43rd 台灣昆蟲學會年會

Annual Meeting of Taiwan Entomological Society

外來入侵生物管理

異蟲崛起

2022. 10. 22-23

國立中山大學理學院

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一路走來．始終如一

第四十三屆台灣昆蟲學會年會

The 43rd Annual Meeting of Taiwan Entomological Society

2022年10月22 - 23日

台灣｜高雄｜國立中山大學理學院

Oct. 22 - 23, 2022

College of Science, National Sun Yat-sen University

Kaohsiung, Taiwan

協辦單位：國立中山大學理學院、國立臺灣大學昆蟲學系

各位會員、昆蟲大家庭的先進們，大家好：

感謝大家參加第 43 屆台灣昆蟲學會年會，去年線上年會的記憶猶新，但也讓人更期待實體年會的鬧熱氛圍。今年的主題是「異蟲崛起－外來入侵生物管理」，我們將聚焦在外來入侵種的邊境管制、入侵後的防治和管理。全球貿易及交通旅運的便捷使不同地區的生物得以擴散至原生地以外的區域，外來生物的族群擴大導致與當地原生物種產生食物、棲地和掠食等競爭，甚至造成病菌傳播的問題。而除生態系遭遇失衡的危機外，從農業的角度來看，外來有害生物入侵至非原產國，可能造成當地巨大經濟損失、甚至是糧食危機。因此，如何在全球貿易系統下因應外來入侵物種的防治與管理是至關重要的議題。我們很榮幸邀請到：日本國立研究開發法人森林研究整備機構森林総合研究所的 Dr. Eiriki Sunamura 砂村栄力博士、國立中興大學昆蟲學系楊曼妙教授、國立臺灣大學昆蟲學系曾書萍助理教授以及瑞士洛桑大學的 Dr. Cleo Bertelsmeier，分別從不同入侵生物特性、分類、遺傳、入侵來源與入侵後的適應、防治策略等不同面向切入，提供與會者對於入侵生物有更全面的了解。

顏聖紘教授主持的「入侵昆蟲工作坊：從政策、科學到田間實務」邀請到了產官學研四方專家學者對談，行政院農委會動植物防疫檢疫局的陳子偉組長、林務局保育組劉泰成先生、臺灣大學昆蟲學系許如君主任、臺灣大學農藝學系莊汶博教授、文化大學森林保育學系謝佳宏教授等專家學者討論外來入侵生物的風險評估與防治，對未來農業上如何因應外來有害生物提供具體的建議與做法。

本次也將是蘇南耀昆蟲學學術獎於 2019 年設立後的首次頒獎，獲獎者為日本京都大學的 Kenji Matsuura 松浦健二教授。松浦健二教授是一位卓越的昆蟲學家，在社會生物學、行為生態學、族群遺傳學都有開創性的進展，是首位發現白蟻蟻后會以孤雌生殖複製第二代蟻后的學者，他所發表的“Asexual Queen Succession (AQS)”的機制隨後也在不同的白蟻與螞蟻物種上被發現，這項研究是我們了解社會性生物生殖系統關鍵的一步。我們將與蘇南耀教授連線，頒贈蘇南耀昆蟲學學術獎及台灣昆蟲學會榮譽會員予松浦健二教授，以表彰他的學術成就與貢獻，並由松浦教授為我們帶來一場專題演講。

今年由李後鋒教授主持的「與學生對談」，邀請到中興大學昆蟲學系的譚景文助理教授、農業試驗所陳怡如助理研究員和台灣巴斯夫（股）公司的王若璇經理等三位不同領域的學者專家，從自身的成長背景與經驗出發，進一步分享女性在昆蟲學領域發展所遇到的挑戰。而「職涯發展與企業分享」將由三間長期支持昆蟲學研究及發展的成功企業，介紹公司營運方向、產品及服務，值得求學階段的與會者們作為未來職涯發展和學習及研究方向的參考。

在今年 8 月份的全國科學展覽會，台灣昆蟲學會與正瀚生技股份有限公司聯合設立了「台灣昆蟲學會正瀚創新獎」，總共評選出 4 件以昆蟲為題材及 1 件農業科學的優秀作品，各頒發獎金 2 萬元及獎狀，鼓勵昆蟲學及農業科學的創新與發展。我們很開心邀請到其中兩個獲獎的優秀團隊：慈濟大學附屬高中和台南小新國小的師生參與年會，他們的作品將於海報區展示，歡迎大家蒞臨指教，也不吝給予鼓勵。

最後，再次歡迎各位朋友參與年會，同時感謝贊助廠商的支持與本屆理監事和工作團隊的辛勞，祝福大家在年會中有豐碩的收穫，度過心滿意足的週末。

理事長

蕭旭峰

敬上

2022 年 10 月 22 日

第43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, National Taiwan University
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	張明陽 Ming-Yang Chang	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
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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, National Chung Hsing University

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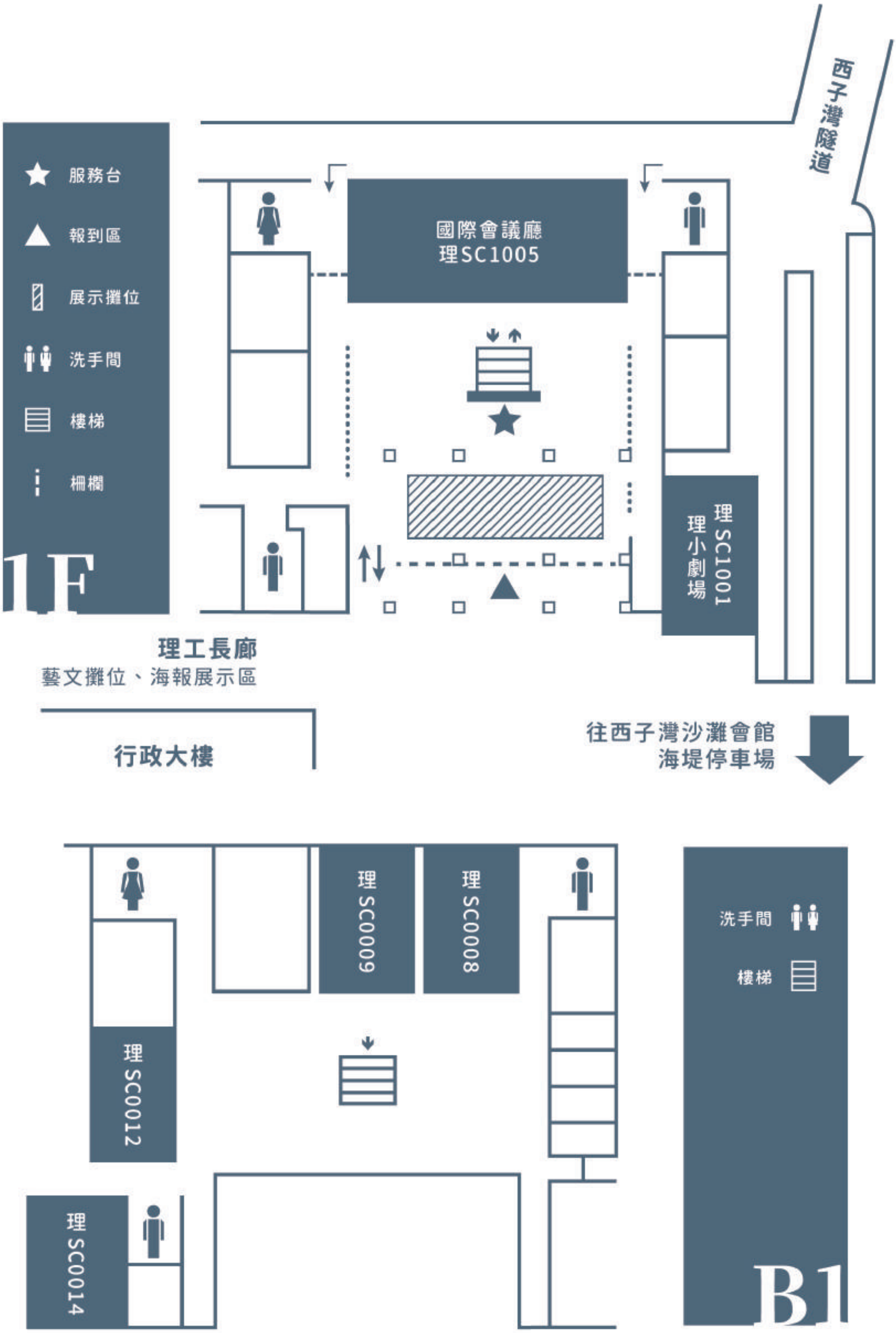
第 43 屆台灣昆蟲學會年會摘要集

會議地點 Meeting Venue

國立中山大學理學院
College of Science, National Sun Yat-sen University



大會資訊 **Meeting Information**

大會地點 Meeting Venue

本屆大會於國立中山大學 (高雄市鼓山區蓮海路 70 號) 舉行。主要場地包括 1 樓理小劇場 (SC1001) 與 B1 普通教室 (SC0008、SC0009、SC0012)、理工長廊。

The conference will be held at National Sun Yat-sen University, NSYSU. The venue includes 1F Theatre (SC1001); B1 Classroom SC0008, SC0009, SC0012 and the 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，所有講者務必提前至報告場地，由工作人員協助將檔案匯入電腦。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。

PC (Windows system) and projectors are provided for all meeting rooms. All presentations must be brought to the symposium venue on a USB-key in advance of the session. The staffs will assist you to import the file. Each speaker has 15 minutes (including your preparation time), 12 minutes of oral presentation and 3 minutes of Q&A.

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

請自行準備您的海報，並於第一天報到後至理工長廊依編號張貼。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在海報旁介紹研究內容並回答問題，並務必於 10 月 23 日 15:00 前自行將海報撤下。

The posters should be mounted before the Poster Session on Oct. 22. Pushpins are provided on site. During the poster sessions (16:10-17:00), 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 15:00 on October 23.

大會專題演講 Keynote Speech

時間：10 月 22 日 (六) 9:10-10:10

Alien longhorn beetles as rising pests in Asia: their biology and control

Dr. Eiriki Sunamura 砂村 榮力 博士

Senior Researcher

Department of Forest Entomology
Forestry and Forest Products Research Institute, Japan

日本森林綜合研究所 高級研究員

大會專題演講 Keynote Speech

時間：10 月 22 日 (六) 10:10-11:10

Psyllids, gallers and their origin: issues with taxonomy and origin of invasive alien species
木蝨、蟲癭及牠們的產地：談外來入侵種的分類及溯源問題

Dr. Man-Miao Yang　楊曼妙 博士

Professor

Department of Entomology,
National Chung Hsing University, Taiwan

國立中興大學昆蟲學系 教授

大會專題演講 Keynote Speech

時間：10月23日(日) 9:00-10:10

Exploring the frontiers of termite biology and beyond

Dr. Kenji Matsuura 松浦 健二 博士

Professor
Assistant Director

Laboratory of Insect Ecology,
Graduate School of Agriculture,
Kyoto University, Japan

日本京都大學大學院農學研究科 教授

大會專題演講 Keynote Speech

時間：10 月 23 日 (日) 14:30-15:30

How genetic data aid invasive pest management: present and future

Dr. Shu-Ping Tseng 曾書萍 博士

Assistant Professor

Department of Entomology,
National Taiwan University, Taiwan

國立臺灣大學昆蟲學系 助理教授

大會專題演講 Keynote Speech

時間：10 月 23 日 (日) 15:30-16:30

Global dispersal and niche shifts in invasive insects

Dr. Cleo Bertelsmeier

Assistant Professor

Department of Ecology and Evolution,
University of Lausanne, Switzerland

瑞士洛桑大學生態與演化學系 助理教授

議程大綱

Oct. 22, 2022（Sat.）				
時間/地點	理小劇場 SC1001			
8:30-9:10	報到（理學院門口）、壁報張貼（理工長廊）			
9:00-9:10	開幕、合照			
9:10-10:10	大會專題演講（線上） Alien longhorn beetles as rising pests in Asia: their biology and control **Dr. Eiriki Sunamura**			
10:10-11:10	大會專題演講 木蝨、蟲癭及牠們的產地：談外來入侵種的分類及溯源問題 **Dr. 楊曼妙**			
11:10-11:20	換場			
時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
11:20-12:20	OS_01-OS_04 系統分類、族群遺傳、演化	OE_01-OE_04 行為、生理、個體生物學	OA_01-OA_04 農業昆蟲學	職涯發展與企業分享
時間/地點	理學院 1 樓中庭			
12:20-13:50	與學生對談			
	休息用餐／12:30-13:30 理監事會 (SC0014)			
13:50-15:50	小黑蚊工作坊	OE_05- OE_12 行為、生理、個體生物學	OA_05-OA_12 農業昆蟲學	OM_01-OM_08 醫學昆蟲學
15:50-16:10	茶敘（理學院 1 樓中庭）			
16:10-17:00	海報時間（理工長廊）			
17:00-18:00	入侵昆蟲工作坊：從政策、科學到田間實務	OU_01-OU_04 都市昆蟲	OB_01-OB_04 生物多樣性、族群與群聚生態學	

議程大綱

Oct. 23, 2022（Sun.）				
時間/地點	理小劇場 SC1001			
8:30-9:00	報到			
09:00-10:10	蘇南耀昆蟲學學術獎頒獎典禮 大會專題演講（線上） Exploring the frontiers of termite biology and beyond **Dr. Kenji Matsuura**			
10:10-10:20	換場			
時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
10:20-11:50	OB_05-OB_08 生物多樣性、族群與群聚生態學	OA_13-OA_18 農業昆蟲學	OS_05-OS_10 系統分類、族群遺傳、演化	OM_09-OM_12 醫學昆蟲學
11:50-13:10	休息用餐／12:00-12:30 會員大會（理小劇場 SC1001）			
13:10-13:55	OE_13-OE_15 行為、生理、個體生物學	OS_11-OS_13 系統分類、族群遺傳、演化	OA_19-OA_21 農業昆蟲學	OA_22-OA_24 農業昆蟲學
13:55-14:30	茶敘（理學院 1 樓中庭）			
時間/地點	理小劇場 SC1001			
14:30-15:30	大會專題演講 How genetic data aid invasive pest management: present and future **Dr. 曾書萍**			
15:30-16:30	大會專題演講 Global dispersal and niche shifts in invasive insects **Dr. Cleo Bertelsmeier**			
16:30-17:10	閉幕暨頒獎典禮／抽獎			

Program at a Glance

Oct. 22, 2022（Sat.）				
Time/Place	SC1001			
8:30-9:10	Registration/ Poster mounted/ Booths settled			
9:00-9:10	Opening Welcome/ Group Photo			
9:10-10:10	Keynote Speech (Online) Alien longhorn beetles as rising pests in Asia: their biology and control **Dr. Eiriki Sunamura**			
10:10-11:10	Keynote Speech Psyllids, gallers and their origin: issues with taxonomy and origin of invasive alien species **Dr. Man-Miao Yang**			
11:10-11:20	Room Switching			
Time/Place	SC1001	SC0008	SC0009	SC0012
11:20-12:20	OS_01-OS_04 Systematics, Population Genetics and Evolution	OE_01-OE_04 Ethology, Physiology and Organismic Biology	OA_01-OA_04 Agricultural Entomology	Career Development and Product Sharing
Time/Place	1F			
12:20-13:50	Career counselling for students			
	Lunch Break／12:30-13:30 Board of Directors Meeting (SC0014)			
13:50-15:50	Workshop on *Forcipomyia taiwana*	OE_05- OE_12 Ethology, Physiology and Organismic Biology	OA_05-OA_12 Agricultural Entomology	OM_01-OM_08 Medical Entomology
15:50-16:10	Tea Break (1F)			
16:10-17:00	Poster Time (1F Gallery)			
17:00-18:00	Workshop on invasive insects: From policy, science to field practice	OU_01-OU_04 Urban Entomology	OB_01-OB_04 Biodiversity, Population and Community Ecology	

Program at a Glance

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<tr><td>8:30-9:00</td><td colspan="4">Registration</td></tr>
<tr><td>09:00-10:10</td><td colspan="4">Nan-Yao Su Entomology Research Award Ceremony
Keynote Speech (Online)
Exploring the frontiers of termite biology and beyond
Dr. Kenji Matsuura</td></tr>
<tr><td>10:10-10:20</td><td colspan="4">Room Switching</td></tr>
<tr><td>Time/Place</td><td>SC1001</td><td>SC0008</td><td>SC0009</td><td>SC0012</td></tr>
<tr><td>10:20-11:50</td><td>OB_05-OB_08
Biodiversity, Population and Community Ecology</td><td>OA_13-OA_18
Agricultural Entomology</td><td>OS_05-OS_10
Systematics, Population Genetics and Evolution</td><td>OM_09-OM_12
Medical Entomology</td></tr>
<tr><td>11:50-13:10</td><td colspan="4">Lunch Break／12:00-12:30 Annual General Meeting (SC1001)</td></tr>
<tr><td>13:10-13:55</td><td>OE_13-OE_15
Ethology, Physiology and Organismic Biology</td><td>OS_11-OS_13
Systematics, Population Genetics and Evolution</td><td>OA_19-OA_21
Agricultural Entomology</td><td>OA_22-OA_24
Agricultural Entomology</td></tr>
<tr><td>13:55-14:30</td><td colspan="4">Tea Break (1F)</td></tr>
<tr><td>Time/Place</td><td colspan="4">SC1001</td></tr>
<tr><td>14:30-15:30</td><td colspan="4">Keynote Speech
How genetic data aid invasive pest management: present and future
Dr. Shu-Ping Tseng</td></tr>
<tr><td>15:30-16:30</td><td colspan="4">Keynote Speech (Online)
Global dispersal and niche shifts in invasive insects
Dr. Cleo Bertelsmeier</td></tr>
<tr><td>16:30-17:10</td><td colspan="4">Award Ceremony & Farewell / Raffle</td></tr>
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編碼對照表

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

論文宣讀總表

底線為論文宣讀者，粗體為參加競賽

Oct. 22, 2022（Sat.）				
時間/地點	理小劇場 SC1001			
8:30-9:10	報到（理學院門口）、壁報張貼（理工長廊）			
9:00-9:10	開幕、合照			
9:10-10:10	大會專題演講（線上） Alien longhorn beetles as rising pests in Asia: their biology and control **Dr. Eiriki Sunamura** 【主持人：蕭旭峰博士】			
10:10-11:10	大會專題演講 木蝨、蟲癭及牠們的產地：談外來入侵種的分類及溯源問題 **Dr. 楊曼妙** 【主持人：楊恩誠博士】			
11:10-11:20	換場			
時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
主題	系統分類、族群遺傳、演化 【主持人：陸聲山、林聖豐博士】	行為、生理、個體生物學 【主持人：林明德、唐政綱博士】	農業昆蟲學 【主持人：林明瑩、曾慶慈博士】	職涯發展與企業分享 【主持人：謝佳宏博士】
11:20-11:35	**OS_01** **臺灣產撚翅目新紀錄科與新紀錄屬的發現** **梁兆榮，蕭旭峰**	**OE_01** **圖形對蜜蜂著陸行為的影響** **謝祥文，楊恩誠**	**OA_01** **黃斑粗喙椿象與蘇力菌共同防治秋行軍蟲之效果評估** **楊又臻，林彥伯**	中西化學工業股份有限公司 美嘉儀器股份有限公司 頂響能多潔股份有限公司

11:35-11:50	**OS_02** **臺灣產寡毛實蠅族 (雙翅目：果實蠅科) 之分類學研究** **黃千育，蕭旭峰**	**OE_02** **畸翅病毒改變腺苷信號影響蜜蜂工蜂分工之研究** **張維展，吳岳隆**	**OA_02** **臺灣家白蟻分解廢棄菇包之可行性評估** **陳慕璇，冨田敬宣，李後鋒**	
11:50-12:05	**OS_03** **New recorded species of genus *Callicera* Panzer (Diptera: Syrphidae) in Taiwan** **Tsung-Hsueh Wu, Shiuh-Feng Shiao**	**OE_03** **穀蠹 (鞘翅目：長蠹蟲科) 麥芽糖酶之生理功能** **陳昀莊，陳美娥**	**OA_03** **短期高溫對瓜實蠅產卵量與死亡率之影響** **洪傳捷，周明儀，黃毓斌，翁壹姿，陳素琴，許如君**	
12:05-12:20	**OS_04** **以 ddRAD-seq 核酸多態型資料研究台灣南部埃及斑蚊在小尺度的族群結構以及親緣關係** **曾奕承，丁柔心，李亞哲，黃于庭，鄭惠菁，何欣頤，游宗翰，黃旌集，王弘毅**	**OE_04** **Regulation of host replication through baculovirus DNA helicase gene *P143*** **許淳閔，吳岳隆**	**OA_04** **Identification of mutations associated with insecticide resistance in *Plutella xylostella* (Lepidoptera: Plutellidae) populations from Taiwan** **Rameshwor Pudasaini, Cheng Chang, Ming-Yi Chou, Shu-Mei Dai**	
時間/地點	理學院 1 樓中庭			
12:20-13:50	與學生對談 【主持人：李後鋒博士】 與談人： 譚景文博士（中興大學昆蟲學系） 陳怡如助理研究員（農業試驗所） 王若璇經理（BASF）			
	休息用餐／12:30-13:30 理監事會 (SC0014)			

時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
主題	小黑蚊工作坊 【主持人：楊恩誠博士】	行為、生理、個體生物學 【主持人：陳美娥、鍾成傧博士】	農業昆蟲學 【主持人：宋一鑫、廖治榮博士】	醫學昆蟲學 【主持人：唐政綱、劉威廷博士】
13:50-14:05	1 台灣鋏蠓 (*Forcipomyia taiwana*) 飼養及與防治技術研究 羅怡珮，黃榮南，詹美鈴 2 台灣鋏蠓基因體組裝與建置其基因體與轉錄體分析入口網站 林明德，莊佳憲，高寘昕，陳淑華，陳冠宇，呂怡萱，謝秉衡，王思捷，李政怡，呂美曄，林仲彥 3 台灣鋏蠓生活史多位點阻斷生物防治技術之研發 林春福，倪念彤，乃育昕 4	**OE_05** **以 nano-CT 技術探討蜜蜂工蜂蕈狀體的體積變化** **扶尚睿，楊恩誠**	**OA_05** **造癭昆蟲之天敵寄生蜂多樣性與棲地組成—以刺桐釉小蜂為例** **洪嘉謙，林聖豐，楊曼妙**	**OM_01** **The habitat changes and distribution expansion of *Collesius hatorii*** **康書維，蔡坤憲**
14:05-14:20		**OE_06** **A study of imidacloprid and adenosine effects on the flight behavior and physiological mechanism of *Apis mellifera*** **林鈺淳，吳岳隆**	**OA_06** **對甲基丁香油不敏感之東方果實蠅族群生殖潛力** **葉懋男，吳文哲，許如君**	**OM_02** **Retrospective investigation of cat flea-associated *Rickettsia felis* in Taiwan** **Nicholas T. Minahan, Yang-Ta Chien, Kun-Hsien Tsai**
14:20-14:35		**OE_07** **台灣產瘤顎家蟻屬與邵氏分針蟻共生關係之探討 (膜翅目：蟻科)** **蔡裴軒，林宗岐**	**OA_07** **偽菜蚜 (半翅目：常蚜科) 於三種寄主上之生活史與族群介量** **魏紹華，李佳穎，彭韋喆，林明瑩**	**OM_03** **硼酸餌劑對抗藥性野外埃及斑蚊之影響** **邱孟頡，游謹嘉，廖一璋，梁國汶**
14:35-14:50		**OE_08** **Evaluation of potential entomopathogenic fungi, *Beauveria bassiana* for controlling coffee berry borer *Hypothenemus hampei* (Ferrari) (Coleoptera: Curculionidae)** **張方旻，呂曉鈴，乃育昕**	**OA_08** **昆蟲寄生真菌紅綬麴菌在蟻害物種疣胸琉璃蟻中盛行率的研究** **陳子嘉，林宗岐**	**OM_04** **Effects of far-UVC light (222 nm) on *Aedes* mosquito vectors of dengue** **陳盈瑄，蕭旭峰，蔡坤憲**

14:50-15:05	以經皮無針式 DNA 疫苗治療台灣鋏蠓 (小黑蚊) 過敏之研究 陳怡行，李美芳 5 台灣鋏蠓 (*Forcipomyia taiwana*) 非農藥防治資材研究 黃榮南，楊騰志，黃祥庭，陳祈融，楊達瑢 6 小黑蚊的餵血器誘引與抗藥性研究 戴淑美	**OE_09** **Caffeine produced in nectar strengthens energy metabolism and neural transmission in honey bees by activating cAMP signaling pathway** **Yun-Heng Lu, Yueh-Lung Wu**	**OA_09** **在臺灣以推拉技術防治秋行軍蟲之可行性** **羅珮綺，胡芳瑜，宋長霖，王芷露，蔡元卿，張世融，莊汶博**	**OM_05** **臺灣埃及斑蚊電壓門鈉離子通道基因型對除蟲菊酯類殺蟲劑抗性之角色** **Han-Hsuan Chung, Cheng-Hui Tsai, Hwa-Jen Teng, Kun-Hsien Tsai**
15:05-15:20		**OE_10** **Identification of differential DNA methylated regions between different development of entomopathogenic fungi, *Beauveria bassiana* NCHU-157, by nanopore sequencing** **李頤瑄，張如君，嚴明仁，乃育昕**	**OA_10** **帶抗褐飛蝨基因 *Bph17* 水稻品系之蛋白質體分析** **宋長霖，王芷露，胡芳瑜，李益，郭政佑，吳泓熹，賴建成，莊汶博**	**OM_06** **Detection of Rickettsiae in ticks from companion animals in Hualien, eastern Taiwan** **Jing-Syuan Huang, Hsi-Chieh Wang, Kun-Hsien Tsai**
15:20-15:35		**OE_11** **球背象鼻蟲近緣種間的生殖隔離** **何芸，廖鎮磐，Ace Kevin S. Amarga，曾惠芸**	**OA_11** **暖化和乾旱對大豆表現與蚜蟲、螞蟻、瓢蟲互動關係的影響** **蕭獻鴻，何傳愷**	**OM_07** **Effects of *Coelomomyces* spp. on vectorial capacity of *Aedes albopictus* (Diptera: Culicidae)** **林芳伶，蕭旭峰，蔡坤憲**
15:35-15:50		OE_12 熱帶火蟻探索行為中的個體差異 賴一德，趙子嫣，徐崇斌，賴麗娟	OA_12 Black soldier fly is the answer of the protein crisis! The development of an alternative protein source in Japan 劉家銘，霜田政美，安藤忠，石原賢司，羽野健志，世古卓也	**OM_08** **臺北市立動物園廄刺蠅幼蟲孳生地調查及成蟲防治技術初探** **王嘉鴻，李芳爾，曾皓佑，蔡昀陵，鄭惟仁**

15:50-16:10	茶敘（理學院1樓中庭）			
16:10-17:00	海報時間（理工長廊）			
時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
主題	入侵昆蟲工作坊：從政策、科學到田間實務 【主持人：顏聖紘博士】	都市昆蟲學 【主持人：詹美鈴、許峰銓博士】	生物多樣性、族群與群聚生態學 【主持人：孫烜駿、廖一璋博士】	
17:00-17:15	與談人： 陳子偉組長（防檢局植防組） 劉泰成先生（林務局保育組） 謝佳宏博士（文化大學森林暨自然保育系） 許如君博士（臺灣大學昆蟲學系） 莊汶博博士（臺灣大學農藝學系）	**OU_01** **一種可殺死抗百滅寧埃及斑蚊幼蟲之假單孢菌屬細菌** **李琵亞，王惠亮，路光暉，戴淑美**	**OB_01** **台灣土白蟻的巢群取食範圍和繁殖結構** **林玟俊，李後鋒**	
17:15-17:30		**OU_02** **The insecticide resistance of field German cockroaches under different management interventions** **潘尼塔，梁國汶**	**OB_02** **莖癭喜楠癭蚋 *Daphnephila truncicola* (雙翅目:癭蚋科) 的蟲癭大小是否受寄生性天敵之影響?** **王釋玄，林聖豐，楊曼妙**	
17:30-17:45		**OU_03** **疣胸琉璃蟻的遷巢動機** **林為詮，梁國汶**	**OB_03** **兩種平腹小蜂種間競爭關係對荔枝椿象生物防治策略之影響** **蔡竣燁，許如君，曾惠芸**	
17:45-18:00		OU_04 入侵性白蟻在台灣的現況 李後鋒，吳佳倩，陳冠豫	**OB_04** **不同劑量的柚子葉片萃取物對蝴蝶產卵行為的影響** **蔡漢祥，黃紹毅**	

