主要在夏季婚飛季節出現，此工蟻型雄蟻在型態上與一般工蟻相似，較難以觀察且存在比例不高。但與有翅型雄蟻一樣具有交尾器，因此推測該型態是為了與族群內生殖型工蟻或是蟻后交配，提高族群量，幫助族群在夏季蟻巢個體成長階段更穩定。因此白足扁琉璃蟻超級群落所造成飛蟻疫情事件的推測，認為降雨雖能帶給物種更多的資源和合適的環境，但也有可能抑制族群成長，甚至成為一種環境逆境。此外，當婚飛季來臨時，有翅型個體會視路燈中藍光及紫光為月光，聚集於燈下，數量高達上千隻，進而侵入住家環境中，影響居民生活。藉由實驗結果可以得知白足扁琉璃蟻各階級個體存在比例與環境降雨量之關係。進而分析物種群落結構和生殖週期，利用餌劑施灑達到防治效果。

關鍵詞(Keywords)：白足扁琉璃蟻(*Technomyrmex albipes*)、降雨量(precipitation)、工蟻型雄蟻(wingless male)、入侵種螞蟻(invasive ant)

PB04

伯格曼法則與拉波波特法則能否解釋臺灣尾尺蛾屬(鱗翅目：尺蛾科)體型大小與海拔分布的關係？

Can Bergmann’s and Rapoport’s rule explain the relationship between body size and elevational distribution of *Ourapteryx* (Lepidoptera: Geometridae) in Taiwan?

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背景/研究問題/材料方法

The climatic niche of an organism is reflected in its phenology, latitudinal and elevational distribution, and long-term shift of distribution under climate changes. Two rules are often used to describe how organisms adapt to different climatic conditions at different altitudes: Bergmann’s rule predicts that organisms develop larger body sizes in colder regions, and the elevational Rapoport’s rule states that the elevational range size of species increases with altitude. We compiled records from social networks, museum specimens, and published studies to examine if body sizes and elevational distributions of Taiwanese *Ourapteryx*, a geometrid moth genus with wide elevational and geographic ranges, conform to these two rules. To see if the elevational ranges of *Ourapteryx* species are restricted by their phylogenetic relationships, we also used public COI gene sequences retrieved from GenBank and BOLD public databases to conduct a preliminary phylogenetic analysis of the *Ourapteryx* species worldwide.

結果/結論/應用啟示

Elevational occurrences of the 15 *Ourapteryx* species in Taiwan range from 1230 to 3255 m, and the species abundance is the highest between 2000 and 2500 m. Linear regression and Pearson correlation analysis indicated that there was no significant correlation between the body size of Taiwanese *Ourapteryx* and the altitude, mean annual temperature, temperature seasonality and annual rainfall ($p > 0.05$). The elevational ranges were positively correlated with highest elevational occurrences (r^2 = 0.31, p = 0.03), but were negatively correlated with mean elevations (r^2 = 0.43, p = 0.007). Neither Bergman’s nor Rapoport’s rule completely explains the relationship between body size and distributional elevation of Taiwanese *Ourapteryx*, demonstrating climate is not the only factor determining their adaptation and evolution of size. The elevational ranges of Taiwanese *Ourapteryx* are not related to their phylogenetic relationships reconstructed with maximum likelihood, implying the formation of their climatic niches might be evolutionarily plastic.

關鍵詞(Keywords)：尾尺蛾屬(*Ourapteryx*)、氣候棲位(climate niche)、外溫動物(ectotherm)、親緣分析(phylogenetic analysis)、演化可塑性(evolutionary plasticity)

PB05

臺灣蝴蝶的特有性與鄰近蝶相之遺傳差異
Endemism of Taiwan butterflies and genetic differences among neighbors

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背景/研究問題/材料方法

臺灣島屬於年輕的大陸島嶼，莫約 500 萬年前浮出海面，島上的生物相隨之成形。臺灣生物相形成時間相較鄰近地區晚近，然而島上的生物卻有高比例的特有種。以蝴蝶為例，已記載的台灣蝴蝶中特有種及特有亞種種數超過六成。此一現象顯示臺灣蝶相的形成過程具有其特殊性。過往的蝶相分析大多呈現與中國大陸的組成較為相似，少部分則為海洋島嶼來源或島內種化之蝶種，然而實際物種來源的佔比為何,卻未有明確證據支持,尤其廣泛分布的蝶種的來源未能確定其來源。

結果/結論/應用啟示

為評估臺灣蝶相來源及與其它地區的蝴蝶差異，我們利用生物條碼、基因淺層定序方法獲得臺灣蝴蝶的遺傳訊息以探討 1) 臺灣特有蝶種多少比例為古特有種 (臺灣島形成前即已完成種化)及新特有種，以及這些特有蝶種的來源? 2)臺灣亞種與其它地區亞種之間的序列差異。目前結果發現大部分的蝶種多為臺灣島形成之前完成種化，亞種之間的差異大多小於 2%。後續將補足尚未取得的樣本序列，以完成臺灣蝴蝶相起源及形成演化歷史之探究。

關鍵詞(Keywords)：島嶼生物地理學(island Biogeography)、散佈(dispersal)、冰河時期(ice age)、博物館基因體學(museumoics)、鳳蝶總科(Papilionoidea)

PB06

活體寵物昆蟲輸入風險評估的科學基礎

The scientific basis of risk assessments for importing exoitc pet insects

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背景/研究問題/材料方法

昆蟲被作為寵物已經有長久的歷史，然而在以寵物或觀賞為由引入外來昆蟲而造成外來入侵種問題之後，外來寵物昆蟲的貿易管制就成為除了一般植物有害生物防疫之外的新議題。隨著電子商務的發達，任何一個國家的活體昆蟲都能夠輕易地被由旅客行李或郵包夾帶入境，又因昆蟲體型小又不具備內骨骼，因此不易以一般的 X 光機所檢獲。此外，由於外來活體動物邊境管理在權責上具有相當的複雜性，因此過去一般民眾經常混淆野生動物保育法與植物防疫檢疫法在邊境控管外來活體昆蟲上的角色。國貿局於 2013 年與 2022 年分別公布了約 5000 與約 8000 種禁止輸入之活體動物，其中大多數物種為昆蟲。而行政院也擬於 2023 年再度公告第三波的禁止輸入動物清單以維護國內農業與自然生態環境。然而外界對於評估的流程以及所採用的科學方法並不熟悉，因此本研究擬說明所有寵物用昆蟲類群被評估之科學基礎與決策方式，並說明生態棲位模擬在昆蟲入侵風險與貿易管制上所扮演的角色。

結果/結論/應用啟示

我們在檢視了已被公告禁止輸入的昆蟲類群以及其生態棲位模擬結果後發現，絕大多數物種的適存氣候機率皆屬中或高度。其中被禁止的非植食性昆蟲通常具有中度適存氣候機率，而植食性昆蟲除具有中至高度的適存氣候機率外，多數物種皆為廣食性，其食物資源在台灣廣泛出現在全島中低海拔地區，因此其入侵風險甚至較非植食性昆蟲更高。此外我們也盤點了每一類昆蟲在台灣的昆蟲飼養社群中的能見度，以及是否有必要進行國內管理或監測之芻議，以利外來入侵種管理的完整。

關鍵詞(Keywords)：外來入侵種(invasive species)、野生動物保育法(wildlife conservation law)、植物防疫檢疫法(plant protection and quarantine act)、風險評估(risk assessment)、生態棲位模擬(ecological niche modelling)

PB07

探討隱密入侵與其成功的機制－以疣胸琉璃蟻族群為例

Cryptic invasion and the underlying mechanisms: a case study of the black cocoa ant, *Dolichoderus thoracicus* (Smith, 1860), in Taiwan

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背景/研究問題/材料方法

了解生物入侵的現況和機制是生態保育和棲地管理的重要議題。以台灣的螞蟻為例，相較於本土的疣胸琉璃蟻 (*Dolichoderus thoracicus*) 族群，近年來外來入侵的疣胸琉璃蟻族群已在中部建立具生態競爭優勢的超級聚落 (supercolony)，騷擾危害農村環境，是一個隱密入侵 (cryptic invasion) 的例子。為探討外來疣胸琉璃蟻族群的入侵現況，以及造成其生態優勢的可能機制，我們在台灣 93 個地點採集野外的螞蟻樣本，進行以下實驗: 1)利用粒線體親緣分析，確認入侵族群的分布地點；2)進行種內侵略行為實驗，探討本土族群和入侵族群之間的行為差異；3)分析本土和入侵族群工蟻個體的表皮碳氫化合物 (CHCs) 組成，以釐清 CHCs 對同伴識別的影響。

結果/結論/應用啟示

粒線體親緣分析結果釐清本土及入侵疣胸琉璃蟻在台灣的分布現況，種內侵略行為的實驗結果顯示入侵族群之間有較低的攻擊性，有助形成具優勢的超級聚落，而 CHCs 分析暗示入侵族群之間較低的攻擊性可能與一些低濃度的碳氫化合物有關。整體而言，本研究揭露的隱密入侵現況與背後機制將有助於此種螞蟻及相關入侵生物的經營管理。

關鍵詞(Keywords)：隱密入侵(cryptic invasion)、超級聚落(supercolony)、表皮碳氫化合物(cuticular hydrocarbons)、蟻科(Formicidae)

PB08

台灣澎湖群島產螳螂(昆蟲綱：螳螂目)名錄建立

Checklist on Mantises (Insecta: Mantodea) of Penghu islands, Taiwan

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背景/研究問題/材料方法

澎湖群島位於台灣海峽，介於台灣和中國之間。澎湖群島過往的生物多樣性研究多集中於海洋生物、候鳥及蝦蟹類調查，節肢動物相關資料尤其是昆蟲則鮮為人知。本研究基於2020-2021年間對澎湖群島直翅目昆蟲的調查，對直翅目昆蟲主要獵食者之一的螳螂亦有詳細紀錄。此外，如要了解台灣地區的螳螂多樣性，則有必要了解各離島的螳螂分布狀況。本研究綜合2020-2023年間澎湖群島採集資料及相關文獻回顧，建立澎湖群島的螳螂名錄。

結果/結論/應用啟示

歷年採集成果與文獻回顧發現，澎湖群島的螳螂目昆蟲為1科4屬5種。其中除了細胸大刀螳 *Tenodera superstitiosa* (Fabricius, 1781)為已記錄種外，寬腹斧螳 *Hierodula patellifera* (Serville, 1838)、薄翅螳 *Mantis religiosa* (Linnaeus, 1758)、小靜螳 *Statilia apicalis* (Saussure, 1871)及枯葉大刀螳 *Tenodera aridifolia* (Stoll, 1813)皆為新紀錄種，本研究建立檢索表供檢視使用。結果也顯示澎湖群島的螳螂多樣性多於原先認知，除缺乏系統性的調查研究外，也可能和島上的氣候與多樣的草本植被結構有關；澎湖群島的螳螂組成也和台灣本島中南部海濱的螳螂組成非常相似。若要全面了解台灣地區螳螂物種組成及結構，金門、馬祖、小球球、綠島及蘭嶼等離島的螳螂組成，均有需要調查建立基本資料。

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

PB09

台灣產之瓜實蠅白蛹品系的應用性評估

Evaluation of the white pupa melon fly strain (*Zeugodacus cucurbitae*) (Diptera: Tephritidae) from Taiwan

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背景/研究問題/材料方法

白蛹基因為不孕性蟲技術(Sterile insect technique (SIT))中分辨雌雄蟲的重要特徵，此性狀能與野生型的褐色蛹作區別，透過育種產生性聯遺傳的品系。目前國際上針對瓜實蠅進行的區域性撲滅計畫與白蛹基因分析研究，皆是來自美國夏威夷的 GSS (Genetic sexing strain)品系。台灣有本土所建立的瓜實蠅白蛹品系，為純白蛹雙性性狀，與國際使用的 GSS 單性品系並不相同。目前尚未有任何相關研究，特與野生型褐蛹品系的台灣產瓜實蠅比較，探討可能的應用潛力。

結果/結論/應用啟示

孟德爾遺傳實驗的結果，發現 F1 雜交的子代均為褐色蛹，F2 子代的蛹色比為 1 : 3.05(白色：褐色)，認為台灣品系的白蛹性狀屬於隱性基因座的遺傳模式。定溫試驗得知白蛹品系在 25℃的孵化率最高為 82.05 ± 1.32 %，顯著高於 20℃ (76.36 ± 0.47 %)、25℃ (64.95 ± 1.34 %)下的數值。另外比較幼蟲期的生長部分，得知白蛹品系於 20℃、25℃下的發育時間短於褐蛹品系。選擇 25℃做最適溫度的生命表分析，發現白蛹品系的平均繁殖率(*F*)為 1265.585 子代/♀，較褐蛹品系的數值(1167.364 子代/♀)高，又平均世代時間(*T*) (33.25 /天)比褐蛹品系的 36.33 /天短。兩品系間的交尾測試之相容性指數(The isolation index)為 -0.14 ± 0.09，屬於隨機交尾模式，且品系間的交尾數高於品系內。綜合以上數據顯示該品系在大量飼養、追蹤用標記、SIT 計畫上具有應用潛力。

關鍵字(Keywords)：瓜實蠅(*Zeugodacus cucurbitae*)、不孕性蟲技術(sterile insect technique)、生命表(life table)、相容性指數(the isolation index)、大量飼養(mass rearing)