<table>
<tr><th colspan="5">Oct. 23, 2022（Sun.）</th></tr>
<tr><td>時間/地點</td><td colspan="4">理小劇場 SC1001</td></tr>
<tr><td>8:30-9:00</td><td colspan="4">報到</td></tr>
<tr><td>09:00-10:10</td><td colspan="4">蘇南耀昆蟲學學術獎頒獎典禮
大會專題演講（線上）
Exploring the frontiers of termite biology and beyond
Dr. Kenji Matsuura
【主持人：蕭旭峰博士】</td></tr>
<tr><td>10:10-10:20</td><td colspan="4">換場</td></tr>
<tr><td>時間/地點</td><td>理小劇場 SC1001</td><td>普通教室 SC0008</td><td>普通教室 SC0009</td><td>普通教室 SC0012</td></tr>
<tr><td>主題</td><td>生物多樣性、族群與群聚生態學
【主持人：林柏安博士】</td><td>農業昆蟲學
【主持人：黃榮南博士】</td><td>系統分類、族群遺傳、演化
【主持人：吳立偉、鄭任鈞博士】</td><td>醫學昆蟲學
【主持人：梁國汶博士】</td></tr>
<tr><td>10:20-10:35</td><td>OB_05
台灣蝶類整體多樣性上升但群聚組成受氣候變遷與棲地類型影響而改變
林承旲，韋家軒，姜信宏，王國權，朱汶偵，林彥博，陳奕穎，陳一菁</td><td>OA_13
我國新紀錄種蟲生線蟲於秋行軍蟲生物防治之應用潛力初探
黃紹綺，郭浩宇，張翔，胡芳瑜，莊汶博，楊爵因</td><td>OS_05
台灣鋸蟻形蜂亞科 (膜翅目：蟻形蜂科) 雄性生殖器的多樣性及探討
廖浩全，寺山守，江口克之</td><td>OM_09
Investigation and identification on sand fly of medical importance in eastern Taiwan
Yu-Feng Tsai, Shiuh-Feng Shiao, Kun-Hsien Tsai</td></tr>
<tr><td>10:35-10:50</td><td>OB_06
台北植物園與中和四號公園授粉網絡及都市棲地營造之比較
謝龥，葉文琪，陸聲山</td><td>OA_14
利用 AI 智慧感知技術建構溫室番茄關鍵害蟲管理專家系統
林鳳琪，吳俊霖，范耀中，姚銘輝</td><td>**OS_06**
臺灣產 *Prosthodocis* 亞屬 (膜翅目：姬蜂科：柄卵姬蜂亞科：擬瘦姬蜂屬) 整合分類學研究
陳玄樸，蕭旭峰</td><td>OM_10
台灣牛隻庫蠓媒介病毒的發生、跨境傳播及病媒昆蟲綜述
曾皓佑，丁履紉，廖癸閔，杜武俊</td></tr>
</table>

10:50-11:05	OB_07 以 DNA 條碼與高通量條碼作為工具研究臺灣落葉甲蟲 Martin Fikáček, Fang-Shuo Hu, Bin-Hong Ho, My-Hanh Le, Jen-Pan Huang	OA_15 小圓胸小蠹蟲 (鞘翅目：象鼻蟲科) 於台灣田間之季節動態 Yi-Chang Liao, Paul Rugman-Jones, Fan-Ling Liu, Lan-Yu Liu, Yu-Hung Yang, Shu-Jen Tuan, Richard Stouthamer	**OS_07** **台灣脈翅目褐蛉科的分類修訂** **蕭世祥，蕭旭峰**	OM_11 以形態與分子方法鑑別臺灣產日本斑蚊複合群及其族群地理分布 劉鎮，黃旌集，蔡坤憲
11:05-11:20	OB_08 植物、昆蟲、環境變遷 林柏安	OA_16 粉斑螟蛾 (*Cadra cautella*) 以四種穀物副產物飼育之生活史探討 王泰權，洪桂香，李錦霞，馮文斌，姚美吉	OS_08 Identification of fruit flies (Diptera: Tephritidae) using species-specific primer pairs targeting the Internal Transcribed Spacer 2 (*ITS2*) gene Prakriti Regmi, Wen-Bin Yeh	OM_12 Autophagy is activated through AMPK/TSC/TOR signaling pathway in *Aedes aegypti* after infection with dengue 2 virus 劉威廷，邱紀涵，盧彥璋，杜武俊，陳正成
11:20-11:35		OA_17 柑橘類揮發物利用於柑橘木蝨誘引劑的可能配方探討 黃竑繻，黃榮南，蕭旭峰	OS_09 Developed DNA microarray for simultaneous identification thrips Watchalawalee Boonmee, Wen-Bin Yeh	
11:35-11:50		OA_18 以最大熵模型 MaxEnt 評估兩種水稻害蟲：馬來西亞稻黑蝽 *Scotinophara coarctata* 及水稻癭蚋 *Orseolia oryzae* 入侵可能性之初探 范姜俊承，黃毓斌	OS_10 利用粒線體總基因體組方法建構臺灣蝴蝶相的譜系關係 吳立偉，陳明玉	
11:50-13:10	休息用餐／12:00-12:30 會員大會 (理小劇場 SC1001)			

時間/地點	理小劇場 SC1001	普通教室 SC0008	普通教室 SC0009	普通教室 SC0012
主題	行為、生理、個體生物學 【主持人：郭祺筠博士】	系統分類、族群遺傳、演化 【主持人：黃仁磐博士】	農業昆蟲學 【主持人：曾惠芸博士】	農業昆蟲學 【主持人：林彥伯博士】
13:10-13:25	OE_13 共生菌 *Buchnera aphidicola* 參與豌豆蚜 *Acyrthosiphon pisum* 之生殖細胞發育 鍾成侑，張俊哲，Shuji Shigenobu	OS_11 球背象鼻蟲的親緣基因體學及斑紋演化 陳釤珉，Ace Kevin S. Amarga，Reagan Joseph T. Villanueva，曾惠芸	OA_19 Effective strain screening of entomopathogenic fungi *Beauveria bassiana* on banana pseudostem weevil, *Odoiporus longicollis* (Coleoptera: Dryophthoridae) 黃柏誠，蕭旭峰	OA_22 警戒費洛蒙應用於文旦薊馬防治效果評估 陳怡樺，林立
13:25-13:40	OE_14 Host synchronous hatching as an anti-parasite defence strategy in burying beetles 孫烜駿，Rebecca M. Kilner	OS_12 Revisiting the diversity of non-termite Blattodea in Taiwan 許至廷，葉文斌	OA_20 臺灣木瓜上的節蟎 申屠萱，廖治榮，石憲宗	OA_23 從茶刺粉蝨發生與入侵歷史看適生區的預測與風險管理 寧方俞，廖治榮
13:40-13:55	OE_15 什麼因素會影響掠食者對不利獵物的迴避程度？ 郭祺筠	OS_13 臺灣產細頸蟖屬分類研究 (蟖目：長角棒蟖科：長角枝蟖亞科) 張書銘，蕭旭峰	OA_21 臺東地區有機水稻栽培之稻黑椿象管理 蔡恕仁，王誌偉	OA_24 昆蟲作為動物飼料的研究趨勢 林柏文，張淑貞，石憲宗
13:55-14:30	茶敘（理學院 1 樓中庭）			
時間/地點	理小劇場 SC1001			
14:30-15:30	大會專題演講 How genetic data aid invasive pest management: present and future **Dr. 曾書萍** 【主持人：吳岳隆博士】			

15:30-16:30	大會專題演講（線上） Global dispersal and niche shifts in invasive insects **Dr. Cleo Bertelsmeier** 【主持人：梁國汶博士】
16:30-17:10	閉幕暨頒獎典禮／抽獎

Conference Agenda

Underline denotes speakers, Bold denotes competition

Oct. 22, 2022（Sat.）				
Time/Place	SC1001			
9:00-9:10	Opening Welcome			
9:10-10:10	Keynote Speech (Online) Alien longhorn beetles as rising pests in Asia: their biology and control **Dr. Eiriki Sunamura** 【Host: Dr. Shiuh-Feng Shiao】			
10:10-11:10	Keynote Speech Psyllids, gallers and their origin: issues with taxonomy and origin of invasive alien species **Dr. Man-Miao Yang** 【Host: Dr. En-Cheng Yang】			
11:10-11:20	Room Switching			
Time/Place	SC1001	SC0008	SC0009	SC0012
Topics	Systematics, Population Genetics and Evolution 【Hosts: Dr. Sheng-Shan Lu, Dr. Sheng-Feng Lin】	Ethology, Physiology and Organismic Biology 【Hosts : Dr. Ming-Der Lin, Dr. Cheng-Kang Tang】	Agricultural Entomology 【Hosts: Dr. Ming-Ying Lin, Dr. Ching-Tzu Tseng】	Career Development and Product Sharing 【Host: Dr. Chia-Hung Hsieh】
11:20-11:35	**OS_01** **A discovery of newly-recorded strepsipteran families and genera (Insecta: Strepsiptera) in Taiwan** **Chao-Jung Liang, Shiuh-Feng Shiao**	**OE_01** **Effects of pattern on honey bee landing behavior** **Hsiang-Wen Hsieh, En-Cheng Yang**	**OA_01** **Evaluation of efficacy of combining *Bacillus thuringiensis* and *Eocanthecona furcellata* (Hemiptera: Pentatomidae) against *Spodoptera frugiperda* (Lepidoptera: Noctuidae)** **You-Zhen Yang, Yen-Po Lin**	Chung Hsi Chemical Plant, Ltd. Major Instruments Co., Ltd. Rentokil Ding Sharn Co., Ltd.

11:35-11:50	**OS_02** **A taxonomic study of Dacini fruit flies (Diptera: Tephritidae) of Taiwan** **Chien-Yu Huang, Shiuh-Feng Shiao**	**OE_02** **Alteration of adenosine signaling by DWV affects division of labor in honey bees (*Apis mellifera*)** **Wei-Chan Chang, Yueh-Lung Wu**	**OA_02** **The possibility of decompose spent mushroom substrate with soil feeding termite** **Mu-Xuan Chen, Tomita Takanori, Hou-Feng Li**	
11:50-12:05	**OS_03** **New recorded species of genus *Callicera* Panzer (Diptera: Syrphidae) in Taiwan** **Tsung-Hsueh Wu, Shiuh-Feng Shiao**	**OE_03** **The physiological function of maltase in *Rhyzopertha dominica* (Coleoptera: Bostrichidae)** **Yun-Chuang Chen, Mei-Er Chen**	**OA_03** **Effects of short-term high temperatures on egg production and adult mortality in melon fly *Zeugodacus cucurbitae* (Coquillett) (Diptera: Tephritidae)** **Chuan-Chieh Hung, Ming-Yi Chou, Yu-Bing Huang, Yi-Tzu Weng, Su-Chin Chen, Ju-Chun Hsu**	
12:05-12:20	**OS_04** **Fine-scale geographic structure and relatedness patterns of the major arbovirus vector, *Aedes aegypti*, in Southern Taiwan inferred by ddRAD-seq SNPs** **Yi-Cheng Tseng, Jou-Hsin Ting, Ya-Zhe Lee, Yu-Ting Huang, Hui-Ching Cheng, Hsin-Yi Ho, Tsung-Han Yu, Chin-Gi Huang, Hurng-Yi Wang**	**OE_04** **Regulation of host replication through baculovirus DNA helicase gene *P143*** **Chun-Min Hsu, Yeah-Lung Wu**	**OA_04** **Identification of mutations associated with insecticide resistance in *Plutella xylostella* (Lepidoptera: Plutellidae) populations from Taiwan** **Rameshwor Pudasaini, Cheng Chang, Ming-Yi Chou, Shu-Mei Dai**	

Time/Place	1F			
12:20-13:50	Career counseling for students 【Host: Dr. Hou-Feng Li】 Panelists: Dr. Ching-Wen Tan (Department of Entomology, National Chung Hsing University) Yi-Ju Chen, Assistant Research Fellow (Taiwan Agricultural Research Institute, Council of Agriculture) Jo-Hsuan Wang, Manager (BASF)			
	Lunch Break／12:30-13:30 Board Meeting (SC0014)			
Time/Place	SC1001	SC0008	SC0009	SC0012
Topics	Workshop on *Forcipomyia taiwana* 【Host: Dr. En-Cheng Yang】	Ethology, Physiology and Organismic Biology 【Hosts: Dr. Mei-Er Chen, Dr. Chen-yo Chung】	Agricultural Entomology 【Hosts: Dr. I-Hsin Sung, Dr. Jhih-Rong Liao】	Medical Entomology 【Hosts: Dr. Cheng-Kang Tang, Dr. Wei-Ting Liu】
13:50-14:05	1 Laboratory rearing and control strategies for the biting midge, *Forcipomyia taiwana*. Yi-Pey Luo, Rong-Nan Huang, Mei-Ling Chan 2 A web portal for genome browsing and transcriptome analysis based on the *de novo*	**OE_05** **Study of volume change of honey bee mushroom bodies by nano-CT** **Shang-Jui Fu, En-Cheng Yang**	**OA_05** **Habitat composition and the diversity of parasitoid wasps of *Quadrastichus erythrinae*** **Chia-Chien Hung, Sheng-Feng Lin and Man-Miao Yang**	**OM_01** **The habitat changes and distribution expansion of *Collesius hatorii*** **Shu-Wei Kang, Kun-Hsien Tsai**
14:05-14:20		**OE_06** **A study of imidacloprid and adenosine effects on the flight behavior and physiological mechanism of *Apis mellifera*** **Yu Chun Lin, Yueh Lung Wu**	**OA_06** **Reproductive potential in methyl eugenol non-sensitive male oriental fruit fly, *Bactrocera dorsalis*** **Mao-Nan Yeh, Wen-Jer Wu, Ju-Chun Hsu**	**OM_02** **Retrospective investigation of cat flea-associated *Rickettsia felis* in Taiwan** **Nicholas T. Minahan, Yang-Ta Chien, Kun-Hsien Tsai**

14:20-14:35	assembled *Forcipomyia taiwana* genome Ming-Der Lin, Chia-Hsien Chuang, Chih-Hsin Kao, Shu-Hwa Chen, Guan-Yu Chen, I-Hsuan Lu, Ping-Heng Hsieh, Szu-Chieh Wang, Jeng-Yi Li, Mei-Yeh Lu, Chung-Yen Lin 3 Bio-control *Forcipomyia taiwana* by blocking multi-site of its life cycle Chuen-Fu Lin, Nian-Tong Ni, Yu-Shin Nai 4 Needle-free epicutaneous For t 2 DNA vaccine is effective for preventing and treating biting midge (*Forcipomyia taiwana*) allergy in a murine model Yi-Hsing Chen, Mey-Fann Lee 5 The studies of nonsynthetic resources for *Forcipomyia taiwana* management	**OE_07** **Symbiotic relationship between Taiwanese *Strumigenys* and *Ectomomyrmex sauteri* (Hymenoptera: Formicidae)** **Pei-Shiuan Tsai, Chung-Chi Lin**	**OA_07** **The life history and population parameters of *Lipaphis erysimi* (Hemiptera: Aphididae) on three hosts** **Shao-Hua Wei, Chia-Ying Li, Wei-Je Peng, Ming-Ying Lin**	**OM_03** **The effect of boric acid toxic sugar bait on field *Aedes aegypti*** **Meng-Chieh Chiu, Jin-Jia Yu, Yi-Chang Liao, Kok-Boon Neoh**
14:35-14:50		**OE_08** **Evaluation of potential entomopathogenic fungi, *Beauveria bassiana* for controlling coffee berry borer *Hypothenemus hampei* (Ferrari) (Coleoptera: Curculionidae)** **Fang-Min Chang, Hsiao-Ling Lu, Yu-Shin Nai**	**OA_08** **The prevalence of entomopathogenic fungus *Aspergillus nomius* in its pest ant host *Dolichoderus thoracicus*** **Tzu-Chia Chen, Chung-Chi Lin**	**OM_04** **Effects of far-UVC light (222 nm) on *Aedes* mosquito vectors of dengue** **Ying-Hsuan Chen, Shiuh-Feng Shiao, Kun-Hsien Tsai**
14:50-15:05		**OE_09** **Caffeine produced in nectar strengthens energy metabolism and neural transmission in honey bees by activating cAMP signaling pathway** **Yun-Heng Lu, Yueh-Lung Wu**	**OA_09** **The availability of push-pull technology for fall armyworm pest control in Taiwan** **Pei-Qi Luo, Fang-Yu Hu, Chang-Lin Sung, Chih-Lu Wang, Yuan-Ching Tsai, Shyh-Rong Chang, Wen-Po Chuang**	**OM_05** **The role of voltage-gated sodium channel genotypes in pyrethroid resistance in *Aedes aegypti* in Taiwan** **Han-Hsuan Chung, Cheng-Hui Tsai, Hwa-Jen Teng, Kun-Hsien Tsai**

15:05-15:20	Rong-Nan Huang, Teng-Zhi Yang, Hsiang-Ting Huang, Chi-Rong Chen, Da-Syuan Yang 6 Investigation of blood-feeder attraction and insecticide resistance in *Forcipomyia taiwana* Shu-Mei Dai	**OE_10** **Identification of differential DNA methylated regions between different development of entomopathogenic fungi, *Beauveria bassiana* NCHU-157, by nanopore sequencing** **Yi-Hsuan Li, Ju-Chun Chang, Ming-Ren Yen, Yu-Shin Nai**	**OA_10** **Proteomics analysis of rice lines with brown planthopper resistance gene *Bph17*** **Chang-Lin Sung, Chih-Lu Wang, Fang-Yu Hu, Yi Li, Cheng-Yu Kuo, Hung-Hsi Wu, Chien-Chen Lai, Wen-Po Chuang**	**OM_06** **Detection of Rickettsiae in ticks from companion animals in Hualien, eastern Taiwan** **Jing-Syuan Huang, Hsi-Chieh Wang, Kun-Hsien Tsai**
15:20-15:35		**OE_11** **Reproductive isolation of two sibling species of *Pachyrhynchus* weevils** **Yun Ho, Chen-Pan Liao, Ace Kevin S. Amarga, Hui-Yun Tseng**	**OA_11** **Effects of warming and drought on soybean performance and soybean aphid-ant-lady beetle interactions** **Xian-Hong Xiao, Chuan-Kai Ho**	**OM_07** **Effects of *Coelomomyces* spp. on vectorial capacity of *Aedes albopictus* (Diptera: Culicidae)** **Fang-Ling Lin, Shiuh-Feng Shiao, Kun-Hsien Tsai**
15:35-15:50		OE_12 Individual differences in *Solenopsis geminata* exploration Yi-De Lai, Tzu-Yen Chao, Chorng-Bin Hsu, Li-Chuan Lai	OA_12 Black soldier fly is the answer of the protein crisis! The development of an alternative protein source in Japan Chia-Ming Liu, Masami Shimoda, Tadashi Andoh, Kenji Ishihara, Takeshi Hano, Takuya Seko	**OM_08** **Investigation of the larval habitat of *Stomoxys calcitrans* (Diptera: Muscidae) and comparison of physical control methods for adults in Taipei Zoo** **Jia-Hong Wang, Fang-Er Li, Hao-You Zeng, Yun-Ling Tsai, Wei-Jen Cheng**
15:50-16:10	Tea Break			
16:10-17:00	Poster Time (Gallery)			

Time/Place	SC1001	SC0008	SC0009	SC0012
Topics	Workshop on invasive insects: From policy, science to field practice 【Host: Dr. Shen-Horn Yen】	Urban Entomology 【Hosts: Dr. Mei-Ling Chan, Dr. Feng-Chuan Hsu】	Biodiversity, Population and Community Ecology 【Hosts: Dr. Syuan-Jyun Sun, Dr. Yi-Chang Liao】	
17:00-17:15	Panelists: Tse-Wei Chen, Director (Bureau of Animal and Plant Health Inspection and Quarantine) Mr. Tai-Cheng Liu (Conservation Branch, Forestry Bureau) Dr. Chia-Hung Hsieh (Department of Forestry and Nature Conservation, Chinese Culture University) Dr. Ju-Chun Hsu (Department of Entomology, National Taiwan University) Dr. Wen-Po Chuang (Department of Agronomy, National Taiwan University)	**OU_01** **A *Pseudomonas* bacterium that kills permethrin-resistant *Aedes aegypti* larvae** **Piyatida Leelagud, Hui-Liang Wang, Kuang-Hui Lu, Shu-Mei Dai**	**OB_01** **Colony foraging area and breeding structure of *Odontotermes formosanus*** **Wen-Jun Lin, Hou-Feng Li**	
17:15-17:30		**OU_02** **The insecticide resistance of field German cockroaches under different management interventions** **Kruaysawat Panida, Kok-Boon Neoh**	**OB_02** **Are gall sizes of *Daphnephila truncicola* (Diptera: Cecidomyiidae) affected by parasitoids?** **Shih-Syuan Wang, Sheng-Feng Lin, Man-Miao Yang**	
17:30-17:45		**OU_03** **Nest relocation motivation of *Dolichoderus thoracicus*** **Wei-Chuan Lin, Kok-Boon Neoh**	**OB_03** **Effects of interspecific competition between two *Anastatus* species on biological control strategies for litchi stink bugs (*Tessaratoma papillosa* (Drury))** **Jiun-Ye Tsai, Ju-Chun Hsu, Hui-Yun Tseng**	
17:45-18:00		OU_04 Current status of invasive termites in Taiwan Hou-Feng Li, Chia-Chien Wu, Guan-Yu Chen	**OB_04** **Effects of different doses of pomelo leaves extraction to the butterfly oviposition behavior** **Han-Hsiang Tsai, Shaw-Yhi Hwang**	

Oct. 23, 2022（Sun.）				
Time/Place	SC1001			
09:00-10:10	Nan-Yao Su Entomology Research Award Keynote Speech (Online) Exploring the frontiers of termite biology and beyond **Dr. Kenji Matsuura** 【Host: Dr. Shiuh-Feng Shiao】			
10:10-10:20	Room Switching			
Time/Place	SC1001	SC0008	SC0009	SC0012
Topics	Biodiversity, Population and Community Ecology 【Host: Dr. Po-An Lin】	Agricultural Entomology 【Host: Dr. Rong-Nan Huang】	Systematics, Population Genetics and Evolution 【Hosts: Dr. Li-Wei Wu, Dr. Ren-Chung Cheng】	Medical Entomology 【Host: Dr. Kok-Boon Neoh】
10:20-10:35	OB_05 The overall diversity of butterflies in Taiwan has increased, but species composition has been reorganized due to climate change and land use type. Cheng-Hao Lin, Chia-Hsuan Wei, Shin-Hung Jiang, Kuo-Chuan Wang, Wen-Chen Chu, Yen-Po Lin, Yi-Ting Chen, I-Ching Chen	OA_13 Assessment of the biological control potential of new record entomopathogenic nematode species against fall armyworm Shao-Chi Huang, Hao-Yu Kuo, Siang Chang, Fang-Yu Hu, Wen-Po Chuang, Jiue-in Yang	OS_05 Discussions about various male genitalia of Taiwanese Pristocerinae (Hymenoptera, Bethylidae) Hauchuan Liao, Mamoru Terayama, Katsuyuki Eguchi	OM_09 Investigation and identification on sand fly of medical importance in eastern Taiwan Yu-Feng Tsai, Shiuh-Feng Shiao, Kun-Hsien Tsai
10:35-10:50	OB_06 Comparison of pollination network and urban habitat establishment between	OA_14 Constructing an expert system for greenhouse tomato key pest management based on AI Smart Sensing Technology	**OS_06** **Integrative taxonomy of subgenus *Prosthodocis* (Hymenoptera: Ichneumonidae: Tryphoninae:**	OM_10 Overview of occurrence, transboundary transmission, and potential vectors of

	Taipei Botanical Garden and Zhonghe Park Tien Hsieh, Wen-Chi Yeh, Sheng-Shan Lu	Feng-Chyi Lin, Jiunn-Lin Wu, Yao-Chung Fan, Ming-Hwi Yao	**_Netelia_) in Taiwan and its systematic implications** **Hsuan-Pu Chen, Shiuh-Feng Shiao**	bovine *Culicoides*-borne viruses in Taiwan Hau-You Tzeng, Lu-Jen Ting, Keui-Ming Liao, Wu-Chun Tu
10:50-11:05	OB_07 DNA barcoding and metabarcoding as tools to study Taiwanese leaf litter beetles Martin Fikáček, Fang-Shuo Hu, Bin-Hong Ho, My-Hanh Le, Jen-Pan Huang	OA_15 Seasonal dynamics of *Euwallacea fornicatus* species complex (Coleoptera: Curculionidae) in the field of Taiwan Yi-Chang Liao, Paul Rugman-Jones, Fan-Ling Liu, Lan-Yu Liu, Yu-Hung Yang, Shu-Jen Tuan, Richard Stouthamer	**OS_07** **Taxonomical revision of Hemerobiidae (Neuroptera) from Taiwan** **Shih-Hsiang Hsiao, Shiuh-Feng Shiao**	OM_11 Identification of *Aedes* (*Finlaya*) *japonicus* complex by morphological and molecular methods and their geographic distribution in Taiwan Jhen Liu, Chin-Gi Huang, Kun-Hsien Tsai
11:05-11:20	OB_08 Plants, insects, and environmental changes Po-An Lin	OA_16 Research on the life cycle of almond moth (*Cadra cautella*) rearing in four kinds of by-product of grains Tai-Chuan Wang, Kuei-Hsiang Hung, Chin-Hsia Lee, Wen-bin Feng, Me-Chi Yao	OS_08 Identification of fruit flies (Diptera: Tephritidae) using species-specific primer pairs targeting the Internal Transcribed Spacer 2 (*ITS2*) gene Prakriti Regmi, Wen-Bin Yeh	OM_12 Autophagy is activated through AMPK/TSC/TOR signaling pathway in *Aedes aegypti* after infection with dengue 2 virus Wei-Ting Liu, Chi-Han Chiu, Yen-Chang Lu, Wu-Chun Tu, Cheng-Chen Chen
11:20-11:35		OA_17 The promising formula of citrus volatile compounds that attract *Diaphorina citri* Kuwayama (Hemiptera: Liviidae) Hong-Ru Huang, Rong-Nan Huang, Shiuh-Feng Shiao	OS_09 Developed DNA microarray for simultaneous identification thrips Watchalawalee Boonmee, Wen-Bin Yeh	

11:35-11:50		OA_18 An explore of MaxEnt modeling used to evaluate the invasion potential of two rice pests: *Scotinophara coarctata*, and *Orseolia oryzae*. Chung-Cheng Fanjiang, Yu-Bing Huang	OS_10 Reconstructing phylogeny of Taiwan butterflies by using mitochondrial meta-genomic method Li-Wei Wu, Ming-Yu Chen	
11:50-13:10	Lunch Break／12:00-12:30 Annual General Meeting (SC1001)			
Time/Place	SC1001	SC0008	SC0009	SC0012
Topics	Ethology, Physiology and Organismic Biology 【Host: Dr. Chi-Yun Kuo】	Systematics, Population Genetics and Evolution 【Host: Dr. Jen-Pan Huang】	Agricultural Entomology 【Host: Dr. Hui-Yun Tseng】	Agricultural Entomology 【Host: Dr. Yen-Po Lin】
13:10-13:25	OE_13 Endosymbiont *Buchnera aphidicola* participates in germline development of the pea aphid *Acyrthosiphon pisum* Chen-Yo Chung, Chun-Che Chang, Shuji Shigenobu	OS_11 Phylogenomics and pattern evolution of colorful *Pachyrhynchus* weevils on oceanic islands Shan-Min Chen, Ace Kevin S. Amarga, Reagan Joseph T. Villanueva, Hui-Yun Tseng	OA_19 Effective strain screening of entomopathogenic fungi *Beauveria bassiana* on banana pseudostem weevil, *Odoiporus longicollis* (Coleoptera: Dryophthoridae) Po-Cheng Huang, Shiuh-Feng Shiao	OA_22 Study of control effect on thrips with alert pheromone application in wendan pomelo orchard Yi-Hua Chen, Li Lin
13:25-13:40	OE_14 Host synchronous hatching as an anti-parasite defence strategy in burying beetles Syuan-Jyun Sun, Rebecca M. Kilner	OS_12 Revisiting the diversity of non-termite Blattodea in Taiwan Chih-Ting Hsu, Wen-Bin Yeh	OA_20 Eriophyid mite (Acari: Eriophyidae) on papaya from Taiwan Hsuan Shentu, Jhih-Rong Liao, Hsien-Tzung Shih	OA_23 From occurrence and invasion history of tea spiny whitefly: prediction of suitable distribution areas and pest risk management Fang-Yu Ning, Jhih-Rong Liao

13:40-13:55	OE_15 What determines the degree of predator avoidance towards unprofitable prey? A meta-analysis. Chi-Yun Kuo	OS_13 Taxonomic study of genus *Sipyloidea* (Phasmatodea: Lonchodidae: Necrosciinae) in Taiwan Shu-Ming Chang, Shiuh-Feng Shiao	OA_21 Management of black rice bug on organic paddy rice cultivation in Taitung Shu-Jen Tsai, Chih-Wei Wang	OA_24 The trend of research on insects as animal feed Bo-Wen Lin, Shu-Chen Chang, Hsien-Tzung Shih
13:55-14:30	Tea Break			
Time/Place	SC1001			
14:30-15:30	Keynote Speech How genetic data aid invasive pest management: Present and future **Dr. Shu-Ping Tseng** 【Host: Dr. Yueh-Lung Wu】			
15:30-16:30	Keynote Speech (Online) Global dispersal and niche shifts in invasive insects **Dr. Cleo Bertelsmeier** 【Host: Dr. Kok-Boon Neoh】			
16:30-17:10	Award Ceremony & Farewell / Raffle			