壁報展示：行為、生理、個體生物學
Posters: Ethology, Physiology and Organismic Biology

PE01

影響長腳捷蟻出芽分巢因素探討

The factors of colony budding in yellow crazy ant, *Anoplolepis gracilipes*

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背景/研究問題/材料方法

長腳捷蟻(*Anoplolepis gracilipes*)為世界百大入侵螞蟻之一，在全臺中低海拔區域皆能見其蹤跡。過去的研究發現，長腳捷蟻之所以能快速且穩定的發展群落，仰賴於其特殊的族群結構－超級群落 (Supercolony)，而具有超級群落特徵的螞蟻，能透過一種被稱為出芽分巢(Colony budding)的方式，穩定且有效的擴展整個蟻群。然而過去的研究對於出芽分巢的探討甚少，產生分巢的成因也僅以部分觀察結果進行假設與推測。故本研究以：(1)改變工蟻(后)數量與巢內密度實驗與(2)野外蟻后標記再捕捉法(Mark-recapture methods)等方法，對產生出芽分巢的因素及季節進行探討。

結果/結論/應用啟示

研究結果顯示，在常溫 25 ºC (± 0.17)下，以 7 cm*7 cm*1cm、8 cm*8 cm*1 cm 及 9 cm*9 cm *1 cm 等三種不同體積的巢體大小進行實驗，整體工蟻數量約達到 900～1500 隻時，蟻后便會從原始巢體移動至連接的空巢體，此外，移動後約 4 ～ 5 天的時間，原始巢與新巢皆達穩定狀態(蟻后與工蟻不再移動且連通管內無工蟻)。然而空間大小的差異並無影響產生分巢時的工蟻數量，惟工蟻數量到達一定值後，即出現分巢現象。另外，於墾丁野外蟻后標記再捕捉的實驗結果顯示，蟻后於春末夏初時開始出現分巢現象，將分巢率(再捕獲率)與當地平均溫度、相對濕度及累積降雨量等因子進行對比，發現以累積降雨量為最相關因子(R^2 = 0.95)，相對濕度其次(R^2 = 0.88)，平均溫度最末(R^2 = 0.71)。未來在進行防治相關作業時，若能針對長腳捷蟻的分巢季節進行防治，或許能提高野外蟻巢的移除率。

關鍵詞(Keywords)：長腳捷蟻(*Anoplolepis gracilipes*)、入侵種螞蟻(invasive ants)、超級群落(supercolony)、出芽分巢(colony budding)、標記再補捉法(mark-recapture methods)

PE02

紋白蝶顆粒病毒全基因定序與分析

Whole-genome sequencing and analysis of granulovirus from cabbage white butterfly (*Pieris rapae*)

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背景/研究問題/材料方法

Pieris rapae granulovirus (PrGV) can infect and kill larvae of *Pieris rapae*, which is a worldwide pest of Brassicaceae crops. There are some published PrGV genomes; however, the study of PrGV in Taiwan remain unclear. In this research, the diseased *Pieris rapae* larvae were found in fields of Xiushui (Changhua County) and subjected to molecular identification by Kimura-2-parameter (K-2-P) distance analysis based on *lef-8* and *lef-9*genes. Therefore, the PrGV was confirmed in the dead *Pieris rape* larvae (named as PrGV-TW) and then whole genome was sequenced by Oxford Nanopore sequencing Technology (ONT) and next generation sequencing (NGS). The sequencing data were then assembled by Unicycler and annotation of PrGV-TW was performed by ORFfinder on NCBI, then were compared with those of China and Korea PrGV genomes.

結果/結論/應用啟示

The whole genome of PrGV-TW is 128,631 bp, with a GC 33%. There were 229 primary predicted ORFs were compared with 120 ORFs of China PrGV genome (isolate Wuhan and strain WV1010) and Korea PrGV genome (GenBank accession number JX968491 on NCBI) by blastn. The result of blastn indicated that all 120 ORFs from published PrGV genome exist in PrGV-TW and 3 of 229 ORFs were function indeterminate and may imply some unique protein exists in PrGV-TW. This study reveals the features of PrGV-TW genome and provide more information for pest control.

關鍵詞(Keywords)：顆粒體病毒(granulovirus)、紋白蝶(*Pieris rapae*)、基因體定序(genomic sequencing)、微孔粒定序法(Oxford nanopore technology (ONT))、次世代定序法(next generation sequencing (NGS))

PE03

利用桿狀病毒表面展示技術開發細胞焦亡診斷系統

Development of a pyroptosis diagnosis system through baculovirus surface display technology

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背景/研究問題/材料方法

Baculoviruses are one of the major insect pathogens characterized by their large rod-like shape, envelope, and double-stranded DNA genome. These viruses have been employed in baculovirus expression vector system (BEVS) for expressing recombinant proteins and surface-displaying proteins on insect cells. Here, we demonstrate the application of baculovirus surface display technology in a human infectious disease. Sepsis, a host immune disorder due to incomplete elimination of bacteria by the immune system, which can lead to life-threatening tissue damage and organ dysfunction. Pyroptosis is one of the programmed cell death mechanisms aiding in eliminating pathogens, but overwhelming pyroptosis-associated inflammatory might induce sepsis-related organ dysfunction. Therefore, detecting the degree of pyroptosis activation is very crucial in treating septic patients. We designed a blood-diagnosis system using recombinant baculovirus to detect pyroptosis degree in septic patients. Since pyroptosis is mediated by inflammatory caspases, we constructed a recombinant baculovirus to display a series of reporters on the surface of *Spodeptera frugiperda* cell line Sf21 insect cells to detect inflammatory caspase activity for reflecting the degree of pyroptosis.

結果/結論/應用啟示

A recombinant baculovirus containing the coding sequence of an enhanced green fluorescent protein (EGFP), caspase-recognition regions, secreted embryonic alkaline phosphatase (SEAP), and transmembrane protein was successfully generated. Expression and surface display of the construct in insect cells were examined after virus infection. We hypothesized that in the presence of active inflammatory caspases, green fluorescence and SEAP activity should be detectable in the supernatant. Blood cells will be collected from septic patients to evaluate the efficacy of this pyroptosis detector. By using baculovirus surface display technology, this insect cell-based detector can be easily produced without tedious purification process. Our aspiration is that this pyroptosis-detecting system can facilitate an exploration of the interplay between pyroptosis and sepsis, ultimately evolving into a high-throughput diagnostic tool for septic conditions.