壁報展示總表 Poster List

編碼	論文標題（Title）	作者（Authors）
生物多樣性、族群與群聚生態學 Biodiversity, Population and Community Ecology 【評審：李奇峯博士、廖浩全博士】 【Judges: Dr. Chi-Feng Lee, Dr. Hau-Chuan Liao】		
PB_01	**以不同土壤介質養殖黑翅土白蟻並分析其生存率與蟻道發育比例** **Breeding *Odontotermes formosanus* in different soil media and analyzing its survival rate and ant channel development ratio**	**賴麗婷，武亞晴，賴吉永** **Li-Ting Lai, Ya-Ching Wu, Ji-Yong Lai**
PB_02	**探討台中市區國、高中生對食用昆蟲的態度現況** **To explore the situation of attitudes towards edible insects among junior and senior high school students in Taichung City**	**吳幸珊** **Shin-Shan Wu**
PB_03	**暖化及土壤水分境況對蘿蔔苗 (*Raphanus sativus*) 與桃蚜 (*Myzus persicae*) 之影響** **Effect of warming and soil water regime on radish seedlings *Raphanus sativus* and green peach aphid *Myzus persicae***	**詹佳純，丘明智，郭美華** **Chia-Chun Chan, Ming-Chih Chiu, Mei-Hwa Kuo**
PB_04	**氣候變遷對濁水溪流域膜翅目授粉者棲地變化之影響** **Distribution range shift of pollinators (Hymenoptera) under climate change in the Choshui River Basin**	**黃冠瑋，曾惠芸，楊恩誠，陸聲山** **Guan-Wei Haung, Hui-Yun Tseng, En-Cheng Yang, Sheng-Shan Lu**
PB_05	Analyzing possible niche shift in alien populations of the Indochina mantis (*Hierodula patellifera*)	Mattia De Vivo, Jen-Pan Huang
PB_06	高溫蒸氣處理對設施土壤內瓜實蠅幼蟲及蛹之影響 Effects of steam treatment on the soil-borne larvae and pupae of *Zeugodacus cucurbitae* (Coquillett) in the greenhouse	陳宇樂，周明儀，翁壹姿，陳素琴，許如君 Yu-Le Chen, Ming-Yi Chou, Yi-Tzu Weng, Su-Chin Chen, Ju-Chun Hsu
PB_07	台北地區焚燒豬屍之昆蟲相演替初探 Preliminary study on the insect succession of burnt pig carcasses in Taipei	莊子平，張光維，蕭旭峰 Tzu-Ping Chuang, Guang-Wei Zhang, Shiuh-Feng Shiao
PB_08	2022 年臺灣登革熱病媒蚊分布調查 Survey on the distribution of dengue vector mosquitoes in Taiwan in 2022	鄭惠菁，楊詠丞，蔡宗儒，李詩雅，施亭君，鄧庭軒，郭又瑄，丁柔心，吳逸鈞，蔡湘沂，林宜穎，林書弘，邱彥傑，杜武俊，黃旌集 Hui-Ching Cheng, Yung-Cheng Yang, Tsung-Ju Tsai, Shi-Ya Li, Ting-Chun Shih, Ting-Xuan Deng, You-Syuan Guo, Jou-Hsin Ting, Yi-Jun Wu, Siang-Yi Tsai, Yi-Ying Lin, Shu-Hung Lin, Yen-Chieh Chiu, Wu-Chun Tu, Chin-Gi Huang

系統分類、族群遺傳、演化 Systematics, Population Genetics and Evolution 【評審：李奇峯博士、廖浩全博士】 【Judges: Dr. Chi-Feng Lee, Dr. Hau-Chuan Liao】		
PS_01	**台灣產新紀錄種短尾馬尾繭蜂短記** **Notes on *Euurobracon breviterebrae* Watanabe, 1934 (Hymenoptera: Braconidae), a new record of Taiwan.**	**林豈弟，蕭旭峰** **Kai-Ti Lin, Shiuh-Feng Shiao**
PS_02	**臺灣偽圓跳蟲科 (Dicyrtomidae) 之分類學研究** **Taxonomy of Dicyrtomidae (Collembola: Symphypleona) of Taiwan**	**鄭欣如，張智涵** **Hsin-Ju Cheng, Chih-Han Chang**
PS_03	斑蛾科螢斑蛾亞科的首個分子親緣關係假說以及對分類體系及特徵演化推測的影響 The first molecular phylogeny of Chalcosiinae (Zygaenidae) and its influence on classification and inference of character evolution	Shen-Horn Yen, Chung-Te Cheng, Chia-Hsuan Wei
PS_04	尺蛾科枝尺蛾亞科潔尺蛾屬的整合分類學揭示台灣與東南亞產五個新物種的發現 Integrated taxonomy of the genus *Genusa* (Geometridae, Ennominae) reveals discovery of 5 new species from Taiwan and southeast Asia	Shann-Ru Wei, Chung-Te Cheng, Shen-Horn Yen
PS_05	原生種短斑偽菜蛾以及入侵種札幌偽菜蛾在台灣的發現以及在珠蔥害蟲防治上的意義 Discoveries of the indigenous *Acrolepiopsis brevipenella* (Moriuti, 1972) and the invasive *A. sapporensis* (Matsumura, 1931) in Taiwan and the implication for pest control of leek	Shen-Horn Yen, Chung-Te Cheng, Tzu-Po Lin
PS_06	臺灣巨波眼蝶亞種間之系統分類問題探討 Discussion on systematic problems between two subspecies of *Ypthima praenubila* in Taiwan	陳璋臨，徐堉峰 Zhang-Lin Chan, Yu-Feng Hsu
PS_07	應用 DNA 分子證據台灣地區長肛屬竹節蟲的分類地位與地理變異 Using DNA molecular evidence to analysis the phylogenetic and taxonomic status of *Entoria* stick insects (Phasmida: Phasmatidae: Clitumninae) in Taiwan	黃品華，葉文斌 Pin-Hua Huang, Wen-Bin Yeh
PS_08	食孢展足蛾亞科 (Cuprininae) 之系統分類學研究及蕨類昆蟲演化關係之探討 Systematics and evolution dynamics of insect-fern interaction in the specialized fern-spore feeding Cuprininae (Lepidoptera, Stathmopodidae)	沈宗諭，周明勳，徐堉峰，黃仁磐 Zong-Yu Shen, Ming-Hsun Chou, Yu-Feng Hsu, Jen-Pan Huang
PS_09	台灣產霜天蛾屬的分類訂正 Taxonomic revision of *Psilogramma* Rothschild & Jordan, 1903 (Sphingidae) of Taiwan	Shen-Horn Yen, Chung-Te Cheng, Kai-Ti Lin

行為、生理、個體生物學 Ethology, Physiology and Organismic Biology 【評審：郭祺筠博士、林柏安博士】 【Judges: Dr. Chi-Yun Kuo, Dr. Po-An Lin】		
PE_01	**使用鳥類掠食者檢驗鱗翅目身體與翅膀斑紋在警戒性產生上之相對貢獻** **Relative contribution between body and wing patterns in formation of aposematism of the Lepidoptera by using birds in predation experiment**	**陳俊博，顏聖紘** **Jun-Bo Chen, Shen-Horn Yen**
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PE_04	**Mass production and purification of GAL1-Melittin fusion protein in a baculovirus expressing vector system**	**Yao-Kuang Tseng, Yueh-Lung Wu, Rong-Nan Huang**
PE_05	***doublesex* 在咖啡果小蠹的選殖及定性** **Isolation and characterization of *doublesex* gene in the coffee berry borer *Hypothenemus hampei***	**蘇姿瑜，吳翊彥，呂曉鈴** **Tzu-Yu Su, Yi-Yan Wu, Hsiao-Ling Lu**
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都市昆蟲學 Urban Entomology		
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大會專題演講

Keynote Speech

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Alien longhorn beetles as rising pests in Asia: their biology and control

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Recently, the incidence of alien longhorn beetles infesting live trees has globally increased. These beetles spend most of their lives inside trees, where they can cause serious damage. Therefore, they are difficult to access from the outside, making their control challenging. Being a neighbor of Taiwan, Japan has been invaded by three longhorn beetle species from continental Asia since 2011: 1) the red-necked longhorn beetle *Aromia bungii*, which infests stone fruit trees, such as plums and peaches; 2) the Asian longhorn beetle *Anoplophora glabripennis*, which infests various hardwood trees, such as willows and maples; and 3) the rusty-spotted longhorn beetle *Apriona swainsoni*, which infests legume trees and others. All the three species are significant tree pests in their native ranges and have already caused damage to Japanese trees. Moreover, *An. glabripennis* interferes with the reproduction of the related species, *An. chinensis,* threatening the ecological balance. Although drastic felling of infested trees is the ideal approach to eradicate these beetles, as adopted in North America and Europe against *An. glabripennis*, it is cost prohibitive and unrealistic in Japan. This situation has driven studies aimed at a population reduction by IPM and the development of chemical, physical, and biological control techniques. In this presentation, I introduce the biology and control of the invasive alien longhorn beetles, with a special focus on the case studies in Japan.

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木蝨、蟲癭及牠們的產地：談外來入侵種的分類及溯源問題
Psyllids, gallers and their origin: issues with taxonomy and origin of invasive alien species

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在全球化的當今，隨著國際交流益加頻繁，外來種昆蟲的入侵案例在近年來不斷增加，尤其是小型或取食習性隱匿的昆蟲，很容易隨著貨物進口等各種方式夾帶進入非原生分佈地，而牠們往往也鑑定不易，其中我長期以來主要從事研究的兩類對象，即木蝨與造癭昆蟲，正符合這類的特性，因此在我過去從事牠們的分類演化與生物多樣性之基礎研究時，也不免涉及此類外來昆蟲的鑑定與防治問題。此次演講將以我過往處理台灣發生的外來入侵種木蝨、造癭昆蟲及其相關生物的分類與生物學案例，說明分類鑑定過程往往不是直接而明顯，並藉由這些案例的啟發，探討外來種鑑定與溯源的問題。

In the Era of Globalization, increasing global trade and transportation have enhanced the magnitude of biological invasions, especially those insects with small body size and conceal feeding habit. They are hard to find and identify. The two systems of my major research focus, the psylloids and gall-inducing insects, completely fit these categories. Although my expertise is the fundamental studies, mainly in systematics, evolution, and biodiversity, however, it is incumbent to involve with the related identification and control when there are invasive cases of these organisms. In this talk, I will share my experience on handling the invasive cases of psylloids, gall-inducing insects and their associates in Taiwan and discuss the issues with invasive insect taxonomy and the discovery of its origin.

關鍵詞（Keywords）：鑑定（identification）、系統發生學（phylogeny）、生物學（biology）、癭學（cecidology）、綜合學科研究法（multidisciplinary approach）

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How genetic data aid invasive pest management: present and future

曾書萍
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Globalization has resulted in accelerated rates of introductions of alien species, threatening native biodiversity, human health, and affecting the global economy. Understanding the biology of invasive species can provide vital information that could be used to assist policymakers in developing management, prevention, and restoration strategies. Population genetics has emerged as a powerful tool to elucidate many aspects of an organism’s life history, ecology, and evolution, and is now being used with increasing frequency to understand the biology of invasive species. In this keynote lecture, I will use invasive insects as applied examples of how genetic methods can be integrated to generate information managing invasive pests more effectively. Specifically, I will discuss how genetic tools are used in: (1) tracing the spread of invasive pests, (2) understanding the ecology of insect pests, (3) assessing the efficacy of pest management, and (4) characterization of insecticide resistance mechanisms in field populations. With continuous improvement of molecular techniques, we can expect accelerating advances in the application of genetic tools to manage pest invasions in the future.

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Global dispersal and niche shifts in invasive insects

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Increased international trade and human movement, particularly since the Industrial Revolution, have resulted in the accidental movement of species worldwide at an unprecedented scale. Even though it has been recognized for a long time that humans introduce invasive species, invasion biologists have mostly focussed on the role of factors directly linked to the biology of organisms rather than human-mediated dispersal. Understanding how globalization affects the accidental transport of invasive species is urgent, because biological theory alone cannot explain current invasions, or predict those likely to happen in the future. In this presentation, I will focus on temporal dynamics, complex introduction histories and global species flows of invasive insects. In addition to understanding the global dispersal of insects, it is important to explore to what extent invasive species can establish under environmental conditions that are different from those encountered in their native range. In this context, I will present some of our recent work on climatic niche shifts in ants and discuss potential mechanisms underlying these niche shifts.

小黑蚊工作坊

Workshop on *Forcipomyia taiwana*

1

台灣鋏蠓 (*Forcipomyia taiwana*) 飼養及與防治技術研究
Laboratory rearing and control strategies for the biting midge, *Forcipomyia taiwana*.

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背景/研究問題/材料方法

台灣鋏蠓 (*Forcipomyia taiwana*) 是台灣地區重要的騷擾性環境衛生害蟲，本計畫持續精進台灣鋏蠓飼養、交配、產卵、繼代繁殖的流程，並於實驗室篩選可誘引台灣鋏蠓的物質，以進行田間誘引試驗，更探討捕蚊燈於科博館植物園調查成蟲發生可行性。此外，也評估數種幼蟲防治技術成效，包括施灑硫酸銨及芬普尼粒劑於植物園進行田間防治，並以小腿調查及遊客問卷進行防治效益評估。藉由推廣公民科學，從幼蟲棲地管理著手，期能友善環境，又能有效防治台灣鋏蠓。

結果/結論/應用啟示

試驗結果顯示孵化幼蟲以綠藻液餵食可有效發育至化蛹，並順利羽化，雌蟲羽化後 2 天、雄蟲羽化後 1 天即可進行交尾，交尾高峰在清晨開燈後 2 小時，中午過後僅零星台灣鋏蠓進行交尾。交尾後以人工餵豬血方式供給血餐，可使雌性台灣鋏蠓順利產卵於滴加濃縮綠藻液的夯實土壤。以碳酸氫銨、乳酸鈉、異戊酸、八烯醇及芥子酸的組合，開啟 UV 燈及熱源進行田間誘集，3 小時可誘集 6 隻台灣鋏蠓雌成蟲。而捕蚊燈誘集到台灣鋏蠓成蟲共計 7 筆 14 隻 (雌蟲 8 隻，雄蟲 6 隻)，8:00 至 17:00 的誘集比例為 4.55%，17:00 至翌日 8:00 的誘集比例為 95.45%。植物園處理硫酸銨的防治率為 22%，施用芬普尼粒劑的防治率為 37%~50%，需要繼續研議其他棲地改進的方案，以進行全方位的防治。此外，推廣公民科學的概念與精神，讓工作人員及志工標定國立自然科學博物館區內的幼蟲棲地熱點，並妥善管理，可進一步落實友善有效防治的目標。

關鍵詞（Keywords）：台灣鋏蠓（*Forcipomyia taiwana*）、大量飼養（Mass-rearing）、防治技術（Control strategies）、幼蟲棲地（Larvae habitat）、公民科學（Citizen science）

2

台灣鋏蠓基因體組裝與建置其基因體與轉錄體分析入口網站
A web portal for genome browsing and transcriptome analysis based on the *de novo* assembled *Forcipomyia taiwana* genome

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Ming-Der Lin[1, 2¶], Chia-Hsien Chuang[3], Chih-Hsin Kao[3], Shu-Hwa Chen[4],
Guan-Yu Chen[2], I-Hsuan Lu[3], Ping-Heng Hsieh[3], Szu-Chieh Wang[1], Jeng-Yi Li[5],
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背景/研究問題/材料方法

台灣鋏蠓嗜吸人血，被叮咬後可能會產生過敏反應，它的盛行對日常生活與觀光發展造成嚴重干擾。目前，蠓科鋏蠓屬昆蟲的基因體闕如，而蠓科庫蠓屬索諾拉庫蠓的基因體組裝卻十分零碎。為了取得高品質的台灣鋏蠓基因體供台灣研究人員進行基因體與轉錄體的分析，我們由單一雌性台灣鋏蠓所產下的胚胎進行 genomic DNA 萃取，並以超微量程序進行建庫，以 PacBio HiFi-reads 進行基因體組裝，並進行 Scaffolds 間的遺缺修補，進而建構了台灣鋏蠓基因體 2.0。

結果/結論/應用啟示

台灣鋏蠓基因體總長 130 Mb，由 133 個 scaffolds 組成，最大 Scaffold 長度到達 7.56 Mb，相對應索諾拉庫蠓基因體組裝為 10 倍長；Scaffold N50 為 2.6 Mb，相對應索諾拉庫蠓基因體組裝為 29 倍長；昆蟲綱保守基因群的涵蓋度高達 96.1%，為當今蠓科昆蟲組裝最為完整的基因體。依此我們建構了台灣鋏蠓入口網站，使用者能透過 Web 介面，執行序列與關鍵字搜尋、基因表現差異性比對、叢集分析及 KEGG 網路圖等各面向的研究。亦可以自行上傳轉錄體序列分析，並可與網站收錄之轉錄體資料庫交互比對。未來可運用於蠓科昆蟲的分子遺傳學研究，例如抗藥性基因的分子機制探討，或是防治藥物的作用機制分析。我們將持續收錄台灣鋏蠓轉錄體相關研究於入口網站，透過更多研究資料的整合，將可提升台灣蠓科昆蟲研究的國際聲量。

關鍵詞（Keywords）：台灣鋏蠓 (*Forcipomyia taiwana*)、基因體新組裝 (*de novo* whole-genome assembly)、轉錄體分析 (transcriptome analysis)、轉錄體分析入口網站 (web portal for transcriptome analyses)

*台灣鋏蠓基因體與轉錄體分析入口網站:

3

台灣鋏蠓生活史多位點阻斷生物防治技術之研發
Bio-control *Forcipomyia taiwana* by blocking multi-site of its life cycle

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背景/研究問題/材料方法

Forcipomyia taiwana (Diptera: Ceratopogonidae) is a nuisance blood-sucking pest to humans in Taiwan. An *F. taiwana* bite causes itching and redness and usually causes serious harassment to human outdoor activity. In terms of *F. taiwana* control, chemical pesticides are ineffective. Therefore, we developed odor and traps to trap the female *F. taiwana*, and isolated potential soil lactic acid bacteria (LAB) and fungi with algicidal activity and ovicidal, larvicidal potential, respectively for blocking multi-site of its life cycle to bio-control *F. taiwana*.

結果/結論/應用啟示

The results include: (1) Combination of fermentation extract of *Acinetobacter lwoffii*, artificial sweat, and smart traps can achieve a 60% trapping rate to female *F. taiwana* that compare with shank attraction; (2) Soil *Lactococcus lactis* Ba4-2 produced hydrogen peroxide has algicidal potential, which block the development of larvae; (3) *Purpureocillium lilacinum* NCHU-NPUST-175 and *Fusarium verticillioides* NCHU-NPUST-178 had 38% and 50% mortality, respectively was found in concentration (5 × 107 conidia/mL) at fourth instar larvae. In conclusion, the combination of trapping female *F. taiwana*, algicidal activity of soil LAB, and the ovicidal and larvicidal potential entomopathogenic fungi could block the multi-sites of *F. taiwana* life cycle. We expect a potential to apply the odor and microbes for the bio-control of *F. taiwana*.

關鍵詞（Keywords）：台灣鋏蠓（*Forcipomyia taiwana*）、洛菲不動桿菌（*Acinetobacter lwoffii*）、乳酸球菌（*Lactococcus lactis*）、蟲生真菌（entomopathogenic fungi）、生物防治（bio-control）

4

以經皮無針式 DNA 疫苗治療台灣鋏蠓 (小黑蚊) 過敏之研究

Needle-free epicutaneous For t 2 DNA vaccine is effective for preventing and treating biting midge (*Forcipomyia taiwana*) allergy in a murine model

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背景/研究問題/材料方法

Backgrounds: Allergen-specific immunotherapy (ASIT) is capable of inducing immune tolerance to the corresponding allergen, thereby enabling treatment of the root cause of the allergic disease. As the treatment course of protein-based vaccines for ASIT is time-consuming, an easily administered epicutaneous anti-allergic DNA-based vaccine is an attractive method, especially during the COVID-19 pandemic.

Methods: We established a mouse model allergic to the biting midge, *Forcipomyia taiwana*, to test the concept of the epicutaneous DNA vaccine. The experiments were designed using two approaches: therapeutic and prophylactic. Mice were patched with 25mg For t 2 DNA vaccine patches for one hour with a total of three treatments spaced one week apart. Scratch bouts after For t 2 allergen challenge were used as a clinical surrogate of itch and biomarkers for allergic inflammation were examined by ELISA, RT-PCR, and histopathology.

結果/結論/應用啟示

Results: We found that after epicutaneous DNA vaccination, the mice significantly improved with respect to allergen-induced scratch. For t 2-specific IgE, mRNA, and protein of IL-13 and eosinophils infiltration in the targeted skin decreased. For t 2-specific -IgG2a and mRNA expression of FOXP3 increased.

Conclusions: We demonstrated the first needle-free epicutaneous DNA vaccine patch that is effective in preventing as well as treating biting midge allergy in a murine model. The mice showed improvements in their allergic condition both clinically as well as in allergic inflammation. The mode of this anti-allergic DNA vaccine may have the potential for use in other specific immunotherapies for other allergens.

5

台灣鋏蠓 (*Forcipomyia taiwana*) 非農藥防治資材研究
The studies of nonsynthetic resources for *Forcipomyia taiwana* management

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背景/研究問題/材料方法

台灣鋏蠓 (*Forcipomyia taiwana*) 雖不會媒介人類相關疾病，但因其嗜吸人血，引起受害者皮膚瘙癢及紅腫，甚至影響各地區觀光產業，為台灣夏季最重要衛生害蟲之一。防治以環境整頓與棲地管理為主，但發生嚴重時仍不免需要合成藥劑緊急防治，但有環境污染與人類健康問題。亟待其它環境友善替代方案。因此，我們研究非有機合成資材等對藻類及台灣鋏蠓卵、幼蟲及蛹等階段生長的影響。

結果/結論/應用啟示

草木灰對台灣鋏蠓幼蟲賴以維生的小球藻 (*Chlorella* sp.) 有劑量相關的生長抑制作用;而苦茶粕、矽藻土、苦茶粕、硼酸等對台灣鋏蠓的生長發育有抑制效果；此外，多種肥料對卵黑化、幼蟲及蛹的生長發育有明顯抑制作用。蜻蜓雖被認為可抑制台灣鋏蠓族群，但未能於實驗室驗證其捕食作用;而網背蟎 (Stigmaeidae)、蠅虎 (Salticidae) 及螞蟻於實驗室及田間均可證實其寄生或捕食台灣鋏蠓成蟲之潛力，尤其螞蟻多樣性與台灣鋏蠓族群密度具有負相關趨勢。但田間驗證肥料 (硫酸胺) 及大頭家蟻 (*Pheidole* spp.) 對台灣鋏蠓族群的抑制效果不明顯，可能原因及因應對策包括 (一) 台灣鋏蠓族群密度變化大，有待建立適當評估方式，(二) 有機資材不具持續性，需適當的劑型改良，(三) 螞蟻是有效天敵，然應用上需克服大量飼養問題、或就地營造有利螞蟻生存之棲地。

關鍵詞（Keywords）：台灣鋏蠓（*Forcipomyia taiwana*）、有機資材（nonsynthetic resource）、天敵（natural enemy）

6

小黑蚊的餵血器誘引與抗藥性研究
Investigation of blood-feeder attraction and insecticide resistance in *Forcipomyia taiwana*

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背景/研究問題/材料方法

小黑蚊是戶外活動者最感到困擾的吸血性害蟲，受害者除了感到異常騷養疼痛之外，也可能會有紅腫過敏現象。目前防治小黑蚊的方法相當多元，包括：行環境整頓、藥劑防治、物理防治、個人防護與教育宣導等；然而由於小黑蚊的棲地與活動範圍遼闊，行環境整頓或小黑蚊孳生地清除都是難度極高的挑戰，因此小黑蚊的防治大多偏重於藥劑防治。本研究擬以小型定溫人工餵血器誘引小黑蚊，發展誘殺雌成蟲的策略來降低小黑蚊族群密度與減少防治藥劑的使用，並且評估現行藥劑對小黑蚊的防治效果與不同地區小黑蚊的抗藥性發展概況，以利制訂有效的藥劑輪用機制。

結果/結論/應用啟示

結果顯示：(一) 本研究室發展的餵血器，在實驗室中無論使用豬血或雞血，對小黑蚊雌蚊的誘引效果均比糖水佳。但是在戶外的誘引效果卻不如預期，仍須進一步測試改良。(二) 目前測試的兩種有機磷與四種除蟲菊酯類藥劑中，陶斯松對台中科博館、賽滅寧對太平長億高中、賽洛寧對大坑逢甲國小與太平長億高中小黑蚊的致死率均小於80%，有防治失效的可能性。進一步進行抗藥性檢測確實發現：科博館小黑蚊對陶斯松具有 23.4 倍的抗藥性、太平長億高中小黑蚊對賽滅寧具有 19.5 倍的抗藥性、大坑逢甲國小與科博館小黑蚊對賽洛寧分別具有 69 倍與 15 倍的抗藥性，至於太平長億高中小黑蚊對賽洛寧的抗藥性遠超過可評估濃度而無法測得。整題而言，各防治藥劑對不同地區小黑蚊的防治效果不盡相同，各地區小黑蚊對防治藥劑的抗藥性發展程度也各不相同。有效的小黑蚊藥劑防治應奠基於對各藥劑防治效果或各地區小黑蚊的抗藥性發展了解，方能制訂有效的藥劑輪用機制，達到降低小黑蚊騷擾、環藥使用量、環境污染負荷與人類健康風險等多贏目標。

關鍵詞（Keywords）：小黑蚊（*Forcipomyia taiwana*）、抗藥性（Insecticide resistance）、餵血器（Blood feeder）

生物多樣性、族群與群聚生態學

論文宣讀

Oral Session: Biodiversity, Population and Community Ecology

OB_01

台灣土白蟻的巢群取食範圍和繁殖結構
Colony foraging area and breeding structure of *Odontotermes formosanus*

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背景/研究問題/材料方法

Fungus-growing termite, *Odontotermes formosanus*, plays an important role in the nutrient cycle of forests, decomposing dead plant tissue and providing the main protein source for many arthropods, reptiles, bird and mammals. However, its subterranean life style makes it difficult to be studied. Its colony territory size, colony density and breeding structure remain unknown. In the Xiaping Tropical Botanical Garden, 4 monitored plots (50m x 50m), a total of 484 wood stakes is conducted to trace the population activity of *O. formosanus*. We used eight microsatellite markers to identify colony boundaries of *O. formosanus* in Xiaping Tropical Botanical Garden at December 2021, the most active period of *O. formosanus*, and examined their colony breeding structure.

結果/結論/應用啟示

Microsatellite genotype analysis shows that there are at least 29 colonies in the 4 monitored plots, 19 colonies belong to simple colony, containing one pair of reproductives and 10 colonies (10/29, 34.5%) belong to mixed family, containing more than one pair of reproductives. Colony density varied among the four plots, 18, 5, 3 and 3 colonies found in the four plots. There are termite individuals of 28 colonies only be detected in a single wood stake, and maximum foraging distance is less than 5 m and only 1 colony maximum foraging distance is 30 m. Comparing to the Asian subterranean termite, *Coptotermes gestroi* (Wasmann), studied in the same location, which maximum foraging distance is 80 m, 56 m and 0 m, the colony foraging area of *O. formosanus* is quite small. This research can be helpful to trace the population dynamic of *O. formosanus* and is the first study that examined the breeding structure of *O. formosanus* in the field.

關鍵詞（Keywords）：台灣土白蟻（*Odontotermes formosanus*）、微衛星基因（Microsatellite）、覓食範圍（Foraging area）、繁殖結構（Breeding structure）、多雌性（Pleometrosis）

OB_02

莖癭喜楠癭蚋 *Daphnephila truncicola* (雙翅目:癭蚋科) 的蟲癭大小是否受寄生性天敵之影響? Are gall sizes of *Daphnephila truncicola* (Diptera: Cecidomyiidae) affected by parasitoids?

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背景/研究問題/材料方法

蟲癭的外形、顏色、大小等形態表現，被視為造癭物種與其他營養層(寄主、伴生真菌、天敵物種等)長久交互作用之選汰結果，其中，許多研究顯示蟲癭大小受其寄生蜂影響，然寄生蜂對蟲癭大小之選汰影響仍需更多研究的案例來進行佐證。本研究以台灣產莖癭喜楠癭蚋 *Daphnephila truncicola* Tokuda, Yang et Yukawa 的莖部梭狀蟲癭，測試蟲癭大小與寄生蜂之關聯。於 2020 及 2021 年於陽明山地區 (GPS: N25.19, E121.51)，分別取樣 49 及 113 顆蟲癭，並將各年份的蟲癭分為寄生組與非寄生組，比較兩組之間長度、寬度、長寬比是否具有差異。

結果/結論/應用啟示

2020 年寄生組蟲癭 (n = 30) 的長度為 14.23 ± 1.13 mm、寬度為 4.54 ± 0.46 mm，顯著小於非寄生組 ($P < 0.05$)；2021 年寄生組蟲癭 (n = 7)的長度為 15.00 ± 1.00 mm、寬度為 4.97 ± 0.26 mm，顯著大於非寄生組 ($P < 0.05$)。綜上，顯示癭蚋蟲癭的大小受到寄生性天敵的影響，支持天敵影響蟲癭大小的假說，然兩年寄生組蟲癭的結果相異，推測被寄生蟲癭的大小可能因寄生蜂的組成有所差異。此外，本研究亦首次記錄莖癭喜楠癭蚋的三種天敵寄生蜂物種，分屬金小蜂科、釉小蜂科及廣腹細蜂科。

關鍵詞（Keywords）：生態（Ecology）、癭蚋（gall midge）、蟲癭大小（gall size）、交互作用（interaction）

OB_03

兩種平腹小蜂種間競爭關係對荔枝椿象生物防治策略之影響
Effects of interspecific competition between two *Anastatus* species on biological control strategies for litchi stink bugs (*Tessaratoma papillosa* (Drury))

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背景/研究問題/材料方法

Anastatus parasitoids are used for pest management (such as control of *Tessaratoma papillosa*) in Taiwan and many other countries around the world. For example, *Anastatus fulloi* have been released across Taiwan for biological control. Another species, the native *A. formosanus* was found to display interspecific competitive behaviors that drove away other wasps on egg masses, a phenomenon which was not observed in *A. fulloi.* We studied interspecific competition between released *A. fulloi* and native *A. formosanus* to determine if mass-released parasitoids oppress native *Anastatus* populations. In this study, we hypothesized that (1) The fecundity and sex ratio of *A. fulloi* or *A. formosanus* will be affected by interspecific competition with adequate resources. (2) The offspring of *A. fulloi* or *A. formosanus* will be affected by the sequence of parasitism on the same host eggs. We collected *A. fulloi* and *A. formosanus* from the field for mass rearing in our lab, then observed offspring from one egg mass parasitized by two *Anastatus* spp. simultaneously or sequentially.

結果/結論/應用啟示

We found no significant differences between single *A. formosanus* and *A. fulloi* in host egg utilization (parasite rate), but the number of eggs increased with the number of *A. fulloi* individuals. However, different amounts of caged *A. formosanus* displayed similar parasite rates. Furthermore, when two species of parasitoids coexisted, the total parasite rate was lower than that of *A. fulloi* alone, indicating that the competitive behavior of single *A. formosanus* may influence other individuals on the same egg mass, regardless of whether they are the same species. We plan to study whether mass release of *A. fulloi* to achieve strengthened control may cause local extinction of native *A. formosanus* due to compression of living spaces.

關鍵詞（Keywords）：平腹小蜂（*Anastatus*）、種間競爭（Interspecific competition）、生物防治（Biological control）、寄生蜂（Parasitoid wasps）

OB_04

不同劑量的柚子葉片萃取物對蝴蝶產卵行為的影響
Effects of different doses of pomelo leaves extraction to the butterfly oviposition behavior

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背景/研究問題/材料方法

昆蟲與植物間的交互作用，是藉由許多生物和非生物因子來達成，其中，化學物質是一個相當重要的媒介，可以同時誘導多個生理機制的運作。而植物的二次代謝物，就是其中的一類，既可以驅離害蟲以及誘引天敵，同時也可以使昆蟲做為產卵或尋找食物的一個定位記號。本研究藉由酒精萃取柚子葉片當中的物質，製成誘引劑，來誘引大鳳蝶 (*Papilio memnon*) 產卵行為，並分別使用 3 種不同劑量的萃取液，分別為 200µl、100µl 以及 50µl，來探討劑量對誘引效果的影響。

結果/結論/應用啟示

在實驗的結果中，確實可以見到實驗室飼養出的蝴蝶受到植物萃取物的誘引而產生的產卵行為，且在三個劑量下均沒有顯著的差異；然而對於野外直接採集的蝴蝶個體上，三種劑量卻都不起作用，直至加倍到 400µl 才開始有產卵行為。這種植物化學物質與昆蟲間的交互作用，未來可以應用在保育與大量繁殖特定蝶種之用，同時這種關係亦可以應用於科普教育上，推廣化學生態的概念。

關鍵詞（Keywords）：大鳳蝶（*Papilio memnon*）、柚子（*Citrus maxima* (Burm.) Merr.）、產卵行為（oviposition ）

OB_05

台灣蝶類整體多樣性上升但群聚組成受氣候變遷與棲地類型影響而改變
The overall diversity of butterflies in Taiwan has increased, but species composition has been reorganized due to climate change and land use type.

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背景/研究問題/材料方法

全球氣候變遷與棲地受人類開發為生物多樣性喪失之主因，多種生物類群以及主要生物多樣性指標亦指出生物多樣性快速下降之警訊。然而對昆蟲這類生活史較快、族群波動大的類群而言，不論大尺度或各區域的多樣性指標，並無共同之趨勢(增加、減少、群聚組成持續變化皆有)；且目前相關研究集中於歐美國家，低緯度、生物多樣性高的區域反而缺乏適當評估。本研究使用台灣蝶類系統性調查結果 (1993-2021)，共 626 旅次的調查，包含 164 個重複調查樣點 (海拔分布 0-2670m)，記錄到 282 物種，配合長期氣候變化與土地利用類型資料，嘗試找出蝶類族群與群聚的長期變化模式與其驅動因子。

結果/結論/應用啟示

結果發現，台灣整體的蝶類豐富度、生物量與物種數是增加的，在較熱與較乾的地方蝶類多樣性與生物量越增加越明顯，且低溫的群聚對溫度變化較敏感、隨溫度上升增加較顯著，但自然環境的棲地蝶類傾向減少；由物種層級看來，傾向增加的蝶類為分布廣泛、體型較小且偏好低度開發棲地的物種。本研究補足低緯度地區昆蟲多樣性變化的知識缺口，並指出即使蝶類能維持或增加族群量，在特定氣候與棲地的壓力下群聚在發生變化，且物種本身的棲地偏好可能發生改變。

關鍵詞（Keywords）：蝴蝶（Butterfly）、生物多樣性（Biodiversity）、氣候變遷（Climate change）、土地利用類型（Land use type）

OB_06

台北植物園與中和四號公園授粉網絡及都市棲地營造之比較
Comparison of pollination network and urban habitat establishment between Taipei Botanical Garden and Zhonghe Park

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背景/研究問題/材料方法

開花植物在公園綠地除作為景觀用，同時也成為多種訪花昆蟲的食物資源，昆蟲也為植物提供授粉服務。本研究針對都市綠地進行開花植物授粉網絡的研究，以台北植物園代表營造後期環境，以中和四號公園代表營造初期環境，建立兩不同樣區的授粉網絡。各樣點目視調查 20min 紀錄劃定之 3*4m 見方內開花植物物種、訪花昆蟲的種類與訪花事件次數，比較兩樣區訪花昆蟲與開花植物物候資料，以探討不同功能群昆蟲與開花植物交互動態。

結果/結論/應用啟示

調查期間台北植物園共記錄到訪花昆蟲 64 種，包含膜翅目 34 種、鱗翅目 22 種、雙翅目 8 種。中和四號公園共記錄到訪花昆蟲 49 種，包含膜翅目 30 種，鱗翅目 15 種，雙翅目 4 種。膜翅目進一步分為震動花蜂 11 種、非震動花蜂 2 種、巢寄生花蜂 2 種、捕食性蜂類 16 種、葉蜂類 4 種。訪花昆蟲物種多樣性高峰發生於 5 月下旬到 6 月初，結果顯示營造初期的四號公園訪花昆蟲多樣性較低，可能因四號公園管理模式干擾花蜂築巢所需微棲地，以及缺乏鱗翅目幼蟲寄主植物，無法供部分物種完成生活史。棲地營造不能只考量景觀功能，須考量不同功能群生物利用棲地之需求。植栽選擇應可參考訪花事件動態，選擇可作為蜜粉源的物種，同時不宜大量栽種，以免排擠某些非人為種植的原生植物。

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

OB_07

以 DNA 條碼與高通量條碼作為工具研究臺灣落葉甲蟲

DNA barcoding and metabarcoding as tools to study Taiwanese leaf litter beetles

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背景/研究問題/材料方法

Soil arthropods are crucial components of tropical forests, as predators and litter transformers. Their species-rich fauna is sometimes compared to tropical coral reefs. Beetles are the most diverse group of soil arthropods in species numbers, and good indicators of forest history and quality, but we lack data about their biology and ecology. In most cases, we are even unable to identify adults, larvae remain completely unknown, and basic data about species diversity are missing. The goal of our ongoing study is to fill in this gap: to provide easy DNA-based tools for species identification and bring the first data about the species diversity, ecology, and biology of these beetles in Taiwan. We aim at optimizing protocols allowing quick and cheap identification of specimens (barcoding) or samples (metabarcoding), using Oxford Nanopore (ONT) sequencing. We have used samples from central Taiwan (Huisun) and are adding those from across Taiwan now.

結果/結論/應用啟示

The data from Huisun indicate that a single 6-liter sample of sifted leaf litter contains 14–55 beetle species, including 2–9 species present only as larvae. Our sampling in 2019-2021 revealed 147 species per locality on average, representing 52–66 % of the real species richness. 19 % of all species (in 13 families) were represented only by larvae. Only 12 % of species (in 11 families) were found in adults as larvae, and larvae of some diverse or abundant groups (e.g., Pselaphinae, Hydrophilidae, Curculionidae) were not found at all, possibly due to their seasonality and specialized habitat preferences. The discovery of larvae allowed us to perform detailed studies on larval morphology and biology in some species (e.g., *Oxyomus*, *Stenochinus*). Our ONT protocols allow quick and cheap DNA barcoding of leaf litter arthropods, and we are currently working on their adaptation for metabarcoding data.

關鍵詞（Keywords）：biodiversity, identification, nanopore sequencing

OB_08

植物、昆蟲、環境變遷
Plants, insects, and environmental changes

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背景/研究問題/材料方法

It is increasingly recognized that the interactions between plants and insects are mediated by multiple abiotic factors, which are crucial in the climate change context and essential in the general plant-insect interaction contexts.

結果/結論/應用啟示

Using several examples from my previous works, this talk aims to demonstrate the importance of abiotic factors in influencing the ecology and evolution of plant-insect interactions. We will also discuss future directions and critical current topics in plant-herbivore interactions on a global scale.

關鍵詞（Keywords）：植物抗蟲防禦（plant antiherbivore defense）、水（water）、非生物逆境（abiotic stress）、光（light）、植物昆蟲交互作用（plant-insect interactions）

系統分類、族群遺傳、演化

論文宣讀

Oral Session: Systematics, Population Genetics and Evolution

OS_01

臺灣產撚翅目新紀錄科與新紀錄屬的發現
A discovery of newly-recorded strepsipteran families and genera (Insecta: Strepsiptera) in Taiwan

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背景/研究問題/材料方法

The hidden biodiversity of Strepsiptera in Taiwan has barely been discovered since 1985. Only five species belonging to two families of Stylopidae and Xenidae were recorded before, and no other recent study has been conducted. Several newly-recorded species of Strepsiptera in Taiwan are presented in this research based on morphological identification, including two genera from newly-recorded family of Myrmecolacidae, one genus from another newly-recorded family of Elenchidae, and the other two genera from Xenidae. This is an approach to further discovery of Strepsiptera in Taiwan.

結果/結論/應用啟示

Three strepsipteran families were discovered, while two of which are newly-recorded in Taiwan. According to the host specificity and morphological identification, members from Xenidae could be identified as cf. *Deltoxenos iwatai* and cf. *Macroxenos piercei*; members from Myrmecolacidae are *Stichotrema asahinai* and *Myrmecolax* sp.; the member from Elenchidae is identified as *Elenchus* sp. The scarcity of Strepsiptera specimens reflects the demand for more intensive collection in the future. The biodiversity of Strepsiptera underlies deeply within their potential hosts. With more parasitized hosts or free-living males to be found could the discovery of these unique insects keep on going.

關鍵詞（Keywords）：Strepsiptera, Myrmecolacidae, Xenidae, Elenchidae, New records

OS_02

臺灣產寡毛實蠅族 (雙翅目：果實蠅科) 之分類學研究
A taxonomic study of Dacini fruit flies (Diptera: Tephritidae) of Taiwan

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背景/研究問題/材料方法

Fruit flies (Diptera: Tephritidae) are regarded as economically important agricultural pests. Approximately 1/3 of the species which their larvae are fruit borers. Damages to the host plant, including both ovipositor punctures and larval feedings, can lead to fruit rot and premature drop. Severe infestation on commercially produced fruits may cause considerable crop loss. While each of the major pest genera of fruit fly have limited natural distribution, some species have invaded regions beyond their native range.

Threat of the introduction of pest fruit flies necessitates the imposition of restrictions on imported fruits in the world. Species of the tribe Dacini are native to tropical regions including South-East Asia. While non-pest species are associated with a narrow range of known host, certain pest species are polyphagous with wide host range. Thus the taxonomic study on Dacini fruit fly species of Taiwan can be both scientifically and economically important. This study aimed to revise Dacini fruit fly species of Taiwan. Specimen were collected through McPhail trap baited with male attractants methyl eugenol and cuelure. During 2020 to 2021, a total of 404 trapping sites were set up throughout Taiwan, and the samples of fruit fly were collected once every two weeks.

結果/結論/應用啟示

A species checklist of Dacini fruit fly occurring in Taiwan is revised, including 30 previously reported species and one newly recorded species of *Bactrocea abbreviata* (Hardy, 1974). Keys to genera and species of tribe Dacini, along with basic information for each species, namely taxonomic status, global distribution, attractants and host records, is provided.

關鍵詞（Keywords）：果實蠅科（Tephritidae）、寡毛實蠅族（Dacini）、分類學（taxonomy）、臺灣（Taiwan）

OS_03

New recorded species of genus *Callicera* Panzer (Diptera: Syrphidae) in Taiwan

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背景/研究問題/材料方法

Callicera Panzer is a small genus in Syrphidae, only about 12 species have been found in the world till 2020. *Callicera* belongs to Eristalinae, and has beautiful bumblebee-like appearance. It is easily identified from its subfamily by its special and long antennae. Larvae of *Callicera* lived in tree hole with decaying materials, and female adults sometimes visit flowers or appeared around the tree holes for oviposition. In Taiwan, only one species, *C. aenea* (Fabricius, 1781), has been recorded in early 20th century. Considering the separating distribution and similar appearance of *C. aenea* and *C. aurata*, this Taiwanese old record might be a mis-identification and need to be reconfirmed. Specimens was collected mainly by net sweeping, and preserved in 95% alcohol until pinned.

結果/結論/應用啟示

In August, 2021, we collected one unrecorded species which is different from *C. aenea*, but more looked like *C. aurata*. Many *Callicera* male adults hovered on the mountain top of Mt. Yuanzui. In July to September, 2022, this species was also collected in Mt. Yuanzui and Mt. Sanjaoi. We have tried to find their larval habitats near the collecting sites of those male adults, but no female adults and larvae were found in these two years. To know more information about their active period of adults and habitats of larvae, more fieldwork is needed.

關鍵詞（Keywords）：Eristalinae, Callicerini, hover flies, taxonomy

OS_04

以 ddRAD-seq 核酸多態型資料研究台灣南部埃及斑蚊在小尺度的族群結構以及親緣關係

Fine-scale geographic structure and relatedness patterns of the major arbovirus vector, *Aedes aegypti*, in Southern Taiwan inferred by ddRAD-seq SNPs

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背景/研究問題/材料方法

埃及斑蚊 (*Aedes aegypti*) 是登革熱 (Dengue) 等蟲媒病毒主要傳播的途徑，了解埃及斑蚊的分佈及散播有益於控制病媒蚊的傳播。本研究使用台南市、高雄市及屏東縣等三個縣市共 168 個有明確座標的埃及斑蚊樣本，再藉由雙切限制酶片段 DNA 定序法 (double-digest restriction-site associated DNA sequencing, ddRAD-seq) 產生的核酸多態型資料，研究台灣南部埃及斑蚊的族群結構以及親緣關係。首先將樣本依行政區分為不同族群，使用 Stacks v2.59 進行分析，計算出各行政區的埃及斑蚊有效族群量介於 21000 至 24000，遺傳分化指數 (FST) 介於 0.01 至 0.03，族群間幾乎沒有分化。

結果/結論/應用啟示

接著以親緣關係 (Loiselle’s k) 配合樣本的採集座標進行分析，在讀取深度 (depth coverage) 大於 5 的條件下，親緣關係為全手足 (full-sibling, Loiselle’s $k > 0.1875$) 的兩隻埃及斑蚊，最遠相距 523 公尺，而半手足關係 (half-sibling, $0.1875 > k > 0.0938$) 最遠相距則達 17 公里，遠超出文獻中斑蚊在自然情況下可移動的距離。另外在橫跨三個縣市的大尺度地理範圍中，基因距離 (Rousset’s a scores) 與地理距離的自然對數並沒有顯著相關 ($p=0.1$)，然而在僅約 4 平方公里小尺度範圍內，不但基因距離與地理距離的自然對數有顯著相關 ($p < 0.001$)，在不同行政區間也有顯著差異 ($p < 0.001$)。因此推測在小尺度的地理範圍中，地理距離與遺傳分化成正比的關係；但在超過自然情況下可移動的大尺度範圍，人類活動會影響遺傳分化與地理距離間的關係。

關鍵詞（Keywords）：埃及斑蚊（*Aedes aegypti*）、有效族群數量（effective population size）、遺傳分化指數（fixation index (FST)）、親緣係數（Kinship coefficient）、基因距離（Genetic distance）

OS_05

台灣鋸蟻形蜂亞科（膜翅目：蟻形蜂科）雄性生殖器的多樣性及探討
Discussions about various male genitalia of Taiwanese Pristocerinae (Hymenoptera, Bethylidae)

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背景/研究問題/材料方法

蟻形蜂屬於青蜂上科，主要分布於熱帶地區的外寄生性寄生蜂。已知寄生於各種鞘翅目與鱗翅目的幼蟲上。研究顯示在印度及中南美洲各地區皆有投入林業及農業害蟲的寄生試驗。其中鋸蟻形蜂亞科為目前數量及多樣性最大的亞科。先前台灣及琉球群島地區的紀錄種僅有五屬 11 種，多數種的描述也因為顯著的兩性異形而並不完整。因此在本研究裡針對形態觀察及利用分子定序技術整合，將台灣及鄰近地區的鋸蟻形蜂亞科分類學重新檢討。

結果/結論/應用啟示

在此次研究當中所記錄到的包含 3 新種共八屬 24 種。在外部形態觀察上有明顯的種內多樣性。體色的變化、前伸腹節上的隆起有明顯差異，以及雌雄間大顎齒數的不同。另外在雄性生殖器上有呈現明顯的形態多樣性。同屬之間 paramere 所呈現的形態幾乎一致，但插入器前端在種間比較中有明顯不同的表現。並且比較各屬間 basiparamere 與 harps 的融合程度與分子系統樹的結果，已知此亞科內至少有三種以上的分歧存在。根據此次研究的結果，鋸蟻形蜂亞科在台灣及周遭地區各館藏保存的乾燥標本能夠以雄性交尾器作為主要形態分類的根據，並結合分子系統的情報，整合雌雄之間的配對。以利於未來在農業害蟲上的應用研究。

關鍵詞（Keywords）：寄生蜂（parasitoid wasp）、系統樹（phylogeny）、分子（molecular）、形態（morphology）

OS_06

臺灣產 *Prosthodocis* 亞屬（膜翅目：姬蜂科：柄卵姬蜂亞科：擬瘦姬蜂屬）整合分類學研究

Integrative taxonomy of subgenus *Prosthodocis* (Hymenoptera: Ichneumonidae: Tryphoninae: *Netelia*) in Taiwan and its systematic implications

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背景/研究問題/材料方法

Highly diverse nocturnal parasitoid wasps in genus *Netelia* were mainly identified to species-level by their specialized male genitalia structures since the similar external appearances. However, the male genitalia structures of subgenus *Prosthodocis* are simplified while their further descriptions were neglected, making the species delimitations unclear. Konishi has proposed diagnoses for some Taiwanese species and some probable misidentifications in Asia, but precise species identifications of subgenus *Prosthodocis* in Taiwan remain pending, and the relationship between *Prosthodocis* and other subgenera is also unknown. In this study, taxonomy of subgenus *Prosthodocis* in Taiwan is revised by integrative approaches, combining external morphologies, male genitalia structures, egg morphologies as well as the phylogenetic reconstruction by partial sequences of *COI* and *28S* genes and molecular-based species delimitation. Implications for their systematics are also discussed.

結果/結論/應用啟示

Only five species in subgenus *Prosthodocis* were recorded from Taiwan in the past, but we have recognized eight morphospecies in Taiwan based on male genitalia, including two newly recorded species. However, molecular evidence suggested low genetic distance between two morphospecies with distinct male genitalia structures, and cryptic species may exist in subgenus *Prosthodocis*. The subgenus *Prosthodocis* was also resolved as a non-monophyletic group in our study which mixed with the *obesis*-group in subgenus *Apatagium.* In conclusion, the species diversity in subgenus *Prosthodocis* in Taiwan is underestimated, and more comprehensive samplings are needed to revise the taxonomy and clarify the phylogenetic relationship of this commonly-seen nocturnal wasps.

關鍵詞（Keywords）：整合分類學（integrative taxonomy）、姬蜂科（Ichneumonidae）、擬瘦姬蜂屬（*Netelia*）、臺灣（Taiwan）

OS_07

台灣脈翅目褐蛉科的分類修訂
Taxonomical revision of Hemerobiidae (Neuroptera) from Taiwan

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背景/研究問題/材料方法

褐蛉科 (Hemerobiidae) 是脈翅目中的第三大科，全世界約有 600 多個物種。褐蛉食性與草蛉相似，甚至因為他展現更明顯的專食性且成蟲為肉食性而可以和草蛉有不同方向的應用，目前台灣已有單位嘗試開發 *Micromus timidus* 作為防治蚜蟲的材料。對於食性有偏好性的褐蛉來說確認物種身分很重要，然而許多褐蛉僅能用生殖器區分物種，且台灣的褐蛉分類研究已有數十年無人問津。本研究欲檢視標本，以外部形態及粒線體分子特徵確認物種身分，也仔細地回顧文獻修訂台灣現有的物種名錄。

結果/結論/應用啟示

目前的名錄中計有 10 屬 21 種褐蛉，其中有 *Sympherobius* 屬物種未被確認身分，只在一本專書中被記錄過。檢視標本以及文獻回顧中我們確認台灣至少有 10 屬 30 個物種，絕大多數的物種可以透過翅膀色斑的模式，以及過去已知的翅脈的特徵辨識，如前翅前緣區 (costal area) 有沒有橫脈、前翅 MP 和 CuA 脈是否癒合、脛分脈 (Rs vein) 數量等。我們也嘗試使用幾何形態測量學的方法，分析翅脈模式尋找新的可用的形態特徵，如第一脛分脈位置、M 脈分岔處等等，除了幫助更方便以肉眼分辨種類外，也能幫助解決脈翅目分類研究中缺乏量化形態特徵的問題。初步結果中，用 18 個 *Micromus timidus* 和 9 個 *Micromus numerosus* 樣本的分析結果顯示，最後一條 Rs 脈基部的水平位置，以及 CuA 脈第二個分岔點的水平位置對於把兩者分開有較高的解析度。

關鍵詞（Keywords）：幾何形態測量學（Geometric Morphometrics）、脈翅目（Neuroptera）、褐蛉科（Hemerobiidae）、分類學（Taxonomy）、*Micromus timidus*

OS_08

Identification of fruit flies (Diptera: Tephritidae) using species-specific primer pairs targeting the Internal Transcribed Spacer 2 (*ITS2*) gene

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背景/研究問題/材料方法

Many fruit flies damage seriously on fruits and vegetables and have been listed as quarantine pests in the world. Agricultural production can incur massive losses if they are not controlled within the timeframe specified. Through agricultural products or crop transportation, they can establish in newly found localities, posing a global hazard. Eggs and larvae concealed inside agricultural products are usually difficult to detect. Morphologically, immature stages shall be reared to adulthood for identification, which is time-consuming and occasionally unsuccessful. It is critical to identify them promptly, efficiently, and properly to prevent them from spreading. In this study, species-specific primer pairs using internal transcribed spacer 2 sequences were designed for 9 fruit flies, i.e., *Bactrocera minax*, *Anastrepha distincta*, *Bactrocera carambolae*, *Bactrocera caudata*, *Bactrocera cucurbitae*, *Bactrocera dorsalis*, *Bactrocera tau*, *Bactrocera tryoni*, and *Ceratitis capitata*. Authenticity in specificity and capacity of the developed species-specific primers were evaluated by visually analyzing the gel profile for the appearance of a clear band in solely targeted fruit flies.

結果/結論/應用啟示

Results in multiplex PCR showed species-specific primer pairs accurately amplified the targeted fruit flies and did not have cross amplification, i.e., no diagnostic bands were found in the nontargeted fruit fly species. Obviously, the designed species-specific primer can be applied at the quarantine port of crops entry to identify fruit flies at their immature stage. Benefits of these specific-primer applications can be acquired by lowering the DNA sequencing cost and shorting the procedures in experiment time from two days to about four hours.

關鍵詞（Keywords）：Fruit Flies, Quarantine Pests, Multiplex PCR, Internal Transcribed Spacer 2

OS_09

Developed DNA microarray for simultaneous identification thrips

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背景/研究問題/材料方法

Thrips identification traditionally based on adult female, while insufficient recognizable characters usually made identification difficult. Molecular evidences applied to clarify the taxonomic debate has been demonstrated over a lot of species complex of insects. Among the known molecular markers, nuclear internal transcribed spacer (ITS) with high variation was commonly used to distinguish the closely related species. It has widely used to design specific primers for some specific identification as well as probes for a number of insects in terms of DNA chip application. In this study, we developed DNA microarray based on ITS2 to improve the efficiency of traditional molecular identification to identify a number of thrips simultaneously. Species-specific probes in range of one to 21 were developed for 67 thrips species. Both adult and nymphal individuals were examined from countries, including China, France, Indonesia, Japan, Taiwan, Thailand, and the United States.

結果/結論/應用啟示

A total of thirty-two thrips species with recognizable signal intensity more than 100 were examined although not all designed specific-probes shown the specific signal. The cross-hybridization in some probes between *Frankliniella fusca* and *Frankliniella williamsi* within the *Frankliniella* group was observed. In *Thrips* group, a few specific probes of *Thrips hawaiensis* and *Thrips florum* also have cross-hybridization to each other, but the cross signal was lower than the specific ones. Our findings show that a DNA microarray based on an ITS2 specific probe can be a reliable, impartial, and predictive tool for identifying multiple thrips simultaneously, although results shown some designed specific-probes do not have hybridization signal on target species.