關鍵詞(Keywords)：昆蟲桿狀病毒(baculovirus)、桿狀病毒表現載體系統(baculovirus expression vector system)、細胞焦亡(pyroptosis)、敗血症(sepsis)、秋行軍蟲(*Spodeptera frugiperda*)

PE04

利用昆蟲桿狀病毒介導 B 型肝炎病毒感染模式研究隱匿性 B 型肝炎病毒感染之機制

Mechanistic investigation of occult hepatitis B virus infection using baculovirus-mediated HBV infection model

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背景/研究問題/材料方法

Hepatitis B virus (HBV) infection constitutes a significant worldwide health challenge, leading to rising incidence of diseases like liver cirrhosis and hepatocellular carcinoma. Certain HBV-infected patients developed so-called “occult HBV infection”; they exhibited reduced or undetectable HBV surface antigens while still displaying detectable HBV DNA. Next-generation sequencing analysis revealed mutations in the HBV surface antigen of these patients, which may be responsible for occult HBV infection. Since occult HBV infection may lead to accidental viral transmission, it is very important to study its development mechanism. However, existing HBV cell infection models often suffer from low infection efficiency. Insect baculoviruses exhibit remarkable proficiency in mediating gene transfer into mammalian cells, highlighting their significant potential as gene delivery vectors. In this study, we engineered a recombinant baculovirus carrying a 1.3-fold HBV genome that is known for enhancing HBV particle synthesis and transduced the virus into Huh7 cell line to establish a cell model for HBV infection.

結果/結論/應用啟示

A transfer plasmid incorporating 1.3-fold HBV genome was constructed by duplicating specific HBV gene sequences. The plasmid was co-transfected with baculovirus DNA into *Spodoptera frugiperda* cell line Sf21 to produce recombinant baculovirus. Sf21 cells infected with the recombinant baculovirus exhibited expression of HBV surface protein as evaluated via Western blot analysis. Transduction of the recombinant baculovirus into Huh7 cell line resulted in expression of HBV core protein that colocalized with baculovirus transduction sites in immunofluorescence analysis. Our results demonstrate that insect baculovirus containing HBV genome can successfully mediate HBV infection in hepatic cell line and this model can be applied to HBV mechanistic studies by introducing point mutations on HBV proteins. Recombinant baculoviruses harboring surface protein encompassing the mutations identified from patients will be generated to elucidate whether the development of occult HBV infection is attributed to these mutations.

關鍵詞(Keywords)：Baculovirus, Hepatitis B virus, HBV infection cell model, occult HBV infection, *Spodoptera frugiperda* cell line Sf21

PE05

人工噪音對褐翅鉦蟋聲音行為的影響

The effect of artificial noise on the behavior of Ornebius infuscatus (Orthoptera: Mogoplistidae)

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背景/研究問題/材料方法

以聲音作為訊息傳遞的溝通方式在直翅目昆蟲中扮演著舉足輕重的角色，然而隨著都市化程度加劇，利用聲音溝通的生物受到人為噪音的影響也日趨嚴重。本研究以直翅目昆蟲為對象，評估人為噪音干擾對鳴蟲的行為影響。我們以都市周遭常見的直翅目物種褐翅鉦蟋(*Ornebius infuscatus*)為研究對象，評估人為噪音對鉦蟋鳴叫的影響。本研究先使用各頻率能量均勻的白噪音作為處理，設計白噪音與非噪音交錯的室內回播實驗，去測試褐翅鉦蟋在面對間歇出現的人為噪音時是否會避免與白噪音同時鳴叫。我們計算鳴聲的脈衝數量(pulse)重疊於噪音與非噪音的比例，以及每段啁啾(chirp)中，第一聲脈衝(pulse)在噪音與非噪音的比例；並且計算完整一段鳴聲的平均時間長是否會受到噪音影響。

結果/結論/應用啟示

研究結果顯示褐翅鉦蟋傾向於無噪音時鳴叫，脈衝數量於無噪音時顯著高於噪音出現時(p- *value* < 0.05)，且第一聲脈衝開始在無噪音段的比例較高(p- *value* < 0.05)。而無論有沒有與噪音重疊，平均鳴叫時間長皆不受影響。我們的研究結果顯示褐翅鉦蟋會迴避噪音鳴叫，人為噪音會改變直翅目昆蟲的鳴叫行為。本研究未來將比較不同頻率與不同聲壓級的噪音對於褐翅鉦蟋的影響，以進一步釐清影響鉦蟋迴避噪音的因子。

關鍵詞(Keywords)：生物聲學(bioacoustic)、人為噪音(anthropogenic noise)、行為可塑性(behavioral plasticity)、褐翅鉦蟋(*Ornebius infuscatus*)

PE06

miRNA-1-3p 基因對東方果實蠅性別決定上影響
Effect of miRNA-1-3p gene on sex-determining of *Bactrocera dorsalis*

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背景/研究問題/材料方法

東方果實蠅(*Bactrocera dorsalis*)為台灣果樹栽培中最為嚴重害蟲之一，危害寄主植物高達 150 種，在適宜的環境下具高繁殖能力，短期內族群快速增長，造成寄主果實腐爛及落果，對於農業經濟影響甚大。本研究利用 piggyBac 系統將外源 miR-1-3p 基因置入胚胎內，進行熱誘發(Heat shock promoter)的誘發性試驗，觀察轉殖蠅是否因熱誘發(Heat shock promoter)干擾 Bdtraf 功能產生抑雌現象或性別比例上的改變。轉入外源基因的胚胎為 G0，G0 與野生種果實蠅進行回交，使用螢光顯微鏡篩選出帶有紅螢光的 G1，G1 進行 single pair 實驗，篩選出有紅螢光的蛹為 G2，G2 經由自交產生 G3，將 G3 成蟲進行熱誘發(Heat shock promoter)實驗，將採到的卵粒分一半，一半進行 37℃ 熱處理 2 小時，另一半保持在 28℃ 培育，比較有無熱處理之成蟲雌雄性別比例是否出現差異，並與野生種果實蠅作為對照組進行比較。

結果/結論/應用啟示

在卵的熱誘發(Heat shock promoter)實驗中，觀察出熱處理組中基因轉殖品系的雄蟲數量明顯多於雌蟲，而熱誘發(Heat shock promoter)實驗中野生種熱處理組和熱處理組雌雄蟲比例數量相近。由結果呈現外源 miR-1-3p 基因經熱誘發(Heat shock promoter)後可以有效的降低雌蟲的比例，若未來培育出此純品系，並經過動物試驗後，實行田間上的應用，期望可以有效降低東方果實蠅的數量，以利減少對農業經濟所帶來的危害。

關鍵詞(Keywords)：東方果實蠅(*Bactrocera dorsalis,* miRNA-1-3p gene)、熱誘發(heat shock promoter)、性別決定(sex-determination)

PE07

Baculovirus surface display of Clostridioides difficile spore exosporium antigen for monoclonal antibody production

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背景/研究問題/材料方法

Baculoviruses are conventionally used for insect pest control and production of recombinant proteins. Here, we used a baculovirus vector-based system to produce monoclonal antibodies (mAbs) for *Clostridioides difficile* (*C. difficile*), the leading cause of nosocomial antibiotic-associated diarrhea worldwide. *C. difficile* is a Gram-positive, strictly anaerobic, and spore-forming pathogenic bacterium. Symptoms of *C. difficile* infections (CDIs) vary from mild diarrhea to pseudomembranous colitis. Transmissible morphotype of *C. difficile* is dormant spore, therefore spore detection is critical for an accurate assessment of threats to patient health during CDI and implementation of effective environmental disinfection programs. However, there are nearly no antibodies available on the market for detecting *C. difficile* spores. In view of this, we expressed three *C. difficile* spore exosporium antigens, CdeC, CdeM, and CotA, for mouse injection to produce mAbs. These exosporium antigens, known to exhibit hydrophobicity or special modifications, are suitable for expression using the baculovirus expression vector system.