關鍵詞（Keywords）：DNA microarray, Biochip, Molecular identification, ITS2, Thrips

OS_10

利用粒線體總基因體組方法建構臺灣蝴蝶相的譜系關係
Reconstructing phylogeny of Taiwan butterflies by using mitochondrial meta-genomic method

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背景/研究問題/材料方法

臺灣島為年輕島嶼，島上生物相形成相對鄰近陸域年輕，然而島上多樣的蝴蝶卻具有高比例的特有種及特有亞種，係探討種化、生物地理及生物多樣性的良好類群。未達成此一目的需要進行大量蝴蝶定序，並且儘可能獲得大片段 DNA 序列以利臺灣蝴蝶親緣關係之建構。考量有限經費，我們利用粒線體總基因體組方法將不同數量樣本 (n = 30、40、50) 混合成進行次世代定序，所獲得序列資料再以生物資訊分析方法進行組裝，以評估混樣的定序之優劣。

結果/結論/應用啟示

三組混樣組合共成功獲得 87 個粒線體基因體序列，成功率分別為 70% (21/30)、68% (27/40)及 78% (39/50)，顯示此三組混樣組合並未因樣本增加而減少組裝的成功率。然而實際在進行資料分析時樣本數增加時則增加了後端的分析時間。即便如此，整體定序的成果大大減少進行次世代定序時所需的上機序列資料庫建置費用，將有助於臺灣蝴蝶相物種形成來源之討論。此方法亦適用於多樣性高的其它類群昆蟲。

關鍵詞（Keywords）：生物資訊分析（Bioinformatics）、次世代定序（Next-generation sequencing）、島嶼生物地理學（Island biogeography）、鱗翅目（Lepidoptera）、鳳蝶總科（Papilionoidea）

OS_11

球背象鼻蟲的親緣基因體學及斑紋演化
Phylogenomics and pattern evolution of colorful *Pachyrhynchus* weevils on oceanic islands

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背景/研究問題/材料方法

複雜的地理歷史和海洋隔離可能會造成海洋性島嶼物種的適應性輻射，促進物種多樣化以及表型的差異。主要分布於菲律賓群島的球背象鼻蟲 (*Pachyrhynchus*) 具有高度多樣的斑紋，然而斑紋的演化過程仍不清楚，且其親緣關係仍然缺乏較完整的研究，因此本研究藉由親緣基因體學的方式重建球背象鼻蟲的親緣關係，並釐清斑紋的演化過程。本研究使用鞘翅目通用的超保守元素 (UCE) 大量定序目標基因座，共取樣 133 隻球背象鼻蟲重建親緣關係及推估物種分化的分歧時間，使用比較親緣關係方法釐清斑紋的演化過程，檢測球背象鼻蟲的地理分佈與斑紋的關係。

結果/結論/應用啟示

從 133 個樣本中，每個樣本平均獲得 627 (94-782) 個 UCE 基因座。親緣關係分析顯示球背象鼻蟲有八個主要的分支，大多數的物種分化發生在上新世。球背象鼻蟲可能主要由呂宋島起源。特定的斑紋與地理有顯著的關聯性，如方格斑紋常出現於呂宋北方島嶼的物種。此外，斑紋之間的轉換可能是很頻繁的，較常見的圓斑被推估為斑紋的祖先特徵，而網狀斑紋的演化則較保守。每個斑紋的不同演化過程反映出這些特徵可能經歷了不同的選汰壓力。本研究為球背象鼻蟲的分類學研究提供系統性研究的建議，並了解球背象鼻蟲多樣化斑紋的演化歷程。

關鍵詞（Keywords）：球背象鼻蟲（*Pachyrhynchus*）、超保守元素（ultraconserved elements）、斑紋（pattern）

OS_12

Revisiting the diversity of non-termite Blattodea in Taiwan

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背景/研究問題/材料方法

The order Blattodea comprises more than 7500 species worldwide. Most of the species inhabit various environments outdoors with diverse morphologies, ecologies and behaviors; while some of them are being sanitarily and economically significant pests. The taxonomic studies of non-termite cockroaches of Taiwan were first taken out in the 19th century and thriving in the 20th. In these studies, the specimen examinations and descriptions were commonly insufficient, especially for the non-sanitary cockroaches which are usually not easy to collect and have sampling biases; therefore, it is possible that their diversity in Taiwan has been underestimated. On the other hand, many cockroaches bear sexual dimorphism, which gives difficulty in associating the sexes of given species correctly. To have better understandings of non-termite Blattodea of Taiwan, we employed both morphological and molecular data from museum collections and newly obtained materials to identify and delimit cockroach species.

結果/結論/應用啟示

To date, a total of 6 families including 75 species and subspecies in 32 genera of non-termite cockroaches have been recorded from Taiwan. This preliminary investigation revises a few erroneous records, while some new records and undescribed taxa are further proposed. Males and females of some sexually dimorphic species can be successfully matched by COI barcode. Morphological and molecular evidences also demonstrate that the species *Margattea persipicillaris* (Karny) might comprise several separate species and *Blattella karnyi* Princis along with *Blattella formosana* (Karny) is likely to be a species complex. Some basic information and taxonomic issues regarding Taiwanese fauna are also revised and discussed.

關鍵詞（Keywords）：Blattodea, taxonomy, diversity, DNA barcode, Taiwan

OS_13

臺灣產細頸䗛屬分類研究 (䗛目：長角棒䗛科：長角枝䗛亞科)
Taxonomic study of genus *Sipyloidea* (Phasmatodea: Lonchodidae: Necrosciinae) in Taiwan

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背景/研究問題/材料方法

長角枝䗛亞科 (Necrosciinae) 是䗛目中物種多樣性最高的亞科，在臺灣該亞科的物種大部分為樹棲性，採集上較為困難，因此分類與生態研究均尚未完整。其中細頸䗛屬 (*Sipyloidea*) 分布印澳區域，相較本亞科的其他屬具較高多樣性且分布更為廣泛。細頸䗛屬部分物種具有強大的傳播能力，且常見於國際間的寵物市場，然而臺灣目前對於此高風險類群的研究卻不盡完整，未來若有相似的未知種出現在臺灣將難以判斷其是否為外來種，因此有必要釐清臺灣細頸䗛屬現有物種。本研究前往全臺各地的殼斗科原始林進行掃網採集，紀錄寄主植物、飼養以收集卵的形態資料，並以形態與分子證據初步釐清台灣細頸䗛屬之生物多樣性。

結果/結論/應用啟示

過去臺灣正式紀錄的細頸䗛屬僅 2 種，在初步的採集結果中，我們發現至少 8 個形態種，並能以翅的長度與地理分布等特徵明顯區別不同形態種，初步比對 *COI* 序列也支持其可區分為不同物種。目前經由形態比對尚未發現疑似外來種的物種，但仍有鎖定一些疑似其他形態種的照片紀錄，未來將前往該地進行採集，及前往博物館檢視相關標本。

關鍵詞（Keywords）：長角枝䗛亞科（Necrosciinae）、細頸䗛屬（*Sipyloidea*）、分類學（Taxonomy）、臺灣（Taiwan）

行為、生理、個體生物學

論文宣讀

Oral Session: Ethology, Physiology and Organismic Biology

OE_01

圖形對蜜蜂著陸行為的影響
Effects of pattern on honey bee landing behavior

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背景/研究問題/材料方法

已知蜜蜂飛行時會固定外環境產生的視覺角速度，因此通過調整飛行通道兩邊重複性黑白條紋的粗細與頻率，即可影響蜜蜂飛行的速度與位移。且透過改變著陸位置重複黑白圖案的收縮與擴張程度，也會影響蜜蜂著陸的速度。此外，前人研究當背景出現許多重複性的圖案時，若單個重複圖案產生的視角小於兩倍蜜蜂兩個小眼間的角度就會產生視覺的空間混疊。所以令我們感興趣的是，當蜜蜂著陸時會不會因為地面圖案的不同，造成空間混疊，進而產生無法著陸的行為。本研究訓練蜜蜂著陸於固定位置，再使用不同圖案來測試其對蜜蜂著陸行為的影響。

結果/結論/應用啟示

利用會影響蜜蜂飛行的黑白條紋進行初步研究，證實 0.95 公分寬的黑白條紋圖案，明顯地增加了蜜蜂尋找糖水的時間，並導致 60% 的蜜蜂無法在記憶的位置著陸；而使用寬度為 0.475 和 0.23 公分的黑白條紋圖案時，超過 90% 的蜜蜂無法著陸。再透過 3D 軌跡追蹤系統分析在著陸的過程中，蜜蜂與條紋圖案 (在糖水下方) 之間的視角，來確認蜜蜂是否產生空間混疊現象。結果發現，下降到著陸的過程中，圖案的條紋寬度越窄，會產生越高比例的視覺空間混疊。因此，得知條紋圖案產生的空間混疊是影響蜜蜂著陸行為並導致著陸失敗的關鍵因素。

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

OE_02

畸翅病毒改變腺苷信號影響蜜蜂工蜂分工之研究
Alteration of adenosine signaling by DWV affects division of labor in honey bees (*Apis mellifera*)

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背景/研究問題/材料方法

蜜蜂是一種真社會性昆蟲，其特點之一是具備生殖分工工蜂負責蜂巢的營運，除了生殖分工，工蜂還可以依工作內容任務分為內勤蜂和外勤蜂。工作內容隨著日年齡增加而轉變的增長，工蜂會改變任務，新羽化的工蜂在最初的二至三週作為內勤蜂兩周於蜂巢中負責育幼和蜂巢維護，而後這段時間過後，它們便轉為外勤蜂外出覓食，已被證實這與蜜蜂大腦產生的青春激素隨日齡增加有關。有趣的是，在面對生存壓力如病原菌侵襲時，工蜂族群內的各項分工在不同的環境條件下將改變，以對抗各種生存壓力情形會有所不同。前人研究證實，當蜜蜂被畸翅病毒感染後，它們會提前轉換為外勤蜂，然而其機制目前尚未明瞭。我們先前研究表明先前，已證實感染畸翅病毒的蜜蜂大腦之腺苷路徑受到負面影響代謝與健康蜜蜂有很大差異，且受感染的蜜蜂體內能量會從大腦大腦轉移到免疫系統以，協助蜜蜂對抗病原，這種改變可能導致生理機制改變，這是否影響了大腦青春激素的分泌，導致分工狀況不同，是本研究探討的目標。目前尚不清楚畸翅病毒感染如何影響工蜂的分工，本實驗透過測量感染畸翅病毒工蜂之 ATP、腺苷、和醣類濃度和相關基因表現來了解能量代謝的改變，並分析分工相關激素青春激素與相關、基因在不同日齡的變化，嘗試解釋外來病原對能量代謝、激素生理及分工行為上的影響，嘗試解釋對分工行為的影響。

結果/結論/應用啟示

病毒感染後的蜜蜂腦部能量消耗減少，醣類代謝相關基因表現下降，但作為分工依據的青春激素相關基因卻更早受到活化，促使工蜂更快轉變為外勤蜂。本研究點出了病毒感染對蜜蜂能量代謝與青春激素的影響進而導致分工改變的可能，闡明在逆境下相關激素和基因的變化，進而解釋病毒對工蜂分工之影響。

關鍵詞（Keywords）：腺苷（Adenosine）、義大利蜂（*Apis mellifera*）、畸翅病毒（Deformed wing virus）、分工（Division of labor）、能量代謝（Energy metabolism）

OE_03

穀蠹 (鞘翅目：長蠹蟲科) 麥芽糖酶之生理功能
The physiological function of maltase in *Rhyzopertha dominica* (Coleoptera: Bostrichidae)

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背景/研究問題/材料方法

大量穀物於儲存期間將面臨各式各樣害蟲侵擾，穀蠹 (*Rhyzopertha dominica* Fabricius) 為其一重要的初級害蟲。穀蠹的幼蟲與成蟲皆取食穀物，穀物的主要成分為碳水化合物，為了有效利用碳水化合物，穀蠹需分泌消化酵素將其分解為小分子以利吸收。其中將雙醣麥芽糖分解為單醣葡萄糖的消化酵素為麥芽糖酶 (maltase, as known as α-glucosidase)，雖已知麥芽糖酶的化學作用方式，但在穀蠹體內麥芽糖酶所執行的生理功能都仍需進一步探討。本研究選殖穀蠹麥芽糖酶 cDNA，並利用即時定量聚合酶連鎖反應檢測麥芽糖酶基因於穀蠹成蟲組織及生長發育時期之轉錄表現量。

結果/結論/應用啟示

選殖得到兩條穀蠹麥芽糖酶 cDNA，*Rdmaltase1* 及 *Rdmaltase2*，兩序列之相同度為 48.6%、相似度為 64.7%。*Rdmaltase1* 在精巢和雄蟲的表現量皆顯著高於其他組織與發育時期 ($P< 0.01$)，推論與穀蠹雄成蟲的生殖調控相關。*Rdmaltase2* 在組織的表現量以中腸最多，雖然跟前腸無顯著差異，但表現量是前腸的五倍之多；而幼蟲期的表現量顯著高於其他時期 ($P< 0.05$)。幼蟲需要能量以供生長及蛹期之成蟲發育，推論 *Rdmaltase2* 於中腸及幼蟲期大量表現能幫助穀蠹快速分解麥芽糖以獲得能量。為證實上述 *Rdmaltase1* 及 *Rdmaltase2* 於穀蠹生理活動所扮演的角色，未來將利用 RNA 干擾技術探究基因默化後對雄蟲生殖及幼蟲生長發育的影響。

關鍵詞（Keywords）：穀蠹（*Rhyzopertha dominica*）、麥芽糖酶（maltase）、精巢（testis）、中腸（midgut）

OE_04

Regulation of host replication through baculovirus DNA helicase gene *P143*

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背景/研究問題/材料方法

Baculoviruses are often used as biocontrol agents and protein expression vectors. *Autographa californica* multicapsid nucleopolyhedrovirus (AcMNPV) and *Bombyx mori* nucleopolyhedrovirus (BmNPV) are the two most thoroughly studied baculoviruses and both have been extensively applied in the expression of eukaryotic recombinant proteins. Although they share highly similar genome sequences, their host ranges do not overlap. Previous studies have found that amino acid mutations in DNA helicase *P143* enable AcMNPV or BmNPV to infect nonpermissive cell lines. In addition to viral factors, alteration of host carbohydrate metabolism is also an important factor which determines the host specificity of baculoviruses. However, the specifics of this mechanism currently remain unclear. We hypothesized that DNA helicase *P143* may regulate virus host range by affecting host DNA replication processes. We therefore tested host nucleotide biosynthesis relative gene expressions following baculoviruses infection and analyzed newly synthesized DNA of post-infection host cells for verification of this effect through DNA synthesis.

結果/結論/應用啟示

Nucleotide biosynthesis relative gene expressions of permissive host were found to be higher post infection. However, the newly synthesized DNA was suppressed. This indicates that baculovirus may regulate virus host ranges by affecting host DNA replication processes. To clarify the relationship between DNA helicase *P143* and host DNA replication, we plan to test the combination between DNA helicase *P143* and host DNA; if we find that viral DNA helicase combines well with host DNA, this may serve as a basis to discover further information related to infection host ranges that can be used to improve current protein expression systems.

關鍵詞（Keywords）：Baculovirus, Helicase, Host specificity

OE_05

以 nano-CT 技術探討蜜蜂工蜂蕈狀體的體積變化
Study of volume change of honey bee mushroom bodies by nano-CT

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背景/研究問題/材料方法

蜂是真社會性昆蟲，族群內有不同的階級與分工，其中工蜂的行為具有日齡多型性 (age polyethism) 的現象，意即工蜂成蟲在不同日齡階段會執行不同的勤務。例如，年輕的工蜂為內勤蜂在巢內工作，而較成熟的工蜂會成為外勤蜂外出採集資源。由於蜜蜂在巢內與巢外工作所執行的勤務差異甚大，工蜂大腦在不同日齡階段功能性亦不相同，因此推論工蜂的大腦在成蟲階段也會有結構性的改變。前人研究已經證實工蜂成蟲大腦內的蕈狀體 (mushroom body) 體積與日齡有關，然而大腦其他部位體積與形態連續性變化則尚未探討。針對此主題，本研究建立蜜蜂大腦的奈米斷層掃描 (nano-computed tomography) 技術，透過奈米斷層掃描產生蜜蜂腦部結構造影。奈米斷層掃描透過 X 光造影，解析度最高可以達到 400 奈米，能在不破壞外骨骼的狀況下呈現蜜蜂腦部的立體結構，可在免除解剖時影響腦部形態的風險下精準呈現腦部各區域形態並計算體積的目標。

結果/結論/應用啟示

奈米斷層掃描的結果顯示，蜜蜂腦部以磷鎢酸染色後可讓各腦區間的影像有良好對比度，腦區如視葉 (包含 lamina, medulla, lobula)、嗅葉、蕈狀體以及中心複合體的結構均清晰且可區分。透過電腦運算抓取各腦區的立體結構後，我們可以精準計算各腦區體積。目前比較羽化後 6 天、15 天以及外勤蜂的蕈狀體體積，發現同日齡工蜂個體間蕈狀體體積差異不大，但不同日齡間蕈狀體體積有明顯差異。

關鍵詞（Keywords）：蜜蜂（honey bee）、蕈狀體（mushroom body）、日齡多型性（age polyethism）、奈米斷層掃描（nano-computed tomography）

OE_06

A study of imidacloprid and adenosine effects on the flight behavior and physiological mechanism of *Apis mellifera*

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背景/研究問題/材料方法

Honey bees are important pollinators of ecosystem and agricultural systems, but their populations have declined over the past fifty years. The aim of this study was to investigate whether imidacloprid causes physical damage to honey bees, in hopes of finding new ways to rescue honey bee colonies. Our experiments were separated into two parts. In the first part, we sought to understand whether imidacloprid affected the foraging ability and flight behavior of honey bees. In the second part of the experiment, we examined whether addition of adenosine can eliminate the effects of imidacloprid. We treated three groups of honey bees with sugar water, an imidacloprid solution, and imidacloprid mixed with adenosine solution, respectively. Pollen collection volumes, movement trajectory and wing beat frequency were measured, as well as neurotransmitter content and energy metabolism gene expression levels in honey bees flight muscles.

結果/結論/應用啟示

Our results indicated that imidacloprid reduced the pollen collection volumes and affected the foraging ability and flight behavior of honey bees by shortening movement distance and wing beat frequency. Imidacloprid also impacted on nerve conduction, causing a rapid increase of octopamine content and short-term energy metabolism gene expression levels, leading to muscles fatigue and energy imbalance, and lowered honey bee activity over the long-term. Compared to the imidacloprid-only treatment, imidacloprid mixed with adenosine promoted carbohydrate metabolism, allowing cells to produce more energy and reducing the negative effects of imidacloprid. According to our study, we have confirmed that imidacloprid imbalanced the energy supply of the honey bees and caused negative impacts on the flight behavior and physiological mechanism of honey bees; adding adenosine can increase the energy production in the bees and recover their flight ability and foraging abilities. In future, we plan to explore further applications for adenosine in apiculture.

關鍵詞（Keywords）：*Apis mellifera*, imidacloprid, adenosine, flight behavior, energy metabolism

OE_07

台灣產瘤顎家蟻屬與邵氏分針蟻共生關係之探討(膜翅目：蟻科)
Symbiotic relationship between Taiwanese *Strumigenys* and *Ectomomyrmex sauteri* (Hymenoptera: Formicidae)

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背景/研究問題/材料方法

共生現象 (Symbiosis) 在蟻科 (Formicidae) 中是相當重要的生存策略，從互利共生 (mutualism) 到寄生 (parasitism)，幾乎都能發現螞蟻與其他生物共生的例子。近期在台灣發現蟻科 (Formicidae)、家蟻亞科 (Myrmicinae) 瘤顎家蟻屬 (*Strumigenys*) 的兩種瘤顎家蟻 — 六龜瘤顎家蟻 (*Strumigenys liukueiensis*) 及墾丁瘤顎家蟻 (*Strumigenys konteiensis*) 分別與邵氏分針蟻 (*Ectomomyrmex sauteri*) 形成複合巢 (compound nests)。為了解及驗證瘤顎家蟻與邵氏分針蟻共棲之交互關係與機制，針對台灣產七種瘤顎家蟻 —六龜瘤顎家蟻、墾丁瘤顎家蟻、日本瘤顎家蟻 (*Strumigenys solifontis*)、節膜瘤顎家蟻 (*Strumigenys membranifera*)、愛美瘤顎家蟻 (*Strumigenys emmae*)、羅傑瘤顎家蟻 (*Strumigenys rogeri*) 以及新種瘤顎家蟻 (*Strumigenys* sp.) 與邵氏分針蟻分別進行共生試驗與觀察。觀察一對一行為與複合巢行為，及分別探討兩種類螞蟻個體在狹小空間相遇時產生之行為及兩種類螞蟻群落共棲對彼此的交互影響，並針對其結果進行分級。其中，羅傑瘤顎家蟻在複合巢行為試驗中，實驗組之間在生長趨勢及與邵氏分針蟻的互動關係具差異性，因此針對羅傑瘤顎家蟻之實驗組進行氣味分析，使用氣相層析質譜儀技術，探討羅傑瘤顎家蟻與邵氏分針蟻之表皮碳氫化合物 (CHC) 之差異。

結果/結論/應用啟示

依據複合巢行為結果，可將七種瘤顎家蟻分別歸類於四個等級中，等級由小至大以與邵氏分針蟻主要居住位置由近至遠進行分級。墾丁瘤顎家蟻屬於等級 I；六龜瘤顎家蟻為等級 II；等級 III 則有羅傑瘤顎家蟻與愛美瘤顎家蟻；日本瘤顎家蟻則歸類於等級 IV。在氣味分析結果中，實驗組與對照組的表皮碳氫化合物組成比較後，確實有數種表皮碳氫化合物在不同的複合巢結果中有不同的濃度與組成。日後研究可利用此分析結果，進一步探討邵氏分針蟻對不同的氣味是否會產生不同的行為模式。

關鍵詞（Keywords）：共生（Symbiosis）、複合巢（Compound nests）、瘤顎家蟻（*Strumigenys*）、邵氏分針蟻（*Ectomomyrmex sauteri*）、表皮碳氫化合物（Cuticular

hydrocabons）

OE_08

Evaluation of potential entomopathogenic fungi, *Beauveria bassiana* for controlling coffee berry borer *Hypothenemus hampei* (Ferrari) (Coleoptera: Curculionidae)

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背景/研究問題/材料方法

The coffee berry borer (CBB) *Hypothenemus hampei* (Ferrari) is the major pest of the coffee-producing countries in the world and caused economic losses in the coffee industry. With the concern that chemical control is harmful to the ecosystem, an alternative eco-friendly management strategy such as microbial control emerges as the times require. Herein, a total of thirty-three fungi were isolated from CBB cadavers and primarily selected by using larvae of *Tenebrio molitor* Linnaeus (Coleoptera: Tenebrionidae: Tenebrioninae). Two entomopathogenic fungal (EPF) isolates, NCHU-271 and NCHU-272, displaying fast insect-killing activity, were subjected to molecular identification, bioassay, and infestation test against CBBs.

結果/結論/應用啟示

Based on the molecular identification, the two EPF isolates were *Beauveria bassiana* and hereafter named "*Beauveria bassiana* -NCHU-271 (Bb-NCHU-271)" and "*Beauveria bassiana* - NCHU-272" (Bb-NCHU-272). Both of Bb-NCHU-271 and Bb-NCHU-272 caused 100% mortality at 8 days post inoculation (d.p.i.) (LT50= 4 days) by spraying 108 conidia/ml conidia suspension. Furthermore, an infestation test was performed to evaluate the differences in CBB control efficacy between the treatments of "CBBs exposed to EPF first" or "coffee fruits exposed to EPF first". Our results demonstrated that the "CBBs exposed to EPF first" of Bb-NCHU-272 exhibits lower survival rates and higher mycosis rates than those of Bb-NCHU-271 significantly. The control effeteness of Bb-NCHU-271 and Bb-NCHU-272 were slight in the "Coffee fruits exposed to EPF first" treatment. Two EPF isolates showed controlling ability to the CBBs either before or after CBBs borer into berries, while application of EPFs before the CBBs infestation is recommended.

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*）

OE_09

Caffeine produced in nectar strengthens energy metabolism and neural transmission in honey bees by activating cAMP signaling pathway

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背景/研究問題/材料方法

Caffeine is a common secondary metabolite in a rage of plant genus like *Coffea* or *Citrus*. As a protective chemical to plant, caffeine is produced at a level that is toxic to other organisms in leaves or seeds, preventing the consumption by herbivores. Interestingly, caffeine also exists in nectar in non-toxic level, thus pollinators such as honey bees also absorb caffeine during pollination. Previous studies discovered that caffeine combined with sugar reward induced stronger long-term memory and foraging ability of honey bees. However, the mechanism of caffeine to provide the benefits above is still under debate. Here, we focus on the interactions between adenosine receptor and caffeine, the antagonist. Behavioral experiments, chemical assays and molecular approaches were performed to investigate the complex mode of actions of caffeine in honey bees, especially to their central nervous system.

結果/結論/應用啟示

Cyclic AMP (cAMP) assay and proboscis extension response assay results indicated that both caffeine and adenosine exerted comparably biphasic effects and no antagonistic effects was observed. The increasing cAMP level induced the phosphorylation of transcriptional factor CREB and activated the expression of down-stream genes expression related to energy metabolism and synaptic plasticity. Calcium imaging and neurotransmitter analysis results revealed that caffeine intake significantly led to more vigorous neurotransmission activity. In conclusion, consumption of caffeine in nectar by honeybees could boost honeybees' energy metabolism via activating cAMP signaling pathway, and this activation subsequently increased neurological functions and may eventually improve long-term memory. Our study provides a new explanation to the mechanism of caffeine, which is different with previous concepts. The phenomenon of biphasic effects also demonstrates the potential of the interaction between adenosine receptor and another G protein-coupled receptors (GPCRs) in honey bee's brain. If so, this will be one of the first records of GPCR complexes among insect models.

關鍵詞（Keywords）：Honey bees (*Apis mellifera*), Caffeine, Adenosine, Energy metabolism, Neural transmission

OE_10

Identification of differential DNA methylated regions between different development of entomopathogenic fungi, *Beauveria bassiana* NCHU-157, by nanopore sequencing

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背景/研究問題/材料方法

The entomopathogenic fungi (EPF), *Beauveria bassiana* is an important and commonly used entomopathogenic fungi (EPF) for microbial control. The whole genomic DNA methylome of one promising EPF isolate, *B. bassiana* NCHU-157 (Bb-NCHU-157) was investigated by Oxford Nanopore Technologies (ONT) in this study.

結果/結論/應用啟示

The whole genome of Bb-NCHU-157 was resequenced by NGS and ONT. There are 16 contigs with 34.19 Mb and 50% GC content, which composed of 10,848 putative protein coding genes for the first genome draft. In the genome of Bb-NCHU-157, two putative *DNA methyltransferases* (DNMTs) were found, including *Dim-2* and *C-5 cytosine specific DNA methylase.* Both of DNMTs showed higher expression level in mycelium stage than those of conidia stage, besides, the *C-5 cytosine specific DNA methylase* showed much higher expression level than those of *Dim-2* in both different life stages. The whole genomic DNA methylation of Bb-NCHU-157 was unmasked by ONT. The global methylation level of mycelium stage is higher than that of conidia stage in both gene and transposon elements (TE) regions. Furthermore, the TE showed higher methylation frequency than gene region, especially in CHH site. In the gene regions, the high methylation frequency was found around the transcription start site (TSS) and transcription end site (TES). Moreover, the CG and CHG methylation are mainly happened in the promoter an intergenic region, while CHH methylation located in the TE region. Genes located in the DMR are commonly classified into the GO terms of DNA binding (GO:0003677), DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981), nucleic acid binding (GO:0003676) and protein serine/threonine kinase activity (GO:0004674) for hypermethylated in mycelium. The evaluation of DNA methylome in Bb-NCHU-157 by ONT provide new insight in this field. These data will be further validated and explored to the epigenetic regulation during development of *B. bassiana*.

關鍵詞（Keywords）：Oxford Nanopore Technologies (ONT), entomopathogenic fungi (EPF), *Beauveria bassiana*, DNA methylation, differential DNA methylated regions (DMR)

OE_11

球背象鼻蟲近緣種間的生殖隔離
Reproductive isolation of two sibling species of *Pachyrhynchus* weevils

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背景/研究問題/材料方法

生殖隔離是物種形成的關鍵因子，包括合子前隔離 (行為隔離、物理隔離或生態隔離) 和合子後隔離 (子代發育遲緩或子代不孕)。球背象鼻蟲 (*Pachyrhynchus*) 在台灣、菲律賓等島嶼上形成高度多樣化的分類群，然而物種如何形成及形成的機制仍然未知。本研究比較兩個近緣物種 *Pachyrhynchus moniliferus* 和 *P. orbifer* 之間合子前隔離 (雄性佔據雌性的時間、次數，同性之間的競爭、雌性抗拒與交配成) 與合子後隔離 (產卵量、孵化率、各齡期存活率、幼蟲與成蟲形態、發育時間與性別比) 的差異，探討個體是否偏好與同種交配，及純種後代是否比雜交後代具有更高的適存度。

結果/結論/應用啟示

在合子前隔離實驗中，雄性 *P. orbifer* 和雌性 *P. moniliferus* 偏好與同種交配，而雌性 *P. orbifer* 和雄性 *P. moniliferus* 與異種交配的機率比與同種高。同種交配時，異種的競爭強度較低，但雜交時，同種的競爭強度顯著較高。雌性 *P. moniliferus* 與同種交配時的抗拒強度顯著高於 *P. orbifer* 與同種交配時的抗拒強度。而合子後隔離實驗表明，從羽化到性成熟的雜交個體存活率顯著低於兩個純種。產卵量、孵化率、其餘齡期存活率、體長與發育時間在雜交與純種間並無顯著差異。本研究顯示 *P. orbifer* 和 *P. moniliferus* 的性擇偏好是不對稱的，可能因兩物種性別比的差異導致不同性別的生殖策略不同，而合子後隔離可能為兩姐妹物種生殖隔離的關鍵。

關鍵詞（Keywords）：雜交種化（hybrid speciation）、球背象鼻蟲（*Pachyrhynchus*）、合子前隔離（prezygotic isolation）、合子後隔離（postzygotic isolation）、種化（speciation）

OE_12

熱帶火蟻探索行為中的個體差異
Individual differences in *Solenopsis geminata* exploration

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背景/研究問題/材料方法

螞蟻被視為超級有機體，因此群體行為常被認為影響個體行為。然愈來愈多研究發現蟻巢內工蟻的行為表現具個體差異，且個體行為和群體行為間存在著關聯性，進而影響整個蟻巢的行為特性。先前研究發現多數熱帶火蟻 (*Solenopsis geminata*) 工蟻在陌生環境下會傾向以同方向繞圈的方式探索，有部分工蟻則會在探索時經常改變方向並花費較多時間。為瞭解工蟻的探索行為是否表現出個體差異，本研究觀察並記錄工蟻在開放環境中，重複三次面對相同情況時的探索行為與路徑變化，並進一步檢驗工蟻個體的探索行為是否影響整體蟻巢的群體探索方式，且不同蟻巢間的探索方式是否具有差異。

結果/結論/應用啟示

研究發現受測工蟻在開放環境下重複三次試驗後，可歸納出五種探索路徑。此五種探索路徑中，工蟻所花費的時間具有明顯差異，但不同蟻巢採取五種探索類型沒有差異。其中，使用彎曲路徑探索的工蟻，在不同蟻巢內其探索時間顯著不同。此外，探索路徑中有改變方向的工蟻個體比例在不同巢間有差異。在探索行為中，工蟻探索時間具有個體差異，不同蟻巢的探索平均時間具有顯著差異。熱帶火蟻工蟻在開放環境下採取的探索路徑多樣，此顯示工蟻採用不同的探索方式，增加其發現標的物的機會。當工蟻在探索時間上具有個體差異時，推測個體將影響同巢內群體的探索方式。

關鍵詞（Keywords）：熱帶火蟻（*Solenopsis geminata*）、工蟻（Worker）、探索行為（Exploration）、個體差異（Individual differences）

OE_13

共生菌 *Buchnera aphidicola* 參與豌豆蚜 *Acyrthosiphon pisum* 之生殖細胞發育

Endosymbiont *Buchnera aphidicola* participates in germline development of the pea aphid *Acyrthosiphon pisum*

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背景/研究問題/材料方法

In the asexual viviparous pea aphid *Acyrthosiphon pisum*, we have pinpointed the route of PGC migration which leads the germ cells to reach the embryonic gonads. However, we have not identified what signals guide the PGC migration. We observe one unique feature of PGC migration in the asexual *A. pisum*: the migrating PGCs are closely associated with the primary endosymbiont *Buchnera aphidicola* throughout embryogenesis ever since its initial invasion to the gastrulating embryo. We thus hypothesize that *B. aphidicola* may play a role in transmitting the attractive signals released from the embryonic gonads or producing repulsive signals to restrict PGCs on the right route of migration.

結果/結論/應用啟示

By eliminating *B. aphidicola* with antibiotics and tracing the germ cell development with the germline marker gene *Apvas1*, an orthologue of the conserved *Drosophila vasa* (*vas*), in the asexual *A. pisum*, we pinned down that the obligate endosymbiont *B. aphidicola* participates in the growth of germ cells during embryogenesis of *A. pisum*. *B. aphidicola* is involved in: (1) the proliferation of PGCs, of which cell proliferation of PGCs in the aposymbiotic *A. pisum* slowed down during invagination of the germ band and at the following stages, and (2) the germ plasm synthesis in the embryo with the formed germ band and the subsequent developments. These findings reveal that *B. aphidicola* is essential for aphid germline development and firstly indicate a developmental role of *Buchnera* in insects.

關鍵詞（Keywords）：豌豆蚜（*Acyrthosiphon pisum*）、巴克納氏菌（*Buchnera aphidicola*）、內共生生物（endosymbiont）、生殖細胞（germ cells）、生殖細胞移動（germline migration）

OE_14

Host synchronous hatching as an anti-parasite defence strategy in burying beetles

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背景/研究問題/材料方法

Group formation is key to group survival as a potential anti-predator strategy that dilutes the risk of attack per individual. For many egg-laying animals, within-clutch egg hatching demonstrates substantial variation, ranging from asynchrony to synchrony, thereby resulting in emergence of temporally different group sizes of offspring. While synchronous hatching is generally assumed to be adaptive in response to predation risk, direct evidence testing this hypothesis remains rare. Here, we hypothesised that synchronous egg hatching counteracts parasitism by the mites *Poecilichirus carabi* in the burying beetles *Nicrophorus vespilloides*. Burying beetles transport mites to carrion resource upon which both species breed, but mites could predate newly-hatched beetle larvae.

結果/結論/應用啟示

We showed that eggs hatched more synchronously when female beetles reproduced in the presence of mites than their absence. We further tested the adaptive significance of hatching synchrony by experimentally manipulating the hatching patterns as highly synchronous, synchronous, and asynchronous broods, in the presence or absence of mites. We found that mites reduced the reproductive success of beetles only when the larvae hatched asynchronously, which in turn, resulting in higher reproductive success of mites. Our results suggest that female beetles can adjust egg hatching patterns as a defensive strategy to swamp the mite predation risk, thereby enabling more offspring to survive.

關鍵詞（Keywords）：捕食風險（predation risk）、同步孵化（synchronous hatching）、埋葬蟲（burying beetles）、附生蟎（phoretic mites）、寄生（parasitism）

OE_15

什麼因素會影響掠食者對不利獵物的迴避程度？
What determines the degree of predator avoidance towards unprofitable prey? A meta-analysis.

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背景/研究問題/材料方法

Predators can often learn to avoid unprofitable prey through conditioned learning. The degree of predator avoidance towards a certain prey can be quantified as their attack probabilities - a low attack probability would signify high avoidance. Although it would be intuitive to hypothesize that prey unprofitability is an important determinant of predator attack probability, a few other factors can also play a role, such as property of the unconditioned stimulus (toxin or bitterness), the manner in which predators encounter prey (sequential or simultaneous), and the property of the conditioned stimulus (color, pattern, color and pattern, color and other [size, taste, and odor]). To test whether these factors determine predator attack probabilities against prey, I meta-analyzed 46 avoidance learning studies that quantified predator attack probabilities in an avoidance learning context. I used generalized linear mixed models, with attack probability as the response variable and the three aforementioned factors as predictors.

結果/結論/應用啟示

Overall, toxic prey resulted in moderately lower attack probilities than prey that were only bitter in taste. The attack probailities were also moderately lower when unprofitable prey were associated solely with colors, compared to when pattern cues are used or when color cues are coupled with either size, taste, or odor. Using both color and pattern cues as conditioned stimulus elicited highest attack probabilities, suggesting that these cues were less effective for predator education. Lastly, predators had lower attack probabilities when unprofitable prey were presented simultaneously with profitable prey. This suggested that predators which encounter prey in a more sequantial manner in nature (e.g., sit-and-wait predators or when prey do not congregate) might avoid unprofitable prey to a lesser extent. These findings have important implications to predator-prey interactions and the ecology and evolution of warning signals, highlighting the fact that predator avoidance is more than a consequence of prey unprofitability.

關鍵詞（Keywords）：avoidance learning, classical conditioning, warning signals,

aposematism, predator-prey interactions

農業昆蟲學

論文宣讀

Oral Session: Agricultural Entomology

OA_01

黃斑粗喙椿象與蘇力菌共同防治秋行軍蟲之效果評估

Evaluation of efficacy of combining *Bacillus thuringiensis* and *Eocanthecona furcellata* (Hemiptera: Pentatomidae) against *Spodoptera frugiperda* (Lepidoptera: Noctuidae)

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背景/研究問題/材料方法

鱗翅目 (Lepidoptera)、夜蛾科 (Noctuidae) 之秋行軍蟲 (*Spodoptera frugiperda* (J. E. Smith)) 於 2019 年入侵台灣，嚴重危害玉米等禾本科 (Poaceae) 作物生產。蘇力菌 (*Bacillus thuringiensis*) 為目前防治此害蟲最常用之病原微生物，雖較於有機合成化學農藥，其對環境友善，但防治效力易受到田間微環境及同時施用之其他藥劑等外在因素干擾。此外，大量施用蘇力菌製劑對於常存於田間的本土捕食性天敵之影響亦未知。這些天敵具可自行繁殖、主動尋找躲藏的害蟲等優點，若與蘇力菌製劑共同使用且不為拮抗，則可為害蟲整合管理 (IPM) 之重要操作模式，加速落實政府農藥減量政策。因此，本研究試以田間常見半翅目椿象科 (Hemiptera: Pentatomidae) 捕食性天敵黃斑粗喙椿象 (*Eocanthecona furcellata* (Wolff)) 及鮎澤品系 (aizawai strain) 蘇力菌進行共同防治秋行軍蟲測試，記錄椿象取食量、存活率及蛻皮狀況，評估兩種防治方法並行下對此害蟲之防治成效。

結果/結論/應用啟示

在黃斑粗喙椿象一齡若蟲接觸蘇力菌懸浮液試驗中，實驗組與對照組存活率皆為 100%。而二至四齡若蟲捕食餵食蘇力菌之秋行軍幼蟲試驗中，二、三齡若蟲齡期天數縮短但四齡若蟲不變。整體而言，僅有少數椿象個體死亡，且多數皆為在蛻皮或休息時遭秋行軍幼蟲咬傷導致。因本試驗樣本數較少，故田間是否適宜併用蘇力菌與此椿象防治秋行軍蟲，尚需更多資料佐證。

關鍵詞（Keywords）：秋行軍蟲（*Spodoptera frugiperda*）、蘇力菌（*Bacillus thuringiensis*）、黃斑粗喙椿象（*Eocanthecona furcellata*）、生物防治（biological control）

OA_02

臺灣家白蟻分解廢棄菇包之可行性評估
The possibility of decompose spent mushroom substrate with soil feeding termite

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背景/研究問題/材料方法

根據農委會資料統計，臺灣近 10 年來每年產生超過 10 萬公噸的廢棄菇包，是大宗的農業廢棄物，因其產量甚大，開發其潛在的處理及利用方式是值得探討的議題。本研究以臺灣家白蟻 (*Coptotermes formosanus*) 作為生物材料，以為期四週的試驗測試其取食香菇、木耳、金針菇廢棄菇包後的巢內個體存活率、個體體重變化率及取食效率，結果顯示白蟻去化廢棄香菇菇包效果最佳，因此我們更進一步以香菇菇包進行半年的試驗，了解是否可長期利用白蟻分解纖維素的特性，達到農業廢棄物減量之目的。

結果/結論/應用啟示

經過為期四週的取食測試，臺灣家白蟻取食香菇及木耳廢棄菇包後，皆有大於 70%的存活率，取食金針菇廢棄菇包的存活率則小於 20%；其中取食香菇廢棄菇包的巢群，工蟻的個體重量有顯著增加。香菇、木耳及金針菇三種廢棄菇包的每公克白蟻每日取食量依序為 22.9±3.8mg、21.2±6.7mg 及 13.8±9.2mg，以香菇廢棄菇包的取食量為最多。以香菇廢棄菇包為基質進行半年的白蟻飼養，結果顯示每公克白蟻每日取食廢棄菇包量為 0.15±0.07g；白蟻的個體成長率為 473±197%，蟻后個體重量由 9.1±1.7mg 成長至 28.5±8.5mg，成長率為 315±91%；工蟻個體重量由 1.8±0.3mg 成長至 2.8±0.6mg，成長率為 528±177%，皆有顯著增加。目前結果顯示臺灣家白蟻有分解香菇廢棄菇包的可行性，且有利用香菇廢棄菇包產生動物性蛋白質的潛力；而木耳廢棄菇包亦有進行長期測試的潛力。

關鍵詞（Keywords）：循環經濟（circular economy）、白蟻飼養（termite rearing）、農業廢棄物（agricultural waste）、臺灣家白蟻（*Coptotermes formosanus*）

OA_03

短期高溫對瓜實蠅產卵量與死亡率之影響
Effects of short-term high temperatures on egg production and adult mortality in melon fly *Zeugodacus cucurbitae* (Coquillett) (Diptera: Tephritidae)

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背景/研究問題/材料方法

高溫對昆蟲可能造成個體死亡、繁殖率下降的現象，已廣泛應用於農產品檢疫，以達到滅除瓜實蠅 (*Zeugodacus cucurbitae*) 之目標。依據國際植物防疫檢疫措施標準 (ISPM) 定義，系統性操作係採用搭配 2 種以上獨立的管理措施，如以防蟲網阻隔害物以降低入侵風險，惟溫網室中短期高溫環境對該成蟲是否造成不利的影響尚無文獻紀錄。本研究以實驗室高溫暴露測試瓜實蠅成蟲致死所需之溫度，並模擬溫室高溫變化狀況紀錄對瓜實蠅成蟲所可能造成的死亡率及對產卵之影響，實際溫室田間溫度對成蟲之影響亦在本研究中紀錄，以作為建立非疫生產操作管理技術之參考。

結果/結論/應用啟示

室內以不同高溫處理試驗結果顯示當溫度達 45℃ 處理 1 小時以上可達到所有成蟲全數死亡。模擬溫室溫度試驗結果發現性成熟蟲經三天處理後之死亡率 (30%) 與未性成熟蟲 (10%) 皆顯著高於未經處理之對照組。田間網室試驗結果則顯示經三天處理後，成熟蟲及未性熟蟲之死亡率分別達到 64% 及 70%。經三天網室短暫高溫處理後，成熟雌蟲產卵量較處理前減少達 96%，且顯著低於未經處理之對照組。兩試驗結果顯示連續三天暴露於短暫高溫環境不但顯著提高瓜實蠅成蟲之死亡率，亦對雌蟲造成產卵上的抑制作用。此結果可應用於系統性操作管理的網室非疫生產模式，製造不利於瓜實蠅生存的環境。

關鍵詞（Keywords）：瓜實蠅（*Zeugodacus cucurbitae*）、系統性操作（systems

approach）、非疫生產點（pest-free production site）、檢疫（quarantine）、網室（greenhouse）

OA_04

Identification of mutations associated with insecticide resistance in *Plutella xylostella* (Lepidoptera: Plutellidae) populations from Taiwan

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背景/研究問題/材料方法

The diamondback moth, *Plutella xylostella* (Linnaeus) (Lepidoptera: Plutellidae), is a serious pest of crucifers and notorious for developing resistance to insecticides. The present study investigated the insecticide resistance and mutations frequency of *P. xylostella* populations collected from five major cruciferous growing areas in Taiwan. The mutations frequency in the nicotinic acetylcholine receptor (nAChR), voltage-dependent sodium channel (VDSC) and ryanodine receptor (RyR) to these populations were determined. In nAChR, three amino acid deletion and α6 intron 9 mutations, and in VDSC F1845Y and V1848I were identified. Similarly, in RyR, E1338D, Q4594L, I4790M, I4790 K, and G4946E mutations were detected.

結果/結論/應用啟示

Bioassay results showed high levels of resistance to spinosad, indoxacarb, metaflumizone, and chlorantraniliprole in the surveyed populations except in Taichung. The resistance ratios ranged from 2.376 to 1,236-fold for spinosad and 24.63–1,511-fold for indoxacarb. Similarly, those for metaflumizone and chlorantraniliprole, were 2.563–76.21- and 4.457–683.0-fold, respectively. To date, only G4946E mutation was detected in these field strains. More identifications of mutations frequency are going on, hopefully, all the mutations will be determined in the near future. These findings are useful for the effective control and insecticide resistance management of *P. xylostella*.

關鍵詞（Keywords）：Diamondback moth, Insecticide resistance, Mutation frequency

OA_05

造瘿昆蟲之天敵寄生蜂多樣性與棲地組成—以刺桐釉小蜂為例
Habitat composition and the diversity of parasitoid wasps of *Quadrastichus erythrinae*

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背景/研究問題/材料方法

刺桐釉小蜂 (*Quadrastichus erythrinae* Kim) 造瘿危害刺桐屬 (*Erythrina*) 植物，於 2004 年入侵台灣，目前主要以注射化學藥劑防治，然為避免害蟲產生抗藥性與傳統防治帶來的環境風險，仍宜發展對造瘿害蟲具有高防治效益且對環境影響低的本土天敵及保育型生物防治 (conservation biological control)。本研究針對台灣中部 13 個樣點進行調查，分析樣點周圍 1km 之棲地組成特性，含農、林、交通、水利、建築及其他，並於 2021 年 10 月至 2022 年 1 月每個月進行取樣，每個樣點選擇三棵樹各採一 10-15cm 危害程度較高的帶瘿枝條，置於網箱待寄生蜂羽化後進行鑑定與計量分析，探討寄生蜂多樣性與棲地組成間之關係，進而篩選於各式棲地組成具防治潛力的寄生蜂物種。

結果/結論/應用啟示

冬季四個月分的調查包含 52 筆樣本，共收集 2,582 隻寄生蜂個體，分屬 15 科 53 形態種，其中以釉小蜂科的 *Aprostocetus felix* 佔總數的 58% 且 9 個樣點皆有紀錄，顯示具廣泛分布及高防治潛力。迴歸與聚類分析則顯示寄生蜂多樣性與棲地組成間的關聯性低，即具高比例農及林地的樣點並未具有高寄生蜂物種豐度。但本研究成果提出之優勢寄生蜂仍可作為發展刺桐釉小蜂生物防治之參考，而以目前單一季節分析的初步結果指出，刺桐之造瘿害蟲的寄生蜂多樣性及來源，受鄰近棲地組成影響較小。後續仍需加入其他季節之調查結果，以求完整的評估不同寄生蜂之防治潛力與多樣性。

關鍵詞（Keywords）：刺桐釉小蜂（*Quadrastichus erythrinae*）、棲地組成（Habitat composition）、生物多樣性（Biodiversity）、寄生蜂（Parasitoid wasp）、造瘿昆蟲（Gall inducing insect）

OA_06

對甲基丁香油不敏感之東方果實蠅族群生殖潛力
Reproductive potential in methyl eugenol non-sensitive male oriental fruit fly, *Bactrocera dorsalis*

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背景/研究問題/材料方法

甲基丁香油 (methyl eugenol, ME) 是東方果實蠅 (*Bactrocera dorsalis*) 雄蠅性費洛蒙的前驅物，作為高效率的揮發性誘引物質，為臺灣滅雄法中主要的防治資材。ME 已被使用數十年之久，然近年報告指出野外存在對 ME 不敏感的雄蠅，可能使滅雄法出現破口。對 ME 不敏感的特性具有遺傳性，因此本實驗室經由累代篩選，維持族群中不敏感雄蠅的比例，首次探討對 ME 不敏感雄蠅的生殖行為與潛力。

結果/結論/應用啟示

在實驗室品系群體交尾實驗中，果實蠅雄蠅取食或暴露 ME 後 3 天對雌蠅的吸引力較未接觸 ME 的雄蠅具有顯著上升的現象；單隻雌蠅的交尾選擇實驗中，ME 敏感品系雄蠅經 ME 暴露後，交尾機會顯著高於對 ME 不敏感的雄蠅。此外，雖然對 ME 敏感雄蠅雖經 ME 暴露後其交尾維持時間顯著長於其他未接觸或不敏感品系的雄蠅，但延長交尾時間並不會對其後代的卵數 (繁殖力) 或後代的孵化率 (生育力) 產生正面的影響，反而使卵的孵化率顯著下降。而對 ME 不敏感的雄蠅在經過 ME 的暴露之後一樣出現孵化率下降的現象。然而，目前仍須透過 ME 篩選不敏感雄蠅，因此，沒辦法準確的反映出未受到 ME 影響下，不敏感雄蠅的生殖潛力。而縱使作為有強烈誘引效果的性費洛蒙前驅物，對於雄蠅的生殖潛力卻不盡然完全帶來正面的效果。

關鍵詞（Keywords）：東方果實蠅（*Bactrocera dorsalis*）、甲基丁香油（Methyl eugenol）、交尾機會（Mating chance）、生殖潛力（Reproductive potential）

OA_07

僞菜蚜 (半翅目：常蚜科) 於三種寄主上之生活史與族群介量
The life history and population parameters of *Lipaphis erysimi* (Hemiptera: Aphididae) on three hosts

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背景/研究問題/材料方法

偽菜蚜屬半翅目 (Hemiptera)、常蚜科 (Aphididae)，為刺吸式口器之小型害蟲，可對多種十字花科作物造成危害，於我國蔬菜田區普遍發生。此蟲生活史短，且行孤雌生殖，多數群聚於葉背及新芽吸食危害，造成葉片皺縮、變形，嚴重時呈現乾枯、黃化，影響作物品質及商品價值。本研究於 25°C、相對濕度 80%、光週期 12:12 (L:D) 之條件，以青花菜、甘藍與蘿蔔三種不同十字花科蔬菜為寄主，探討偽菜蚜之生活史及族群介量，瞭解不同寄主對此蟲基礎生態及族群表現之影響。

結果/結論/應用啟示

偽菜蚜於青花菜、甘藍及蘿蔔上，不同齡期若蟲之發育時間皆不具顯著差異。幼期之發育時間分別為 5.14、5.61 及 5.14 日，以甘藍上之發育時間顯著較長。成蟲壽命於青花菜、甘藍及蘿蔔上分別為 14.71、15.47 及 13.17 日。成蟲繁殖前期 (APRP) 及全期繁殖前期 (TPRP) 於甘藍上最短，分別為 0.53 及 6.14 日；繁殖天數 (Reproduction days) 於甘藍上最長，為 13.50 日。於青花菜、甘藍及蘿蔔之平均繁殖量分別為 68.32、77.92 及 47.50 offspring/female，以甘藍之繁殖量最高。族群表現上，青花菜、甘藍及蘿蔔之淨繁殖率 (R_0) 分別為 65.97、73.82 及 38.00 offspring/individual；內在增殖率 (r) 及終極增殖率 (λ) 以甘藍上較高，分別為 0.4065 及 1.5016 day^{-1}；平均世代時間 (T) 於青花菜上為 10.37 日最短，而於蘿蔔上為 11.12 日則最長。

關鍵詞（Keywords）：偽菜蚜（*Lipaphis erysimi*）、青花菜（*Brassica oleracea* var. *italic*）、甘藍（*Brassica oleracea*）、蘿蔔（*Raphanus sativus*）、族群介量（population parameters）

OA_08

昆蟲寄生真菌紅綬麴菌在蟻害物種疣胸琉璃蟻中盛行率的研究
The prevalence of entomopathogenic fungus *Aspergillus nomius* in its pest ant host *Dolichoderus thoracicus*

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背景/研究問題/材料方法

疣胸琉璃蟻 (*Dolichoderus thoracicus*) 為台灣新興蟻害物種，在危害地區形成超級群落 (Supercolony)，主要危害包含對果園、住宅造成干擾，而紅綬麴菌 (*Aspergillus nomius*) 為疣胸琉璃蟻的昆蟲致病真菌，因此以紅綬麴菌做為一具潛力的生物防治製劑，了解其在疣胸琉璃蟻超級群落中的盛行情況、傳播能力以及菌株本身的產毒情況有助於評估其作為生物防治製劑的可行性。因此本研究針對 (1) 疣胸琉璃蟻超級群落內的衛星巢進行樣本採集，並使用微生物培養鑑定 (Microbiological culture) 以及即時聚合酶連鎖反應 (Real-time PCR) 檢測紅綬麴菌的盛行率，(2) 透過施灑分生孢子液，檢測紅綬麴菌的在群落中的盛行率變化，最後 (3) 以電噴灑游離質譜法 (LC-ESI-MS) 對 JYC640 紅綬麴菌菌株進行黃麴毒素 (Aflatoxin) 檢測以評估其作為疣胸琉璃蟻的生物防治製劑的可能性。

結果/結論/應用啟示

本研究總共檢測 33 個衛星巢，微生物培養鑑定與即時聚合酶連鎖反應所測得知盛行率皆為 3.03%；在噴灑分生孢子液後其盛行率在噴灑後第四天提升至 36.4%；LC-ESI-MS 檢測紅綬麴菌 JYC640 菌株，顯示其菌落產生黃麴毒素 B1、B2。本研究顯示施灑紅綬麴菌分生孢子能夠提高疣胸琉璃蟻群落中的盛行率，但同時需考慮其潛在的毒性風險。

關鍵詞（Keywords）：疣胸琉璃蟻（*Dolichoderus thoracicus*）、紅綬麴菌（*Aspergillus nomius*）、盛行率（Prevalence rate）、生物防治（Biological control）

OA_09

在臺灣以推拉技術防治秋行軍蟲之可行性
The availability of push-pull technology for fall armyworm pest control in Taiwan

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背景/研究問題/材料方法

秋行軍蟲為新興入侵鱗翅目害蟲，對我國玉米、高粱等作物造成嚴重危害。由於其咬食習性以及具有長遷特性，如何防治秋行軍蟲成為一個重要課題。本研究利用推拉技術 (push-pull technology) 探討對於秋行軍蟲防治之可行性。推拉技術為田間種植主要作物以及間作忌避植物，透過忌避植物散發揮發性物質產生推力，使害蟲遠離寄主植物或吸引其天敵前來；拉力則是於田周遭種植陷阱植物，亦會散發揮發性物質誘使害蟲前來啃食或產卵，並透過其自身防禦機制使害蟲無法存活。

本研究分兩個部分，第一部分為直接餵食秋行軍蟲不同狼尾草品系，計算其啃食面積及幼蟲存活率，選出適合田間試驗的狼尾草。此外，將狼尾草與玉米進行田間試驗，並依危害程度定期評分，藉此選出對害蟲具較佳吸引力之狼尾草品系；第二部分將陷阱植物及忌避植物分別餵食秋行軍蟲，紀錄幼蟲之重量、存活率、羽化率。

結果/結論/應用啟示

我們已利用幼蟲存活率篩選出數十種不同狼尾草品系並進行田間試驗。此外，餵食陷阱植物及數種忌避植物後，秋行軍蟲幼蟲重量及存活率與餵食玉米相比均有顯著差異，藉此探討忌避植物與陷阱植物在臺灣應用時的成效。

關鍵詞（Keywords）：秋行軍蟲（*Spodoptera frugiperda*）、推拉技術（push-pull technology）、狼尾草（Napier grass）

OA_10

帶抗褐飛蝨基因 *Bph17* 水稻品系之蛋白質體分析
Proteomics analysis of rice lines with brown planthopper resistance gene *Bph17*

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背景/研究問題/材料方法

褐飛蝨 (*Nilaparvata lugens* (Stål)) 為主要的水稻害蟲之一，其主要透過刺吸式口器於稻叢基部取食，危害嚴重時會導致水稻植株大量枯萎，稱為「蝨燒」，進而導致水稻嚴重減產。在實驗室前人研究發現水稻帶有抗褐飛蝨基因 *Bph17* 其抗蟲性不受溫度跟二氧化碳上升及氮肥施用多寡而影響。因此，本研究探討抗褐飛蝨基因 *Bph17* 如何調控水稻生理變化進而進行植物防禦反應。比較水稻感蟲品種 IR24 及帶有 *Bph17* 抗性基因之近同源系 (near-isogenic line) (NIL-*Bph17*) 在水稻處理褐飛蝨後第 0 天、第 1 天、第 4 天利用四極桿飛行時間質譜儀以非標定定量技術 (sequential window acquisition of all theoretical fragment ion spectra；SWATH) 分析其葉鞘蛋白質體表現。

結果/結論/應用啟示

質譜儀上機結果可鑑定出 815 種葉鞘蛋白質，並從其中篩選出訊號品質優良的 192 種蛋白質進行後續分析。透過主成分分析可以發現，樣本會因不同處理、時間、品種分群的趨勢。再進一步比較第 1 天到第 4 天時的蛋白質變化，在兩品種間有 73 個蛋白質具有表現量差異；在褐飛蝨吸食後有 43 個蛋白質出現表現量的變化；第 1 天到第 4 天有 42 個蛋白質出現表現量的改變。在目前的分析中可以知道 IR24 與 NIL-*Bph17* 兩水稻品種面對褐飛蝨吸食產生的生理變化具有差異，這可能使得 NIL-*Bph17* 有更優良的抗蟲性。

關鍵詞（Keywords）：褐飛蝨（Brown Planthopper）、蛋白質體（proteomics）、*Bph17*

OA_11

暖化和乾旱對大豆表現與蚜蟲、螞蟻、瓢蟲互動關係的影響
Effects of warming and drought on soybean performance and soybean aphid-ant-lady beetle interactions

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背景/研究問題/材料方法

Climate change events, such as warming and drought, will occur more often in this century, but their interactive effects on food security (e.g., crop production) and species interactions (e.g., herbivory, mutualism, predation, and antagonism) remain unclear. To help fill this knowledge gap, this study investigated how two climate change events (warming and drought) may interactively affect 1) crop growth and production, and 2) species interactions (e.g., mutualism and predation) on crop plants. Specifically, this study focused on a crop system in Taiwan, including soybean plants (*Glycine max*), aphids (*Aphis glycines*), lady beetles (*Cheilomenes sexmaculata*), and ants (*Anoplolepis gracilipes*). We conducted a laboratory experiment with a 2x2x2x2 factorial design, including the temperature (control/+3°C warming), soil water content (control/drought), ant (presence/absence), and lady beetle (presence/absence) treatments. Note that each replicate of a treatment combination at least had aphids on a caged soybean plant. We recorded crop performance, aphid populations, and ant and lady beetle mortality.

結果/結論/應用啟示

The results show the following: 1) Warming and drought commonly interacted with each other and species interactions and affected crop growth and production, suggesting that any estimation on crop production based on individual factors only may not reflect the reality. 2) Under warming, lady beetles significantly suppressed aphid population, implying that biocontrol of pests (aphids) by natural enemies (ladybeetles) may become more efficient under warming. 3) Under warming, ant mortality increased with lady beetle presence, suggesting that warming may intensify the lady beetle-ant conflict (i.e., predation on pests vs. mutualism with pests). Taken together, the results suggest that evaluating food security this century should consider the interplay between abiotic (climate change) and biotic (species interaction) factors.