結果/結論/應用啟示

DNA fragments encoding speculated CdeC, CdeM, and CotA proteins were successfully amplified from *C. difficile* strains R20291 and BAA-1805 by PCR and inserted into a transfer plasmid for recombinant baculovirus production. We constructed each antigen in two forms, surface display and secreted, resulting in a total of six virus strains. Expression of each construct was examined in *Spodoptera frugiperda* cell line Sf21 after virus infection. Subsequently, we will inject mice either with purified antigen proteins or baculoviruses surface-displaying the spore antigens. By fusing spleen cells from the mice with tumor cells, hybridomas can be generated. Following this, monoclonal antibodies can be isolated for detecting *C. difficile* spores in patients’ feces or ordinary liquid samples. Compared to traditional *C. difficile* culture assays that may require up to 7 days, we provide a fast and accurate method based on the baculovirus vector-based system that produces mAbs to detect *C. difficile* spores.

關鍵詞(Keywords)：baculovirus surface display, *Clostridioides* difficile spore, CDI, monoclonal antibodies, *Spodoptera frugiperda*

PE08

藉由溫控 *RTA-Bddsx* 蓖麻毒素系統表現抑制轉殖東方果實蠅子代雌蟲數量

Repression of female progeny of transgenic *Bactrocera dorsalis* using thermo-controlled *RTA-Bddsx* system

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背景/研究問題/材料方法

東方果實蠅(*Bactrocera dorsalis*)為嚴重農業害蟲之一，因分布廣泛並且寄主植物多達 478 種，對於全球農業經濟危害甚鉅。如何有效的控制東方果實蠅的族群數量已成為目前防治的重要問題，目前已採用化學性、生物性、物理性等防治方法，仍未能完全有效防治。通過了解東方果實蠅 *RTA-Bddsx* LERQ 蓖麻毒素系統，當蓖麻毒素系統在雌蟲體內時，因東方果實蠅性別決定機制，在雌蟲體內會剪接出完整的 RTA 基因，對於雌蟲具有致死特性，而在雄蟲體內則是剪接出不完整 RTA 基因，所以對雄蟲無毒性(Huang *et al*., 2016)。因此本次實驗以蓖麻毒素系統為基礎，再利用預設的 Heat shock promoter 誘發性表現，觀察是否能調節 *RTA-Bddsx* LERQ 蓖麻毒素系統的功能，在熱誘發的情況下對轉殖蠅造成抑雌現象及性別比例改變。利用 piggyBac 系統把外源基因經胚胎顯微注射完成基因轉殖，此為 G0，將 G0 雄蟲與野生種雌蟲 single pair，再使用螢光顯微鏡篩選出帶有紅螢光的 G1，G1 將雄蟲與野生種雌蟲 single pair 並分組，篩選出帶有紅螢光的蛹，此為 G2，G2 成蟲自交產生 G3，G3 各組進行熱誘發實驗，將 1-3 齡幼蟲挑出，一半進行 37℃熱處理 2 小時，另一半保持在 24℃培育，後續觀察比較成蟲雌雄性別比例上有無熱處理之間是否出現差異。

結果/結論/應用啟示

由於實驗尚在初步階段，目前推論若在理想情況下雌東方果實蠅體內在表現出蓖麻毒素會導致死亡，因而造成基因轉殖品系幼蟲在熱誘發實驗後，雌性幼蟲便會死亡，造成在成蟲時期雄蟲數量會多於雌蟲，甚至皆是雄蟲的情況，而沒有經過熱誘發的繼代組別雄雌蟲數量則是接近相同。後續從 gDNA 分析有出現顯著雌雄比的組別，挑出帶有完整轉殖基因片段的成蟲再自交培育出純的品系後代，藉由 qPCR 分析 *Bddsx* 和 *RTA-Bddsx* 在幼蟲和蛹不同階段的基因表現量。在未來應用中，若能培育出純的品系並且大量飼養出雄性子代，在防治上將具潛力及法規容許下，可再進一步進行田間試驗，觀察是否可以有效的降低野生種的東方果實蠅數量。

關鍵詞(Keywords)：*Bactrocera dorsalis*, *RTA-Bddsx*, *transformer*

PE09

Doublesex 在咖啡果小蠹的純化及定性

Isolation and characterization of doublesex gene in the coffee berry borer Hypothenemus hampei

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背景/研究問題/材料方法

咖啡果小蠹 *Hypothenemus hampei* 為咖啡作物之重要經濟害蟲。體型小且於咖啡果實中鑽食，導致不易觀察其生命週期。咖啡果小蠹的族群具有高偏雌之特徵，與其他小蠹蟲科物種類似，且具有兩性異形的現象，而造就此現象的成因目前尚無定論。節肢動物的性別決定在染色體型態與分子調控上展現多種樣貌。咖啡果小蠹的雌雄核型皆為二倍體，但雄蟲的一套染色體失活，其性別決定為功能性單雙套系統。然而其中哪個分子訊息開啟性別決定梯瀑的關鍵基因及兩性開關基因，目前仍屬未知。由於兩性開關基因中 doublesex (dsx) 調控性別決定之功能具有高度保守性，因此我們首先以 dsx 作為分子標記探討咖啡果小蠹的性別調控機制。我們根據咖啡果小蠹的基因體資訊選殖 dsx 基因片段。透過全胚胎原位雜合反應檢測 dsx 基因的發育表現，希望能解釋咖啡果小蠹雌雄兩性異形的調控現象。

結果/結論/應用啟示

我們已初步完成選殖咖啡果小蠹 dsx-1、dsx-2、dsx-3 及 dsx-4 的基因片段。藉由 RACE-PCR 增幅此四個基因全長，將可瞭解在咖啡果小蠹是否具有性別特異性剪接。在胚胎發育時，我們偵測到 dsx-1 在咖啡果小蠹的胚胎前端位置有表現。而 dsx-2 的初步偵測結果顯示基因表現於胚原的部分組織中，位置與 dsx1 迥異。然因咖啡果小蠹胚胎時期的發育圖譜尚未建立，無法正確定義其二基因的表現位置。未來將致力於建構完整胚胎圖譜，並且同時偵測 dsx-3 與 dsx-4 在胚胎表現位置。本研究除了有利於區別各個基因在胚胎的表現位置，對於 dsx 在胚胎發育過程中，可能扮演的功能，將可為小蠹蟲性別決定機制提供新的線索。

關鍵詞(Keywords)：兩性基因(doublesex)、性別決定(sex determination)、兩性異形(sex dimorphism)

PE10

鈴木球金龜(鞘翅目: 駝金龜科: 球金龜亞科)的生活史

Life history of *Madrasostes suzukii* Ochi, Tsai & Masumoto (Coleoptera: Hybosoridae: Ceratocanthinae)

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背景/研究問題/材料方法

Ceratocanthid beetles are renowned for their remarkable ability to tightly roll up into a ball, a behavior traditionally attributed to defense mechanisms. However, the biology of this group, particularly during their immature stages, remains unclear. In Taiwan, two species of Ceratocanthid beetles have been documented: *Madrasostes taiwanense* in Taitung, and *M. suzukii* on Lanyu Island. This study endeavors to elucidate the natural habitats and life history of *M. suzukii*, while redescribing the morphology of *M. suzukii* with a specific focus on its immature stages.