關鍵詞（Keywords）：氣候變遷（climate change）、暖化（warming）、乾旱（drought）、物種交互作用（species interaction）、糧食安全（food security）

OA_12

Black soldier fly is the answer of the protein crisis! The development of an alternative protein source in Japan

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背景/研究問題/材料方法

The black soldier fly (*Hermetia illucens*, BSF hereafter) has been considered a novel protein source because its larvae convert organic wastes into high-quality protein. A large-scale BSF rearing system has been developed in many countries, however, a similar system could not be implemented in Japan because of some social concerns. In addition, the composition of organic wastes in Japan is highly different from those countries. Therefore, it is necessary to establish an applicable rearing system for BSF in Japan. To assess the performance of BSF larvae when they are feeding on organic wastes in Japan, 24 types of wastes including Toufu, Natto, Shochu lees, and coffee residue were used as BSF feeds. Twenty BSF larvae (7-day old) were weighed and fed with organic wastes (100g, water content ca. 70%) under 25°C with 60% RH, and the performance was evaluated after 7 days. Subsequently, the ratio of coffee and bread residue was combined and adjusted for developing an optimum diet for BSF. Finally, the effects of the BSF meal were evaluated by measuring the growth of seabreams (*Pagrus major*) through feeding trials. Several fish feeds, which contained different ratios of fishmeal and BSF meal, were prepared for the trials. The growth rate was recorded individually.

結果/結論/應用啟示

The survival rate of BSF larvae on organic wastes was higher than 85%, but the weight gain varied with different waste categories (0.2 – 148%). In addition, BSF larvae showed the best performance when they feed on a 3:1 ratio of coffee and bread residue. The rearing experiment of seabreams suggests that the substitution of fishmeal with up to 50% of BSF meal does not affect the growth of seabreams negatively. These results indicate that BSF is a promising and sustainable protein alternative for the use of aquaculture.

關鍵詞（Keywords）：黑水虻（black soldier fly）、蛋白質危機（protein crisis）、有機廢

棄物（organic wastes）、替代性蛋白質（protein alternatives）、水產養殖（aquaculture）

OA_13

我國新紀錄種蟲生線蟲於秋行軍蟲生物防治之應用潛力初探
Assessment of the biological control potential of new record entomopathogenic nematode species against fall armyworm

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背景/研究問題/材料方法

The fall armyworm *Spodoptera frugiperda* (FAW) invaded Taiwan in 2019. It caused serious economic production loss of corn, sorghum, and rice, and no effective management method is currently available for organic farms. Many studies have shown the efficacy and discussed the environmentally friendly benefit of applying entomopathogenic nematodes (EPNs) for agricultural pest management. However, no local EPN product are available on the market in Taiwan. Therefore, this study aimed to (1) extract local EPN populations through soil baiting and white trap techniques, (2) identify the EPNs and their symbiotic bacteria through culture-based and molecular methods, including morphological measurements and sequences analysis of ribosomal genes, and (3) evaluate their parasitism efficacy against FAW through inoculation experiments.

結果/結論/應用啟示

During 2019 to 2020, soils from 45 sites in Northern Taiwan were surveyed for EPN. Two new record species, *Pristionchus pacificus* and *Oscheius myriophilus,* were extracted and identified. After further isolation and culture processes with selective media, *Serratia marcescens*and *Achromobacter insuavis* were isolated from *P. pacificus*, and *Cupriavidus* spp, *Pseudomonas* spp. *Variovorax* spp. and *Stenotrophomonas* spp. were isolated from *O. myriophilus*. Among them, *C. malaysiensis* and *V. paradoxus* resulted in 41% and 30% mortality rates after inoculation on FAW 3rd instar larvae, respectively. Moreover, suspensions of 6 bacteria isolates reduced the FAW pupae eclosion rate significantly after injection. These isolates belong to *P. putida*, *C. alkaliphilus* and *C. malaysiensis*. In sum, this study describes two new record EPN species in Taiwan, provide the information of their symbiotic bacteria and the biological control application potential against FAW. Our findings set a foundation for local EPN research and future product development.

關鍵詞（Keywords）：蟲生線蟲（entomopathogenic nematode）、秋行軍蟲（fall armyworm）、生物防治（biological control）、共生細菌（symbiotic bacteria）、新紀錄種（new record species）

OA_14

利用 AI 智慧感知技術建構溫室番茄關鍵害蟲管理專家系統
Constructing an expert system for greenhouse tomato key pest management based on AI Smart Sensing Technology

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背景/研究問題/材料方法

傳統害蟲綜合管理在台灣因面臨從農人口高齡化及缺工問題、害蟲辨識不易、監測費時耗力、防治決策上常因資訊複雜難以分析而錯失防治時機，導致生產者應用意願低，實有必要改進以自動化替代傳統人力決策，提高整體生產效率。本研究應用自動監測裝置監測溫室番茄上關鍵害蟲-銀葉粉蝨 (*Bemisia argentifolii* = *B. tabaci* b type) 發生密度，並以傳統懸掛黃色黏板誘集粉蝨為對照，以綜合管理模式中銀葉粉蝨防治基準為 50 隻/黏板/週，達到防治基準應採防治措施為基礎，透過專家系統提供決策分析，進驗證行應用效果。

結果/結論/應用啟示

結果顯示以自動監測裝置及黃色黏板監測粉蝨族群密度兩者趨勢一致。在粉蝨辨識及計算數量上，以系統自動影像辨識每張黏板為 6 秒，人工辨識計數依誘得蟲數多寡所需時間為 1 至 15 分鐘以上，其所需時間為自動辨識粉蝨之 10-150 倍。自動辨識系統在低於 50 隻/黏板的準確率約為 70-80%，以機器辨識計算的蟲數在防治上具參考價值。於伸港及新社兩溫室驗證以自動監測裝置監測番茄銀葉粉蝨發生族群變動進行管理之依據，結果顯示壓制媒介銀葉粉蝨密度低於 50 隻/黏板，配合清除溫室內病毒株能預防帶毒粉蝨傳播至健康植株，避免病毒蔓延，減少農損。

關鍵詞（Keywords）：銀葉粉蝨（*Bemisia argentifolii* = *B. tabaci* b type）、害蟲綜合管理（integrated pest management）、人工智慧（artificial intelligence）、自動監測（Automatic monitoring）

OA_15

小圓胸小蠹蟲 (鞘翅目：象鼻蟲科) 於台灣田間之季節動態
Seasonal dynamics of *Euwallacea fornicatus* species complex (Coleoptera: Curculionidae) in the field of Taiwan

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背景/研究問題/材料方法

The *Euwallacea fornicatus* species complex, commonly referred to as shothole borers (SHB), is native to South- and Southeast Asia, but has invaded many locations over the globe. This complex includes four cryptic species that infest a wide range of plant species including several economic crops. Their hidden lifestyle inside wood could lead to an underestimation of the impact of these beetles on their host plants, consequently the economic impact of these beetles in crops in Taiwan is unknown. Here, we determine the presence of these beetles in four crops in Taiwan: avocado, cocoa, tea and lychee. Infested logs were collected from each of these crops, and adults emerging from the logs were identified using their COI sequences. We also used sticky traps with attractant lures to monitor their flight dynamics in these crops.

結果/結論/應用啟示

The peak flight activity of the species complex occurred between October and March based on monitoring data from four orchards. The beetles were identified as *E. fornicatus s. s.* Eichhoff, *E. kuroshio* Gomez & Hulcr, *E. perbrevis* Schedl and a taxonomically ambiguous taxon, simply referred to as H22 here. *E. fornicatus s. s.* is the most dominant taxon in Taiwan, followed by *E. kuroshio*, H22 and *E. perbrevis*. Although temperatures in Taiwan were favorable for SHB flight over the majority of the year, the peak flight of the SHB coincided with the driest time of year. In contrast, flight activity during the summer months was consistently low, coinciding with the summer monsoon rainfall, suggesting that precipitation is a key factor affecting their flight activity. This study provides a baseline information of species composition and annual activity of SHB that would be conductive to management of this pest in Taiwan.

關鍵詞（Keywords）：ambrosia beetle, polyphagous shothole borer, Kuroshio shothole borer, tea shothole borer

OA_16

粉斑螟蛾 (*Cadra cautella*) 以四種穀物副產物飼育之生活史探討

Research on the life cycle of almond moth (*Cadra cautella*) rearing in four kinds of by-product of grains

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背景/研究問題/材料方法

粉斑螟蛾 (*Cadra cautella*) 為儲藏性穀物及果乾的重要鱗翅目害蟲，幼蟲可於食物內吐絲生長，造成入侵產品的污染損失。除了害蟲的角色之外，粉斑螟蛾所產下的卵可用於作為大量飼養小黑花椿象及草蛉的食物，為重要的天敵餌料食物來源。本研究以 4 種常見的穀物副產物，分別以米糠、麥麩、粉頭及玉米粉作為食物基質進行飼養，以蘇式人工飼料作為正對照組進行比較，探討粉斑螟蛾於不同食料下的卵期、幼蟲期、蛹期及雌成蟲產卵量，評估粉斑螟蛾於不同穀物副產物之生長狀況，作為未來發展人工飼料之基礎研究。

結果/結論/應用啟示

餵食不同食物基質之粉斑螟蛾卵期約為 3.15～3.24 天。幼蟲期以蘇式人工飼料所飼養的粉斑螟蛾的生長天數最短，僅為 17.8 天；其次為米糠、麥麩及粉頭，分別為 22.73、24.36 及 33.34 天；其中餵食粉頭雖可以羽化成成蟲，但是生長狀況不佳，無法進行後續的試驗；而餵食玉米粉則無法生長。粉斑螟蛾蛹期於各種食物基質餵食下並無顯著差異，約為 5.64～8.24 天。比較羽化交配後的雌成蟲產卵數，約為 183.2～196.4 顆，統計上並無顯著差異。本研究發現不同食物來源僅影響幼蟲之生長天數，並不影響成蟲產卵數量，未來可以考慮將米糠或麥麩作為飼育粉斑螟蛾之飼料基質的成分。

關鍵詞（Keywords）：粉斑螟蛾（*Cadra cautella*）、食物基質（food substrate）、生活史（life cycle）、穀物（grains）、副產物（by-product）

OA_17

柑橘類揮發物利用於柑橘木蝨誘引劑的可能配方探討
The promising formula of citrus volatile compounds that attract *Diaphorina citri* Kuwayama (Hemiptera: Liviidae)

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背景/研究問題/材料方法

亞洲柑橘木蝨 (*Diaphorina citri* Kuwayama) 為柑橘黃龍病的主要傳播媒介，其感染柑橘植株造成重大農業損失。本研究嘗試找尋有效的化合物以製作誘引劑。試驗中分別以四種柑橘類氣味作為誘引氣味樣本，以氣相層析質譜儀 (GC-MS) 進行樣本化合物分析，利用 Y 型管測試柑橘木蝨偏好性，以具偏好性樣本測試黃色黏板提升誘捕率效果。

結果/結論/應用啟示

Y 型管試驗顯示，四種柑橘類氣味柑橘木蝨僅以 62.18 % 顯著偏好甜橙精油，而甜橙精油主要 8 種化合物的四種不同濃度混合物皆無使柑橘木蝨表現偏好性，以 100 ppm 的樣本配置法為基礎，依序移除其中一種化合物，發現柑橘木蝨以 37.43 % 與 37.71 %顯著不偏好移除檸檬烯 (Limonene) 與瓦倫烯 (Valencene) 的氣味，後分別以檸檬烯 (Limonene) 與瓦倫烯 (Valencene) 之混合物與剩餘 6 種化合物之混合物進行誘引性測試，結果發現柑橘木蝨以 62.64 % 對檸檬烯與瓦倫烯混合物產生顯著偏好，而對剩餘 6 種化合物沒有顯著偏好反應；黃色黏版以甜橙精油提升捕獲率試驗表明甜橙精油能在試驗後 3 小時至 8 小時間顯著提升黏板捕捉效率，其捕獲指數在 27.27 ~ 40 間。

試驗結果顯示甜橙精油氣味中的化合物具有發展誘引劑的可能性，尤其以檸檬烯與瓦倫烯可能最具發展潛力，未來若要持續開發柑橘木蝨誘引劑，或許能以此兩種化合物作為基礎，進行進一步的試驗，以獲得更好的誘引劑。

關鍵詞（Keywords）：亞洲柑橘木蝨（Asian citrus psyllid）、柑橘黃龍病（Huanglongbing）、氣相層析質譜儀（Gas Chromatography-Mass Spectrometry, GC-MS）、誘引劑（Attractant）、黃色黏板（Yellow sticky trap）

OA_18

以最大熵模型 MaxEnt 評估兩種水稻害蟲：馬來西亞稻黑蝽 *Scotinophara coarctata* 及水稻癭蚋 *Orseolia oryzae* 入侵可能性之初探。

An explore of MaxEnt modeling used to evaluate the invasion potential of two rice pests: *Scotinophara coarctata*, and *Orseolia oryzae*.

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背景/研究問題/材料方法

馬來西亞稻黑蝽 *Scotinophara coarctata* 及水稻癭蚋 *Orseolia oryzae* 為兩種東南亞重要水稻害蟲且目前尚未分佈於台灣，本研究藉由 SDMs 中最大熵 (Maximum entropy, MaxEnt) 模型，運用 GBIF 蒐集物種於冬南亞地區之分布點位以及 19 種環境變數 (Environment Variable)，推估兩種潛在入侵害蟲於台灣地區之分布機率。

結果/結論/應用啟示

結果顯示兩種害蟲於台灣之分布區域皆以以西部平原、宜蘭平原及花東縱谷等水稻耕作區域為最可能發生區域，其中 *S. coarctata* 適生機率為 0.09-0.53，以恆春半島最南端為分佈機率最高區域；*O. oryzae* 適生機率為 0.17-0.53，以嘉南平原西部沿海及恆春半島南端為發生機率最高區域。本研究以 MaxEnt 模型所推估害蟲適生機率可協助訂定害蟲入侵時之高風險區域，藉此擬定熱點界定及緊急防治策略。

關鍵詞（Keywords）：最大熵模型（Maximum Entropy Model）、物種分布模型（SDMs）、水稻害蟲（Rice Pest）

OA_19

Effective strain screening of entomopathogenic fungi *Beauveria bassiana* on banana pseudostem weevil, *Odoiporus longicollis* (Coleoptera: Dryophthoridae)

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背景/研究問題/材料方法

Banana is not only one of the most important crops in the world but also the fourth valuable edible plants. However, banana plants were often attacked by the stem borer, banana pseudostem weevil (BSW) *Odoiporus longicollis*, causing serious stem damage and economic loss. As the world environmental protection awareness increased, the use of chemical pesticides may cause many external costs. In our observation, *Beauveria* is the most common entomopathogenic fungi which infects *Odoiporus longicollis* in the northern Taiwan. This study is aimed to screen for effective strains of *Beauveria bassiana* collected from the field and compare with the only on stock *Beauveria* strain A1 in Taiwan.

結果/結論/應用啟示

The species of *Beauveria* isolates collected from field are confirmed as *Beauveria bassiana* using ITS, nrLSU, *tef1-a* and *rpb2* sequence. Among all of the isolates, strain SF404 is the most bio-effective, the mortality rate of strain SF404, SF303, SF124 and A1 were respectively 93.3%, 83.3%, 73.3% and 30% at 3 × 10^8conidia/ml concentration on adult BSW after 12 days' infection. The spore germination rate of strain SF124, SF303 and SF404 can all reach over 90% after 24 hours on PDA medium at 24℃ incubation. Based on the experiment data, these new strains of *Beauveria bassiana* provide a potential microbial agent to control BSW.

關鍵詞（Keywords）：香蕉假莖象鼻蟲（*Odoiporus longicollis*）、白殭菌（*Beauveria bassiana*）、蟲生真菌（entomopathogenic fungi）、微生物製劑（microbial control agent）

OA_20

臺灣木瓜上的節蟎
Eriophyid mite (Acari: Eriophyidae) on papaya from Taiwan

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背景/研究問題/材料方法

木瓜 (*Carica papaya*) 為我國重要經濟果樹，除常見大規模網室栽培，也常見於居家少量露天栽培。2021 至 2022 年間，在南投、台中與金門的木瓜植株，發現其下位葉的葉表或葉緣呈現局部不規則狀的黃褐色斑紋，經採集初步鑑定，確認由節蟎引起。國外已記錄四種節蟎 (Eriophyidae) 造成木瓜葉片局部焦黃或捲起 (*Aculops caricae*、*Calacarus brionesae*、*C. citrifolii*、*C. flagelliseta*)；國內未有調查木瓜節蟎的相關報告。本研究透過製作玻片及電子顯微鏡樣本，以光學顯微鏡及電子顯微鏡 (SEM) 分別觀察形態特徵，並描述為害徵狀，以作為學者鑑定及田間防治的參考。

結果/結論/應用啟示

自南投、台中、金門具有前述被害徵狀的木瓜園，從木瓜植株的下位葉上採集節蟎新鮮標本，製成玻片及 SEM 標本，檢視雌蟎形態，以確認節蟎種類。結果確認在臺灣 3 處及金門 3 處採集到的皆為同種節蟎科 (Eriophyidae) 物種，即 *Calacarus* sp.，且在金門其中 1 處與 *Aculops* sp. 有共存情形。此兩種節蟎皆群居於木瓜葉背，刺吸葉背組織造成葉表呈不規則狀黃褐色斑紋，嚴重時造成葉緣捲起至全葉枯萎，未對木瓜全株造成危害。目前標本採集處多為居家栽培。未來將對木瓜葉上的 *Calacarus* sp. 與 *Aculops* sp. 進行物種鑑定，並調查與確認兩種木瓜節蟎在臺灣及所屬島嶼分布、生態及是否危害木瓜產業等資訊，以提供臺灣節蟎物種多樣性及其經濟重要性所需之生態基礎與農業應用資料。

關鍵詞（Keywords）：蟎（Acari）、節蟎科（Eriophyidae）、木瓜（papaya）、鑑定（identification）

OA_21

臺東地區有機水稻栽培之稻黑椿象管理
Management of black rice bug on organic paddy rice cultivation in Taitung

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背景/研究問題/材料方法

臺東縣關山鎮於2020年開始轉行水稻有機耕作，毗鄰面積100公頃，於2021年第2期作收穫時，田間稻株發現大量稻黑椿象成蟲，於水稻收穫後移動至附近住家光源聚集，甚或危害番石榴果樹。2022年1期作初期調查稻黑椿象成蟲族群密度，每公頃平均蟲數約100,000隻，以礦物油、苦參鹼及白殭菌等資材進行防治並無顯著效果，至收穫時每公頃平均蟲數已達2,000,000隻，部分田區發生「椿燒」情形，造成嚴重的產量損失。

結果/結論/應用啟示

期作間發現稻黑椿象之卵寄生蜂，經農業試驗所鑑定為黑卵蜂屬 (*Telenomus* sp.) 種類，田間亦可發現受黑殭菌 (*Metarhizium anisopliae*) 感染死亡之成蟲。2022年第2期作與苗栗區農業改良場合作，利用培育之黑卵蜂進行田間增補釋放；國立中興大學莊益源教授團隊負責黑殭菌的開發利用，亦有不錯的防治效果。未來於該水稻有機專區，將採用釋放天敵黑卵蜂與黑殭菌等蟲害綜合管理方式，以減少稻黑椿象對水稻的為害。

關鍵詞（Keywords）：稻黑椿象（black rice bug）、黑卵蜂（*Telenomus* sp.）、黑殭菌（*Metarhizium anisopliae*）

OA_22

警戒費洛蒙應用於文旦薊馬防治效果評估
Study of control effect on thrips with alert pheromone application in wendan pomelo orchard

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背景/研究問題/材料方法

文旦於花期至小果期常遭受小黃薊馬 (*Scirtothrips dorsalis*) 危害，影響文旦果皮外觀，一般慣行果園施用化學藥劑防治可獲得良好控制，然而針對有機果園的部分，本研究於花蓮縣瑞穗鄉鶴岡村文旦產區測試橡皮帽型薊馬警戒費蒙對於薊馬防治效果。試驗選擇兩塊分別為兩分地和三分地的有機文旦園，自 108 年至 110 年期間每年進行費洛蒙懸掛和調查。試驗組分為警戒費洛蒙處理組 (T) 及無處理對照組 (CK)，每處理組面積約 0.5 分。警戒費洛蒙處理組於每年二月花期前於每棵文旦樹上各懸掛 8 粒費洛蒙，各方位均勻分布吊掛，三至五月以黃色黏紙監測薊馬數量，另於六月份調查文旦中果期被薊馬危害情形，分為 0、1、2 級，0 級為未被危害果實，1 級為表面積被危害 10%以下，2 級為 10%以上，最後以統計方式比較差異，評估防治成效。

結果/結論/應用啟示

兩處有機文旦果園分別各進行兩年和三年試驗調查，進行連續兩年試驗之羅姓農友，於第二年文旦中果期，調查表皮完整果實率分別為警戒費洛蒙處理組 (T) 62.5%、對照組 (CK) 為 0%；另一處黃姓農友果園試驗第三年，完整果實率分別為警戒費洛蒙處理組 (T) 33.3%、對照組 (CK)為 10.83%，顯示警戒費洛蒙對薊馬具有防治效果，若再佐以施用防治薊馬的有機資材輔助，可提升文旦外觀品質。本試驗結果可提供農友除有機資材以外的資材應用參考，並可推廣於一般慣行農戶，減少農藥施用。

關鍵詞（Keywords）：文旦（Pomelo）、警戒費洛蒙（Alarm pheromone）、薊馬（thrips）

OA_23

從茶刺粉蝨發生與入侵歷史看適生區的預測與風險管理
From occurrence and invasion history of tea spiny whitefly: prediction of suitable distribution areas and pest risk management

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背景/研究問題/材料方法

茶刺粉蝨 (*Aleurocanthus camelliae*) 為茶樹的主要粉蝨害蟲，最早於 1960 年代發生於中國大陸華南茶區，1989 年全面發生於中國產茶區，隨後相繼入侵臺灣 (1993)、日本 (2004)、荷蘭 (2017)、印尼 (2019) 及義大利 (2020)，造成樹勢衰弱及經濟損失。本研究目的為預測茶刺粉蝨於世界主要茶區的適生區，評估擴散風險，同時檢視植物檢疫措施如何管理此類害蟲之移動。將全球 142 個茶刺粉蝨發生地座標，使用最大熵演算法 MaxEnt 生態位模型，以入侵時間序分別匯入已知發生位點進行機器學習，預測其在臺灣及日本茶區之適生區，並與文獻紀錄比對驗證，進一步預測其在世界的潛在地理分布。

結果/結論/應用啟示

最大熵演算法結果顯示，以茶刺粉蝨已知發生位點進行未入侵地區的適生區預測時，會有低估風險之情形。專家進行有害生物風險評估時，應合理加權其發生機率。本研究預測其潛在地理分布，發現其在臺灣中高海拔茶區、日本茶區、越南東北部茶區及印尼爪哇島為高度適生區，分布主要受到最暖季度降水量、等溫性及最乾月降水量等生物氣候變量影響。有鑑於茶刺粉蝨長期錯誤鑑定為柑橘刺粉蝨 (*A. spiniferus*) 致使其生態學資料闕如，MaxEnt 生態位模型能在資料有限的情況下取得高精確度之潛在分布區，適於預測外來入侵物種或新興害蟲之分布，作為植物防檢疫措施壓力測試及風險評估的基礎。

關鍵詞（Keywords）：茶刺粉蝨（*Aleurocanthus camelliae*）、適生區（suitable distribution area）、MaxEnt niche model （MaxEnt 生態位模型）、害物風險管理 （pest risk management）

OA_24

昆蟲作為動物飼料的研究趨勢
The trend of research on insects as animal feed

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背景/研究問題/材料方法

以昆蟲蛋白替代動物飼料的大豆粉與魚粉已成全球產業趨勢，預計 2030 年全球昆蟲蛋白之年需求量將成長 50 倍，歐盟則為全球積極發展昆蟲蛋白的區域。為瞭解飼料用昆蟲產業應用趨勢，本文以歐盟與臺灣公告之飼料用昆蟲作為調查標的，並以布林檢索法自 Google Scholar、Web of Science 及 PubMed 等搜尋引擎或文獻資料庫進行搜尋，分析麵包蟲 (*Tenebrio molitor*)、外米擬步行蟲 (*Alphitobius diaperinus*)、大麥蟲 (*Zophobas morio*)、黑水虻 (*Hermetia illucens*)、黃斑黑蟋蟀 (*Gryllus bimaculatus*)、牙買加蟋蟀 (*Gryllus assimilis*)、家蟋蟀 (*Acheta domesticus*)、熱帶家蟋蟀 (*Gryllodes sigillatus*)、家蠶 (*Bombyx mori*) 及家蠅 (*Musca domestica*) 作為動物飼料的發展趨勢，以提供國內開發飼料用昆蟲種類參考。

結果/結論/應用啟示

研析上述 10 種昆蟲和「動物飼料 (animal feed)」於 2011～2021 年相關報告數量，以 Google Scholar 最多，近 10 年均呈指數增長 ($y = 131.95e^{(0.319x), R}2 = 0.9796$)；限縮檢索範圍為「水產飼料 (aquafeed or fish feed)」，亦具相同趨勢 ($y = 37.71e^{(0.349x), R}2 = 0.9919$)。檢索 Web of Science 與 PubMed 的學術研究核心期刊，顯示報告增長數量與年度呈正相關，並以黑水虻及麵包蟲相關研究最多。本文研析結果顯示全球發展較成熟或具產業競爭力的飼料用昆蟲，以黑水虻、麵包蟲、蟋蟀及家蠅為主。我國未來應從國際趨勢與法規，建立適合本土環境的飼料用昆蟲種類與相關配套措施，以積極發展具有國際競爭力的昆蟲蛋白新興產業。

關鍵詞（Keywords）：昆蟲蛋白（Insect-derived protein）、飼料用昆蟲（Insects as feed）、麵包蟲（Yellow mealworm）、黑水虻（Black soldier fly）

都市昆蟲學

論文宣讀

Oral Session: Urban Entomology

OU_01

一種可殺死抗百滅寧埃及斑蚊幼蟲之假單孢菌屬細菌
A *Pseudomonas* bacterium that kills permethrin-resistant *Aedes aegypti* larvae

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背景/研究問題/材料方法

Aedes aegypti is an important vector for transmitting dengue virus, chikungunya, yellow fever, and zika virus. As there is no treatment for the virus, various synthetic chemicals have been used to manage this vector. Pyrethroids are the most widely used insecticides for mosquito control, which are relative accessibility and have low toxicity to mammals. However, *Ae. aegypti* has developed relatively high pyrethroid resistance due to its overuse. To solve this problem, microbial control provides an alternate method for controlling mosquitoes. An entomopathogenic *Pseudomonas* bacterium, which was isolated by Dr. Hui-Liang Wang from a pond sludge, has been investigated to fulfill this goal.

結果/結論/應用啟示

In this study, the 3rd-instar larvae of permethrin-resistant (Per-R) *Ae. aegypti* have been treated with *Pseudomonas* bacterial culture, resulting in a 100% mortality within 24 hrs. The subsequent experiments showed that its insecticidal components were present in the supernatant of the culture. The median lethal time of the culture and supernatant of this *Pseudomonas* bacterium were 4.87 hrs and 5.13 hrs, respectively. These results suggest that this *Pseudomonas* bacterium has the potential to be used as an alternative insecticide to control pyrethroid-resistant *Ae. aegypti*.

關鍵詞（Keywords）：埃及斑蚊（*Aedes aegypti*）、假單胞細菌（*Pseudomonas* bacterium）、抗百滅寧（Permethrin-resistant）、昆蟲病原菌（Entomopathogenic bacteria）

OU_02

The insecticide resistance of field German cockroaches under different management interventions

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背景/研究問題/材料方法

Blattella germanica (L.) receives growing attention owing to its rapid development of insecticide resistance. Problems with decreased efficacy of both spraying and gel bait formulations are becoming increasingly common. 12 field populations of *B. germanica* collected from restaurants which were managed using different strategies, namely, gel bait formulation after spraying formulations failed (gel bait), random insecticide used (random), and insecticide rotation strategies (IRM) were tested against deltamethrin, fipronil, indoxacarb, and imidacloprid using the topical bioassay with diagnostic doses of 1× LD95, 3× LD95 and 10× LD95. We hypothesized that those field populations under the management program of IRM may display low insecticide resistance followed by gel bait and random insecticide used.

結果/結論/應用啟示

Results showed that deltamethrin at the highest dose (10× LD95) caused limited mortality (<40% mortality) towards 50% field populations under random and IRM; while 3× LD95 deltamethrin caused >70% mortality in field populations under gel bait management. Fipronil caused no mortality in 80% field populations at the dose of 3× LD95. Even at the highest dose (10× LD95), 67% populations has moderate to high resistance (mortality <40%). 67% populations showed moderate resistance toward 1× LD95 imidacloprid. However, when the dose increased to 3×, 83% populations recorded > 60% mortality. Among the test insecticides, 58% field populations showed no resistance toward indoxacarb at the lowest dose. The mortality in some resistant populations was further increased to 70% after being exposed to 3× LD95 of indoxacarb. Besides deltamethrin, no evident showed that the development of insecticide resistance was linked to pest management strategies. Contrary to hypothesis, field populations under the IRM were characterized by high resistance toward deltamethrin and fipronil. These findings suggest that treatments using deltamethrin in residual spraying and fipronil in gel bait formulation would fail to control cockroaches. Indoxacarb and imidacloprid (the like of neonicotinoid group) could be alternatives to ensure satisfactory cockroach management.