結果/結論/應用啟示

Both adults and immature stages were discovered within the clay-like materials found in decomposing wood or tree cavities inhabited by the termite *Prorhinotermes flavus* (Bugnion & Popoff). Numerous adult individuals coexisted with larvae in various instars, and a short period of immature phase was observed, suggesting a multivoltine life history with overlapping generations. The study delves into *M. suzukii*'s feeding habits and termitophily in detail. Moreover, based on an extensive collection of adult and immature specimens, this research provides a comprehensive redescription of the morphology at each developmental stage of *M. suzukii*, enriched by scanning electron microscopy (SEM) images and micro-computed tomography (micro-CT) volume data.

關鍵字(Keywords)：球金龜亞科(Ceratocanthinae)、喜白蟻性(termitophily)、喜白蟻巢性(termitariophily)、共生生物(symbiont)

壁報展示：醫學昆蟲學

Posters: Medical Entomology

PM01

大陸與島嶼鼠媒人畜共通傳染病比較
Comparison of rodent-borne diseases on continent and island

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背景/研究問題/材料方法

鼠媒人畜共通傳染病對人類社會、經濟、健康的影響甚鉅，為目前全世界極欲解決的重要公衛議題。全球旅遊與貿易的盛行增加了囓齒類動物擴散到世界各地的機會。囓齒類動物傳播超過 60 種鼠媒人畜共通傳染病，對人類健康帶來嚴重威脅，當這些囓齒類動物攜帶病原體或節肢動物病媒，入侵到島嶼時，是否會加速鼠媒人畜共通傳染病的傳播，鮮少受到關注。影響鼠媒人畜共通傳染病傳播的因素，除了宿主以外，尚包含病原體、病媒、傳染途徑與環境因子等。本研究將利用 R 統計軟體與 PubMed 蒐集相關文獻資料，記錄下所需要的資訊後，利用 QGIS 標示有出現鼠媒人畜共通傳染病的島嶼，接著使用描述性統計：比較不同類型的鼠媒人畜共通傳染病在島嶼上出現的頻度；比較島嶼上外來與原生種囓齒類動物各自帶有哪些鼠媒人畜共通傳染病與節肢動物病媒，並與在大陸上帶原同一種鼠媒人畜共通傳染病的囓齒類動物與節肢動物病媒種類進行比較。

結果/結論/應用啟示

目前得知島嶼上(1)出現直接傳播的鼠媒人畜共通傳染病的機率較間接傳播高；(2)外來鼠種成為鼠媒人畜共通傳染病宿主的機率，高於原生鼠種。

關鍵詞(Keywords)：鼠媒人畜共通傳染病(rodent-borne diseases)、囓齒類動物(rodents)、島嶼(islands)、病媒(vectors)、外來入侵種(invasive species)

PM02

土臭素(Geosmin)和聚二甲基矽氧烷(Polydimethylsiloxane, PDMS)對臺灣鋏蠓產卵偏好之影響

Preliminary evaluation of geosmin and polydimethylsiloxane on oviposition preference of the biting midge, *Forcipomyia taiwana*

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背景/研究問題/材料方法

灣鋏蠓為臺灣重要騷擾性衛生害蟲，因其嗜吸人血，可導致受害者皮膚搔癢、紅腫等過敏反應，對各行業均造成負面影響。目前防治以環境整頓及緊急化學防治為主，然而化學防治不僅成效不彰，亦有環境汙染與人類健康之虞，急需研發環境友善之替代防治方法，本研究試驗影響臺灣鋏蠓產卵偏好訊號。土臭素為環境中常見的微生物代謝物，對蚊子具有誘引產卵效果；聚二甲基矽氧烷(Polydimethylsiloxane, PDMS)是一種高分子有機矽化合物，屬於環境友善的蚊子產卵忌避劑。本研究利用瓊脂覆蓋含藻液之濾紙作為產卵基質，比較土臭素添加與否，及測試不同 PDMS 劑量於添加藻液條件下，試驗對臺灣鋏蠓產卵之影響。

結果/結論/應用啟示

結果顯示土臭素不論加到瓊脂培養皿、或加到含藻液的瓊脂培養皿或土杯中，都有誘引雌蟲產卵的趨勢。甜菜根也含有土臭素成分，甜菜根表皮(epidermis)或皮層(cortex)萃取液，也發現對臺灣鋏蠓產卵具有正面影響，推測土臭素可能為一種臺灣鋏蠓選擇產卵棲地的訊號，而於野外的誘卵效果，仍有待進一步探討。此外，臺灣鋏蠓也偏好產卵在添加 PDMS 及藻液的基質上，尤其含 0.42 mg/cm^2 PDMS 劑量的基質產卵比例最高，但 PDMS 具有黏性，是否因此迫使懷卵雌蟲臨死前將卵大量產出的情形，或何種 PDMS 劑量，具有最佳干擾產卵之效果仍有待釐清。

關鍵詞(Keywords)：台灣鋏蠓(*Forcipomyia taiwana*)、產卵訊號(oviposition cue)、誘卵陷阱(gravitrap)

壁報展示：系統分類、族群遺傳、演化
Posters: Systematics, Population Genetics and Evolution

PS01

怪螳科於台灣的首次記錄(螳螂目：怪螳科)
First record of Amorphoscelididae (Mantodea) in Taiwan

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背景/研究問題/材料方法

怪螳屬 *Amorphoscelis* Stål, 1871 為怪螳科 Amorphoscelididae 下的一個屬，頭部後緣具兩個瘤狀突起，前胸背板方形或近似方形，前足細小，腿節僅一枚中刺、脛節僅一枚端刺，中後足細長無明顯凸起或擴展，尾毛細長末端寬大扁平。本屬物種皆為體長不足3公分的小型螳螂，多棲息在樹幹或枯木上，廣泛分布於非洲、亞洲、歐洲及大洋洲等地，中國及東南亞各國皆有怪螳之分布紀錄。目前全球已知約50餘種怪螳，中國記載有5種。在台灣昆蟲相的調查中，長期缺乏螳螂目的資訊，相關調查中亦未見怪螳的紀錄。

結果/結論/應用啟示

本研究之怪螳標本,係由國立臺灣大學昆蟲學系學生捕獲,位於新北市海拔約800-900公尺山區，以燈光誘集採得之雄性標本。經檢視比對，確認為為台灣第一筆怪螳科怪螳屬物種；生殖器解剖與形態特徵鑑定，初步判定為本屬之新物種。後續將透過形態特徵與DNA序列資料分析，進行物種描述，確認其分類地位；此一新科新種之記錄，代表台灣螳螂目的多樣性還有相當大的探索空間。

關鍵詞(Keywords)：螳螂目(Mantoda)、怪螳科(Amorphoscelididae)、怪螳屬(*Amorphoscelis*)、新紀錄(new record)

PS02

東方蜂微粒子比較基因體研究
The comparative genomics of *Nosema ceranae*

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背景/研究問題/材料方法

東方蜂微粒子 (*Nosema ceranae*) 為蜜蜂微粒子病 (Nosemosis) 主要病原，為絕對胞內寄生真菌，會對蜜蜂造成生理及行為等負面影響，嚴重時會導致蜂群崩解。2004 年首度於西方蜂群中鑑定出東方蜂微粒子，近年似乎趨於潛伏感染，故此研究中我們使用第三代定序 Oxford Nanopore Technology (ONT) 定序，針對台灣，台中地區西方蜂群之東方蜂微粒子進行基因體的重新定序，並與中國已發表基因體進行比對，釐清目前存於臺灣蜂群間的東方蜂微粒子之基因體是否已產生變異，並討論變異對現存蜜蜂微粒子病的影響。

結果/結論/應用啟示

組裝基因體結果顯示，組裝基因體大小為 2,166,462 bp，包含 32 條 contigs。與中國已發表之基因體比較後發現，於台灣蜂群中採樣之東方蜂微粒子基因體已產生變異，共計 2842 個差異基因體區域 (Distinctive genomic gions, DGRs)。篩選大於 500 bp 之 DGRs，共計 1188 個，在相似度小於 60％的 DGRs 中發現 29 個預測性蛋白基因，其中包含 ribosome-associated chaperone zuotin、transposase-like protein 及其餘為 hypothetical protein 的變異基因，相似度分別僅有 54% 及 58%，顯示台灣蜂群中的東方蜂微粒子基因體已與中國之基因體產生區別。在結合過去轉錄體數據後，發現有 9 個基因在成熟孢子及感染蜜蜂後 5、10、20 天具有差異基因表現量。未來將持續探討基因體變異對東方蜂微粒子造成的影響，並期望此研究成果可以為蜜蜂微粒子在早期偵測、治療防治及瞭解蜜蜂健康程度提供貢獻。

關鍵詞(Keywords)：西方蜂(*Apis mellifera*)、東方蜂微粒子(*Nosema ceranae*)、基因體(genome)、比較基因體學(comparative genomics)

PS03

臺灣產擬瘦姬蜂屬 (膜翅目：姬蜂科：柄卵姬蜂亞科)於形態及分子物種界定上的不一致

Incongruences between morphological and molecular species delimitation of the genus *Netelia* (Hymenoptera: Ichneumonidae: Tryphoninae) in Taiwan

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背景/研究問題/材料方法

The species-level taxonomy of the diverse nocturnal darwin wasp genus, *Netelia* Gray, 1860, is mainly based on their unique male genitalia structures due to their similar external appearances. However, the role of their specialized male genitalia structures in speciation remains unknown, and the previous taxonomy based on male genitalia has not been tested with molecular data. In this study, we aim to re-examine the previous taxonomic system and revise the taxonomy of Taiwanese *Netelia* using an integrated taxonomic approach by analyzing more than 70 morphospecies from Taiwan and Japan, and more than 300 *COI* sequences worldwide from the BOLD systems. This combines morphological criteria (external morphologies and male genitalia structures) and molecular criteria (mitochondrial *COI*-based ASAP and bPTP and nuclear *28S* sequences) for species delimitation.

結果/結論/應用啟示

Our results revealed incongruences between morphological and molecular criteria for species delimitation. For example, four morphospecies from the subgenus *Prosthodocis* and three from the subgenus *Netelia* from Taiwan and Japan displayed low genetic divergence. Conversely, within the subgenera *Apatagium* and *Amebachia*, significant genetic divergence was observed among morphospecies with similar morphology. The results suggest that the diversity observed in male genitalia morphology may not accurately reflect species diversity within the genus *Netelia*. The low genetic divergence within certain morphospecies might result from local morphological adaptation or sexual selection-driven diversification. Meanwhile, cryptic species might be present in some *Netelia* groups. For future works, a more comprehensive sampling is needed to clarify the taxonomy of this commonly seen nocturnal wasps.

關鍵字(Keywords)：整合分類學(integrative taxonomy)、物種界定(species delimitation), 姬蜂科(Ichneumonidae)、擬瘦姬蜂屬(*Netelia*)、臺灣(Taiwan).

PS04

近年入侵臺灣的麻子燈蛾(鱗翅目：裳蛾科，燈蛾亞科)之分子鑑識

Molecular identification of Olepa ricini (Fabricius, 1775) (Lepidoptera: Erebidae, Arctiinae), a new invasive species in Taiwan

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背景/研究問題/材料方法

Since 2004, a large and un-recorded arctiine species was discovered in urban Taipei. The species was immediately identified as a species of *Olepa*. Identification of the species, however, become immediately difficult because the male genitalia of *Olepa* exhibits remarkable intraspecific variation, the material for molecular identification was not available, and the competition among different research teams have resulted in descriptions of many new species with doubtful status. Up to date, in total 14 species plus 2 subspecies are already described and since the barcode data has become accessible in recent years, we consider it would be necessary to investigate the taxonomic identity of the *Olepa* species invading Taiwan for years. In the present study, we extracted barcode sequence data from 6 *Olepa* species (54 individuals) and used *Nannoarctia tripartita* as the outgroup. We used both Maximum likelihood and Bayesian methods to reconstruct the tree and used bootstrap and Bayesian inference to evaluate the robustness and reliability of the trees.

結果/結論/應用啟示

The results of phylogenetic analyses show that the Taiwanese population belongs to *Olepa ricini* and the genetic affinity is closer to an individual from Maharashtra of India. The results also show that *Olepa ricini* and *Olepa schleini* should be treated as synonyms and this synonymy also implies that *Olepa ricini* might have dispersed to West Asia and SE Asia since 1980s. Although the invasion pathway from India to Taiwan has not been investigated, the shipping containers may play an important role of carrying moths that can survive for a period of time.

關鍵字(Keywords)：隱藏種(cryptic species)、個體變異(individual variation)、入侵種(invasive species)、生命條碼(barcode of life)、貨櫃(container)

PS05

造成檳榔用藥管理困難的椰子綴蛾(鱗翅目：螟蛾科，蠟螟亞科)究竟是那一種？有幾種？

Which species and how many species of *Tirathaba* (Lepidoptera: Pyralidae, Galleriinae) have caused the problem of pesticide management for betel nut?

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背景/研究問題/材料方法

Betel nut (*Areca catechu*) is one of a significant palm crops in Taiwan since the Austronesian people migrated to this island. The industry of this plant was quickly developed and expanded to almost the entire island after the War II due to the need from the working class. Although the production of betel nut has played an important role in the development of agroeconomy in Taiwan, the industry has raised great concern in many aspects, such as soil water conservation in hilly regions, public heath, food security and ecological damage in agricultural system. Thus, the betel nut industry was an agony for the authorities concerned due to these complicated issues that would require multiple approaches to resolve. In order to resolve the safety issue of the pesticides used on betel nut, ACRI recently announced the guideline for using pesticides on betel nut based on experiments using the so-called "oil palm bunch moth" (*Tirathaba mundella*). When examining the images of the moth used for press, however, we found that the species used for the assay was misidentified and therefore a taxonomic revision of the moths infesting betel nut in Taiwan becomes necessary. In the present study, we aim to investigate which species and how many species cause damages of betel nut flowers and fruits by using both molecular phylogenetic and morphological approaches.

結果/結論/應用啟示

The results of phylogenetic analyses based on Maximum Likelihood and Bayesian methods reveal that at least 3 species of *Tirathaba* occur in Taiwan, but none of them is conspecific with *Tirathaba mundella*, of which the type locality is Sabah (Malaysia). We also found that the larvae of a population in I-lan occasionally infest guava fruit, and this finding may have significant influence on management of the pesticides used for betel nut and other fruits.

關鍵字(Keywords)：隱藏種(cryptic species)、食果性(frugivory)、親緣關係分析(Phylogenetic analysis)、螟蛾科(Pyralidae)、棕櫚(palms)

PS06

白斑翅野螟(鱗翅目：草螟科，斑野螟亞科)是個單模屬且其近緣屬在翅紋上的相似性可能肇因於與鹿蛾間的貝氏擬態關係

The genus *Bocchoris* (Lepidoptera: Crambidae, Spilomelinae) is monobasic and the similarity in wing pattern among related genera is possibly owing to Batesian mimicry with Syntomini moths

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背景/研究問題/材料方法

Defensive mimicry refers to the phenotypic resemblance between sympatric species that receive similar selection pressure through evolutionary history and thus convergence in a certain traits is expected to increase fitness of at least one of them. The characters shaped by convergence due to mimicry, however, often mislead taxonomists to place co-mimicking species into one group with little doubt. In the present study, we present a case showing how the body pattern exhibiting Batesian mimicry may mislead taxonomists for over 130 years. *Bocchoris* Moore, 1885 currently comprises more than 30 species in both the New and Old Worlds. When investigating the taxonomic placement of certain species, we found that the entire genus might not be monophyletic. We therefore obtained the COI sequence data from 9 *Bocchoris* species plus *Ategumia*, *Nankogobinda*, *Diasemia* and *Diasemiopsis* for comparison.

結果/結論/應用啟示

The results of phylogenetic analyses based on Maximum Likelihood and Bayesian methods reveal that *Bocchoris* should be confined to its type species, *inspersalis*, and the rest of the species should be placed in several new genera. The resemblance among *inspersalis, trimaculalis*, and *ciliate* is very likely linked to the mimicry with Syntomini moths in SE Asia, but the potential model in African requires further investigation.

關鍵字(Keywords)：貝氏擬態(Batesian mimicry)、趨同演化(convergent evolution)、親緣關係分析(phylogenetic analysis)、草螟科(Crambidae)、多系群(polyphyletic group)

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PU01

入侵臺灣的東南亞小蜜蜂新型蜜蜂病毒變種發現

Discovery of novel variants of honeybee viruses on invasive dwarf honey bee (*Apis florea*) in Taiwan

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背景/研究問題/材料方法

東南亞小蜜蜂 (*Apis florea*) 在 2017 年疑因船舶運輸進入臺灣南部，雖然是授粉昆蟲，但至今已成為都市地區極具威脅的入侵物種，滋擾民眾的通報數逐年激增，攻擊事件亦頻傳；研究團隊的研究已確認並報導小蜜蜂另攜入欣氏真瓦蟎 (*Euvarroa sinhai*)，以及蜜蜂畸翅病毒 (Deformed wing virus) 之新型變異病毒株。其影響，不僅對於外來植物及雜草傳播擴散之生態影響，另危及民眾的人身安全，以及帶來臺灣養蜂產業風險。本研究分析 2018 年至 2023 年高雄地區移除小蜜蜂的案件，瞭解 6 年間的移除作業與擴散趨勢影響。此外，對於部分移除的蜂群，檢測工蜂中腸、寄生蟎體的畸翅病毒 RNA，並依據該畸翅病毒的多蛋白基因編碼區域，設計長度 855 nt 的專一性引子對，後續搭配現有的畸翅病毒 (378 nt)、黑王台病毒廣效性引子對 (700 nt)，針對 123 個小蜜蜂樣本和 22 個寄生蟎樣本，進行多重聚合酶鏈反應檢測並定序。

結果/結論/應用啟示

歷經中央與地方政府的通力合作，進行大量移除，至 2023 年，小蜜蜂的分布，在高雄市仍不斷發生並逐步往外擴散，現已逾 20 個行政區，顯見未來我們要有與此入侵物種共存的認知，在防治管理策略上建議主管機關提早因應，而鄰近縣市地方政府，建議提前部署管理機制。新型畸翅病毒株的分析，小蜜蜂與欣氏真瓦蟎的病毒株，其序列相似度達 98-99%，與西洋蜜蜂 (*Apis mellifera*) 的原始病毒株僅 87%，已登錄於 GenBank。畸翅病毒廣效性引子對於小蜜蜂工蜂的總檢出率為 81.3% ($n = 123$)，對欣氏真瓦蟎為 81.8% ($n = 22$)，而專一性引子針對新型病毒株的檢出率分別為 49.6% 和 63.6%；此外，對於黑王台病毒總檢出率分別為 83% 及 63.6%；兩種病毒的複合感染率為 67.5% 及 59.1%。同時，黑王台病毒的廣效性引子所增幅的特定片段與 GenBank 已發表的病毒株序列相似度僅 88%，顯示黑王台病毒也有類似於畸翅病毒的變異情況。綜合上述，小蜜蜂身上疑似還攜帶另一種蜜蜂病毒的新病毒株，研究團隊將持續追蹤探討。

關鍵詞(Keywords)：東南亞小蜜蜂(dwarf honey bee)、寄生蟎(parasitic mites)、畸翅病毒(deformed wing virus)、黑王台病毒(black queen cell virus)、變異病毒株(variants)

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