關鍵詞（Keywords）：insecticide rotation management, gel bait, diagnostic dose, residual

insecticide spraying

OU_03

疣胸琉璃蟻的遷巢動機
Nest relocation motivation of *Dolichoderus thoracicus*

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背景/研究問題/材料方法

The outbreak of *Dolichoderus thoracicus* (Hymenoptera: Formicidae) has become a serious problem in Nantou since 2016. *D. thoracicus* causes soot disease owing to their mutualism with aphids, and nuisance to farmers during cultivation and harvesting season. Several human-induced factors might exert budding and nest relocation of ants, including physical disturbance, food depletion, exposure to pyrethroid insecticides or escape from parasites. The budding and nest relocation may indirectly promote colony territorial expansion and thus further complicate pest management programs. In this study, we aim to elucidate the factors exerting nest-relocation of *D. thoracicus* including shading depletion, food depletion and physical disturbance. The experiment set up contained two compartments: a compartment (nest site) where 2 queens, 150 workers and 150 broods of *D. thoracicus* were introduced and acclimatized for three days; another compartment (empty nest) provision with food source and sugar solution which allow the ants to move in. Each factor was replicated three times using different colonies. Relocation of ant (number of queen, workers and brood) from original nest to another nest site was checked on day 1, 3 and 5.

結果/結論/應用啟示

Result demonstrated that only food depletion resulted in significant budding and nest relocation of worker (95%) and brood (100%) when comparing to control group. In addition, most ant colonies relocated within 24 hours. However, shading depletion did not significantly elicit colony relocation. Physical disturbance resulted in insignificant budding and nest relocation of worker (53%) and brood (50%) when comparing to both control group and food depletion. The tests of chemical disturbance especially when insecticide efficacy is incomplete on colony relocation is now underway. The information might be crucial to ensure successful management of *D. thoracicus*.

關鍵詞（Keywords）：疣胸琉璃蟻（*Dolichoderus thoracicus*）, Nest relocation, Shading depletion, Food depletion, Physical disturbance

OU_04

入侵性白蟻在台灣的現況
Current status of invasive termites in Taiwan

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背景/研究問題/材料方法

自上個世紀起，入侵性白蟻已隨著人類活動輸出與輸入台灣，最知名的有台灣家白蟻 (*Coptotermes formosanus*) 入侵美國，而格斯特家白蟻 (*C. gestroi*) 則由東南亞入侵台灣，由於國際貿易頻繁，台灣每年進口大量木材，白蟻入侵風險高。近十年間，我們藉由白蟻公民科學計畫與港口檢疫單位的合作計畫，從台灣都市地區與國境關口取得超過 5,000 筆樣本，隨著台灣產白蟻物種分類研究的進展，讓我們能檢視台灣白蟻入侵物種的現況。

結果/結論/應用啟示

格斯特家白蟻占全國白蟻危害案件的 50.1%，成為台灣最主要的害蟲，從屏東到台中有連續分布，而北台灣與台東開始有零星案例，在台中發現格斯特家白蟻與台灣家白蟻的雜交族群，顯示入侵害蟲與本土害蟲有自然雜交現象；黃肢散白蟻 (*Reticulitermes flaviceps*) 為台灣特有種，在台灣北部能適應都市環境；關門散白蟻 (*R. kanmonensis*) 是台灣的原生物種，在台灣雖無都市危害紀錄，但在韓國與日本則是入侵性的害蟲；從民眾提供的樣本中發現 3 種國際重要害蟲：麻頭堆砂白蟻 (*Cryptotermes brevis*)，小楹白蟻 (*Incisitermes minor*) 以及長鼻白蟻 (*Schedorhinotermes* sp.)，出現在家俱、棧板或分飛活動。港口檢疫在原木也攔截到角象白蟻 (*Nasutitermes corniger*) 與大和散白蟻 (*R. speratus*)，上述證據顯示入侵性白蟻在台灣具有高度流動性，也能改變都市害蟲的物種組成，其潛在的經濟重要性，促使我們持續監測並籌畫預防措施。

關鍵詞（Keywords）：地下白蟻（subterranean termite）、乾木白蟻（drywood termite）、公民科學計畫（citizen science project）、台灣白蟻物種鑑定服務（Taiwan Termite Identification Service）、港口檢疫（port quarantine）

醫學昆蟲學

論文宣讀

Oral Session: Medical Entomology

OM_01

The habitat changes and distribution expansion of *Collesius hatorii*

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背景/研究問題/材料方法

Collessius hatorii, a mosquito species that habitats in rock pools along streams, often been collected with *Ochlerotatus japonicus*, and were originally distributed only around streams at Shidins, Taiwan. However, since 2016, we discovered that *Collessius hatorii* can also be collected in nearby districts and unrecorded habitats: the artificial containers in tea and vegetable plantations. Collections were recorded by our lab in neighboring district, Pinling, for years, with a steady population in containers at a plantation mixed planting tea and vegetables. Therefore, we wanted to know that, since *Ochlerotatus japonicus*, also a rock-pool-habitat specie, was observed a world-wide expansion due to climate change, whether a similar trend occurred on *Collessius hatorii*. To investigate the current status, we started larvae sampling in habitats of the originally-recorded rock pools and new-discovered agricultural-used artificial containers in areas around Taipei City, New Taipei City and Keelong City, in order to draw a distribution map of Northern Taiwan.

結果/結論/應用啟示

Our sampling results showed that in New Taipei City, at Shidin District, *Collessius hatorii* larvae can still be found in rock pools along streams. Also, larvae can be collected in artificial containers in plantations. In Pinling District, larvae can still be collected from the plantation we first found the artificial-container-habitat larvae. As the investigation area spread, we also found that in Wenshan District, Taipei City, larvae can be collected from pothole-like rock pools. Therefore, rock pools of pothole landform had also been in consideration. In pothole landform areas from Qidu District, Keelong City, and Rueifang District, New Taipei City, populations of *Collessius hatorii* larvae were recorded. Our investigation results showed that, *Collessius hatorii* populations tend to expand the distribution and water-body-source usage, which may indicate the expansion of this specie is happening, and it may cause by environmental variation due to climate and land use changes.

關鍵詞（Keywords）：*Collessius hatorii*, habitat, distribution

OM_02

Retrospective investigation of cat flea-associated *Rickettsia felis* in Taiwan

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背景/研究問題/材料方法

Rickettsia felis is an emerging rickettsial pathogen mainly associated with cat fleas (*Ctenocephalides felis*), formerly discovered in the Elward Laboratory (California, USA) cat flea colony in 1990. In Taiwan, *R. felis* was retrospectively detected in laboratory-reared cat fleas from 1991. Since the 2000s, *R. felis* infection rates in cat fleas recovered from dogs and cats have been found to be about 20% in northern Taiwan and, more recently, 4% in eastern Taiwan, with DNA sequences identical to the type strain *R. felis* URRWXCal2 isolated from the Flea Data Inc. (New York, USA) cat flea colony. However, outside of the US, the prevalence of *R. felis* infection has not been reported for wild-caught cat fleas before 1990. Therefore, this study aimed to investigate the prevalence of *R. felis* infecting wild-caught cat fleas in Taiwan dating back to 1964 collected by the late Dr. Jih-Ching Lien. Following morphological identification and DNA extraction of cat fleas, quantitative PCR targeting *Rickettsia*-specific citrate synthase gene (*gltA*) was utilized to determine *R. felis* infection rates, followed by PCR amplification of larger *gltA* fragments and Sanger sequencing to determine sequences for comparison with global *R. felis* sequences deposited on NCBI.

結果/結論/應用啟示

This study serves to clarify the circulation of *R. felis* in wild-caught cat fleas globally before 1990.

關鍵詞（Keywords）：*Ctenocephalides felis*, Emerging pathogen, Historical specimens, Molecular detection, Rickettsial pathogen

OM_03

硼酸餌劑對抗藥性野外埃及斑蚊之影響
The effect of boric acid toxic sugar bait on field *Aedes aegypti*

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背景/研究問題/材料方法

Aedes aegypti (Linnaeus) is a main vector of arbovirus. It is utmost challenge to keep the spread of arboviral disease at bay owing to the rapid development of mosquitoes' resistance to insecticide. While chemical approaches remain the most effective method of rapidly suppressing disease-transmitted vectors when there is outbreak, alternative active ingredient is in urgent need to ensure effective management program. Boric acid toxic sugar bait has been shown an effective alternative for use in sensitive environments to control resistant mosquitoes. In the present study, we tested the efficacy of sugar bait on 6 field populations of resistant *Ae. aegypti* mosquito. In addition, given the high mortality of male mosquito were generally observed at 24 hr after exposure, we were interested to determine the fecundity and insemination rate of female. We further explored the flight activity and wing beat frequency of male after sugar bait exposure.

結果/結論/應用啟示

Results showed that the mortality of 6 field populations of male mosquito was consistently high within 24 hr after exposure. By contrast, female mortality was inconsistent, which more than 70% of female mortality was only recorded at 168 hr. Fecundity and insemination rate of female mosquitoes in the treatment were compared to control. Such decreased in fecundity and insemination rate were in inverse proportion to the sugar bait exposure time. In addition, flight activity and wing beat frequency of treated male were significantly reduced when compared to control counterparts. The results suggested that sugar bait is highly effective in reducing wild male population, and affecting male flight activity and female-seeking behavior, which resulting in reduced fecundity and insemination rate. The sugar bait could be an effective alternative to complement current chemical intervention approaches.

關鍵詞（Keywords）：硼酸餌劑（Boric acid toxic sugar bait）、產卵量（Fecundity）、飛行活力（Flight activity）、登革熱（Dengue fever）

OM_04

Effects of far-UVC light (222 nm) on *Aedes* mosquito vectors of dengue

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背景/研究問題/材料方法

Mosquito is the deadliest animal in the world because of mosquito-borne diseases such as malaria, dengue, and Chikungunya. In Taiwan, there are *Aedes albopictus* and *Aedes aegypti* as vectors for dengue. The integrated vector management, including source reduction, biological control, chemical control and physical control should be systematically considered. Ultraviolet C light (254 nm) has been used to inactivate pathogens, but exposure risk of human skin and eyes to UV light should be seriously concerned. Therefore, 222 nm far-UVC light is developed as a safer alternative in recent years. Moreover, the application of using 222 nm far-UVC on vectors is limited. We evaluated the 222 nm far-UVC light (dosage: 0.753 mJ/cm^2/sec; distance: 10 cm) to irradiate eggs, larvae, and pupae of *Ae. albopictus* and *Ae. aegypti* for bioassay. For bioassay, survival curves, median lethal doses (LD50), and establishment of the criteria for abnormal performances were presented. The qRT-PCR was applied to delineate the relationship between irradiation dosage and gene expression of immunogene (*hsp83*) and light-sensitive genes (*cry2* and *per*). A prototype of larvicidal ovitrap equipped with 222 nm far-UVC light and programmable time controller was designed for laboratory evaluation.

結果/結論/應用啟示

Survival curves of first to fourth instar larvae of *Ae. albopictus* and *Ae. aegypti* indicated significant larvicidal effects. Although bioassay of eggs did not result in significant differences, mortal effects of far-UVC light were convinced on larvae and pupae under irradiation dosage of 45.18 mJ/cm^2 and 1355.40 mJ/cm^2, respectively. In addition, some abnormal performances of larvae were observed, including melanization (83.3%, n=18), behavior of biting anal gills (80.0%, n=15), writhing response, and staggering motion. The qRT-PCR analysis revealed the increasing gene expression of *hsp83* and *cry2*, and decreasing of *per*, although significant difference was not found. Since the prototype of ovitrap poses an significant impact on mosquito larvae with no larva survived after 3 minutes of irradiation (45.67-82.94 mJ/cm^2), the applicational value of pesticide-free larvicidal ovitrap will be further investigated.

關鍵詞（Keywords）：白線斑蚊（*Aedes albopictus*）、埃及斑蚊（*Aedes aegypti*）、遠紫外光（far-UVC light）、222 奈米（222 nm）、物理防治（physical control）

OM_05

臺灣埃及斑蚊電壓門鈉離子通道基因型對除蟲菊酯類殺蟲劑抗性之角色

The role of voltage-gated sodium channel genotypes in pyrethroid resistance in *Aedes aegypti* in Taiwan

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背景/研究問題/材料方法

Background/Question: *Aedes aegypti* is the major vector of dengue that threatens public health in tropical and subtropical regions. Pyrethroid-based control strategies effectively control this vector, but the repeated usage of the same insecticides leads to resistance and hampers control efforts. Therefore, efficient and prompt monitoring of insecticide resistance in local mosquito populations is critical for dengue control.

Methods: We collected *Ae. aegypti* in southern Taiwan in March and October 2016. We analyzed the voltage-gated sodium channel (*vgsc*) genotypes of parentals (G0) and G1 adults after cypermethrin insecticide bioassay. Four alleles (S989P, V1016G, F1534C, and D1763Y) of *vgsc* were genotyped by PCR amplification and sequencing. To evaluate the cypermethrin resistance of mosquitoes, the bioassay followed the small-scale study of WHO guidelines.

結果/結論/應用啟示

Results: Our results showed that four VGSC mutations (S989P, V1016G, F1534C, and D1763Y) associated with resistance were commonly detected in field-collected *Ae. aegypti*. The frequencies of these four mutations in the local mosquito population were significantly higher in October (0.29, 0.4, 0.27 and 0.11) than in March (0.09, 0.16, 0.18 and 0.03). Specific *vgsc* combined genotypes composed of the one to four such mutations (SGFY/SGFY, SVCD/SVCD, SGFY/PGFD, SVCD/SGFY, PGFD/PGFD, and SVCD/PGFD) shifted towards higher frequencies in October, implying their resistance role. In addition, the cypermethrin exposure bioassay data supported the field observations. Moreover, our study observed an association between the resistance level and the proportion of resistance genotypes in the population.

Conclusions/Applications: This is the first study to demonstrate the role of four-locus *vgsc* genotypes in resistance evaluation in a local *Ae. aegypti* population in Taiwan. This alternative method using resistance-associated genotypes as an indicator of practically insecticide resistance monitoring is a useful tool for providing precise and real-time information for

decision makers.

關鍵詞（Keywords）：*Aedes aegypti*, insecticide resistance, VGSC, *kdr*, pyrethroid

OM_06

Detection of Rickettsiae in ticks from companion animals in Hualien, eastern Taiwan

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背景/研究問題/材料方法

Companion animals provide blood source for ticks and fleas, therefore becoming a reservoir for pathogens and damaging human health. Previous studies indicated that ticks serve major roles on transmiting *Anaplasma*, *Borrelia*, *Ehrlichia*, *Rickettsia* spp. and threat human's and animals' health. In Taiwan, tick-borne rickettsiae has been studied in metropolitan cities in northern, central and southern Taiwan but not in eastern Taiwan. In this study, we reported the identification and percent of positive of *Rickettsia* spp. in ticks collected from Hualien city, east Taiwan in 2021. Tick species were identified by morphological and molecular methods. Gene primers of *ITS2* and *16S*genes were applied for species identification. For rickettsia detection, genes of *gltA*, *OmpA* and *OmpB* were amplified to perform the gene diversity and prevalence rate of *Rickettsia* spp. in ticks.

結果/結論/應用啟示

A total number of 36 ticks' specimens were collected from 10 veterinary hospitals in Hualien city from the year of 2021. The prevalence rate of *Rickettsia* in *Rhipicephalus sanguineus* and *Haemaphysalis hystricis* was 0% and 2.7%, respectively. This study identified one novel *Rickettsia* spp. in *Haemaphysalis hystricis* based on the genes of *gltA*, *OmpA*, *OmpB* which showed 99%, 95%, 94% gene sequence similarity to *Rickettsia* sp. (KM386690.1), *Rickettsia slovaca* (JX683121.1), *Candidatus* Rickettsia tasmanensis (GQ223393.1). These results indicate a novel Rickettsia sp. In *Haemaphysalis hystricis*, whether it can infect the humans or not are unknown. As a result, it means that there should be continuous monitoring to ensure the health and safety of both humans and animals in east Taiwan.

關鍵詞（Keywords）：*Rickettsia*, *Rhipicephalus sanguineus*, *Haemaphysalis hystricis*, eastern Taiwan

OM_07

Effects of *Coelomomyces* spp. on vectorial capacity of *Aedes albopictus* （Diptera: Culicidae）

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背景/研究問題/材料方法

Mosquitoes are of great threat to human health because they transmit vector-borne diseases. Integrated vector management for mosquito control have gained interest rather than using chemical insecticides. Obligatory parasitic fungi, species of *Coelomomyces* (Blastocladiomycetes: Blastocladiales), have potential roles for mosquito control based on the advantages of high prevalence and lethal effects. Four partial genomic data of *Coelomomyces* have been identified, however, data in Taiwan has not yet been available. *Aedes albopictus* were collected from northern Taiwan, and *Coelomomyces* were identified by both molecular data and ultramorphologies from scanning electron microscope. The potential of *Coelomomyces* on mosquito control was evaluated based on the survival rate of larvae. Interactions between *Coelomomyces* and dengue virus in female adults were investigated by oral feeding on virus-infected blood. Vector competence of the interaction between dengue virus and *Coelomomyces* in mosquito tissues was quantified by qRT-PCR. The modulation of antifungal immune responses in mosquito larvae to *Coelomomyces* infection were also estimated by qRT-PCR, including *CLSP2*, *TEP22*.

結果/結論/應用啟示

Mosquitoes and intermediate host copepods were co-cultured in the laboratory to maintain *Coelomomyces in vivo*. Sequences of 18S SSU rRNA from three samples shows 88.77, 95.58, and 99.59% similarity to *C. stegomyiae*. The molecular and morphological data indicate that one novel strain of *C. macleayae*, and two strains of *C. stegomyiae* var. *stegomyiae* and *C. stegomyiae* var. *chapmani* were isolated. The infection rate of *Coelomomyces* in the 1st instar larvae (90.67±4.16%, 136/150) was higher than the 2nd instar larvae (60.67±5.77%, 91/150) after incubating with 102.69 resting sporangia/ml solution for 2 days, and the mortality rates were 72.96±9.67% and 47.39±6.20%, respectively. In the 3rd instar larvae, the infection rate was 46.67±6.67%, and the mortality rate was 37.35±5.52% in 103.12 resting sporangia/ml solution (N=90). Preliminary data shows the virus infection in salivary glands with a high Ct value.

關鍵詞（Keywords）：*Aedes albopictus*, *Coelomomyces*, biological control, entomopathogenic fungi

OM_08

臺北市立動物園廄刺蠅幼蟲孳生地調查及成蟲防治技術初探

Investigation of the larval habitat of *Stomoxys calcitrans* (Diptera: Muscidae) and comparison of physical control methods for adults in Taipei Zoo

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背景/研究問題/材料方法

廄刺蠅對動物的危害自 17 世紀即有紀錄，牠的刺吸會造成動物疼痛、產生傷口或導致被叮處化膿潰爛，造成動物之緊迫、進食量及生產力下降等問題。此外，尚有傳播疾病的可能性，因此被視為影響畜產業之重要吸血害蟲。然而，臺灣地區目前並未有其幼蟲棲地的相關調查及紀錄，因此，本次試驗選在臺北市立動物園內，針對先前紀錄廄刺蠅成蟲為害之區域進行幼蟲孳生地的調查。成蟲方面，嘗試使用黏板陷阱、水盤陷阱及非黏性誘捕陷阱等三種不同的陷阱進行物理防治技術探討，比較不同陷阱之間對廄刺蠅誘引能力，以提供後續廄刺蠅成蟲防治的參考。

結果/結論/應用啟示

在調查 32 種動物物種之活動場域及 2 座堆肥場後，總計發現幼蟲孳生地包括植物組織之腐植質堆積 9 處及老熟糞便大量堆積 2 處。成蟲誘捕方面，測試廄刺蠅對顏色趨性試驗結果顯示，白色對廄刺蠅的誘引效能最佳，藍色次之，惟兩者以 LSD 進行比較無顯著差異，然對其他顏色均呈顯著差異。在陷阱構造對廄刺蠅之誘引效率評估中，白色黏板及白色黏球兩者之間無顯著差異，綜合評估廄刺蠅誘捕裝置，以白色黏板之誘集效率最佳，可以具體推薦做為廄刺蠅成蟲誘捕防治技術。

關鍵詞（Keywords）：Stable fly, breeding source, sticky trap, maggot

OM_09

Investigation and identification on sand fly of medical importance in eastern Taiwan

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背景/研究問題/材料方法

Phlebotomine sand fly is a tiny blood-sucking dipteran and natural vector of Leishmaniasis, Bartonellosis, and sand fly fever. Leishmaniasis, especially, is a neglected tropical zoonosis and second only to malaria in the world. In Taiwan, four species of sand flies were reported based on morphological characters in 1970. Although six cases of indigenous cutaneous leishmaniasis were recorded from 1985 to 2009 in Taiwan, research on sand fly species and vector incrimination in Taiwan is pending. Understanding the species and current distribution of Taiwan sand flies is a key for developing and implementing appropriate prevention strategies. This study aims to clarify the distribution and species composition of sand flies in eastern Taiwan. For the sand fly collection, the sampling sites are mainly the scenic sites with intense human activities. Collecting approach is mainly using the light traps that were set up from eve to dawn with carbon dioxide. Wing venation and maxillary palps are the most significant characters and applied to identify collected male adults for morphological identification. The mitochondrial cytochrome c oxidase subunit I (*COI*) gene sequences were extracted from 5 males of each sampling sites to compare with the NCBI database for molecular identification.

結果/結論/應用啟示

After our survey, a total of 333 sand fly samples were successfully collected from 20 sampling sites in 3 Counties (Yilan, Hualien, and Taitung). Preliminary results showed the 16 and 44 specimens belong to *Sergentomyia squamipleuris* and *Se. barraudi* respectively in 65 male specimens via external characters. Species identification of another 5 male specimens are still pending due to their equivocal character states. However, the *COI* sequence identification of the 17 males was divided into two groups: *Se. insularis* and *Se. iyengari.* The contradiction between morphological and molecular identification implies there could have new or new record of sand fly in eastern Taiwan. Our study provides the basic information for the biology of sand flies in Taiwan and will help to realize the disease triangle of sand fly-borne diseases for developing a better and efficient prevention strategy.

關鍵詞（Keywords）：Phlebotominae, neglected tropical diseases, eastern Taiwan, Newstead’s spine, cytochrome c oxidase subunit I

OM_10

台灣牛隻庫蠓媒介病毒的發生、跨境傳播及病媒昆蟲綜述
Overview of occurrence, transboundary transmission, and potential vectors of bovine *Culicoides*-borne viruses in Taiwan

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背景/研究問題/材料方法

庫蠓媒介病毒為重要草食動物病原，這類病毒主要屬於正本雅病毒屬 (*Orthobunyavirus*)、環狀病毒屬 (*Orbivirus*) 及發熱病毒屬 (*Ephemerovirus*) 三屬。在台灣，此三屬病毒僅發現過 7 種，本研究選擇鄰近台灣的周邊地區有紀錄的庫蠓媒介病毒 19 種為監測標的，並透過於 2012-2019 年間在台灣各地所採集之 2,525 池 108,937 隻病媒昆蟲為樣本，利用兩階段聚合酶連鎖反應檢測方法 (two-step PCR approach) 偵測目標庫蠓媒介病毒，以了解台灣庫蠓媒介病毒之發生。

結果/結論/應用啟示

在 19 種目標病毒中檢出 12 種病毒，本別為 6 種正本雅病毒、5 種環形病毒、1 種發熱病毒，其中 6 種為台灣首次發現之病毒，分別為沙門達病毒 (shamonda virus)、蘇佩里病毒 (sathuperi virus)、舒尼病毒 (shuni virus)、流行性出血性疾病病毒第四血清型與第七血清型 (Epizootic hemorrhagic disease virus serotype 4 and 7)，薩圖瓦查里病毒 (Sathuvachari virus)。此外，本研究亦鑑定出 3 種庫蠓、5 種蚊子分別為這些病毒的潛在病媒。另外透過親緣演化分析牛流行熱病毒 G 蛋白以及分析赤羽病毒基因體，發現這兩種病毒可能在八重山群島與台灣之間進行跨境傳播。

關鍵詞（Keywords）：庫蠓（Culicoides biting midge）、蟲媒病毒（arthropod-borne virus）、跨境傳播（transboundary transmission）、病媒（vector insect）

OM_11

以形態與分子方法鑑別臺灣產日本斑蚊複合群及其族群地理分布
Identification of *Aedes* (*Finlaya*) *japonicus* complex by morphological and molecular methods and their geographic distribution in Taiwan

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背景/研究問題/材料方法

Aedes (Finlaya) japonicus, an emerging disease vector of Japanese Encephalitis, have been an invasive species in Europe and North America. Yet, whether different subspecies of *Ae. japonicus* have invaded to non-native Asia countries or not is understudied. According to previous studies, it has been reported only *Ae. japonicus shintienensis* distributed in Taiwan, but this argument based on limited specimens and has not been tested by molecular phylogenetic reconstruction. Therefore, we combined morphological and genetical characters to re-evaluate classification of *Ae. japonicus* complex and its distribution in Taiwan. We recorded 68 populations in different mountain area in Taiwan to analysis their morphology variation, and selected 20 sub-sampling to analysis genetic variation. To analysis morphology variation, we analysis dot pattern on hind femora and wing allometries. To analysis genetic variation, we sequenced *CO1* and *CO2* gene to reconstruct phylogenetic tree including other published subspecies sequences.

結果/結論/應用啟示

The collections included 28 populations with adult specimens and 40 populations with larval specimens. All specimens were collected from artificial sources, and distributed across elevational gradients from 12 m to 2283 m. Based on dot pattern analysis, all individuals are *Ae. japonicus shintienensis*. This study refreshes the distribution of *Ae. japonicus* complex in Taiwan. Furthermore, this research provides a clearer background information for managing an emerging disease vector in the changing world.

關鍵詞（Keywords）：*Ochlerotatus japonicus japonicus*, *Ochlerotatus japonicus shintienensis*, population expansion, ovipositional preference, *Aedes koreicus*

OM_12

Autophagy is activated through AMPK/TSC/TOR signaling pathway in *Aedes aegypti* after infection with dengue 2 virus

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背景/研究問題/材料方法

Autophagy is a self-degradative process that is required for cell survival in response to diverse conditions of stress. It has been reported that infection of dengue 2 virus (DEN2) induced autophagy machinery and resulted in increased viral replication in animal cells and its vector mosquito, *Aedes aegypti*. In mammalian cells, autophagy is regulated by mTOR (mammalian target of rapamycin)-dependent and mTOR-independent pathway. However, it remains unclear how this autophagic process is regulated in *Ae. aegypti* after DEN2 infection. In this study, double-stranded RNA (dsRNA) silencing analysis and chemical drug feeding were used to elucidate the autophagy induction pathway in DEN2-infected mosquitoes.

結果/結論/應用啟示

We found that the induction of autophagy by silencing of IMPase, an important factor in the TOR-independent pathway, did not significantly affect the replication of DEN2 in *Ae. aegypti*. On the other hand, the induction of autophagy by feeding the mosquitoes with 10% sucrose containing A-769662 to activate AMPK, the major control point in AMPK/TSC/TOR pathway, significantly elevated the replication of DEN2 in *Ae. aegypti*. In addition, we also found that the inhibition of autophagy by feeding mosquitoes with 10% sucrose containing SC-79 to activate Akt, an important factor in PI3KC1/Akt/TSC/TOR pathway, did not significantly reduce the replication of DEN2. In conclusion, our results suggest that autophagy is activated through AMPK/TSC/TOR signaling pathway in *Ae. aegypti* after infection of DEN2.

關鍵詞（Keywords）：*Aedes aegypti*, autophagy, signaling pathway, dengue virus, replication

生物多樣性、族群與群聚生態學

壁報展示

Posters: Biodiversity, Population and Community Ecology

PB_01

以不同土壤介質養殖黑翅土白蟻並分析其生存率與蟻道發育比例
Breeding *Odontotermes formosanus* in different soil media and analyzing its survival rate and ant channel development ratio

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背景/研究問題/材料方法

在野外，黑翅土白蟻 (*Odontotermes formosanus*) 會與蟻巢傘菌屬 (*Termitomyces*) 真菌共生。但在實驗室中人工養殖黑翅土白蟻的死亡率很高，其中土壤的特性對於共生系統來說可能是影響其蟻巢發育的因素之一，因此本研究透過改變不同的土壤介質 (黃土、滅菌黃土、滅菌紅土、椰纖土、滅菌椰纖土、泥黃土、滅菌半紅黃土) 來養殖黑翅土白蟻，並分析不同土壤中蟻巢的生存率與建築蟻道的比例。我們假設土壤對蟻巢的影響有 1.含有機質的土壤 (泥炭土或是椰纖土) 可以提供黑翅土白蟻氮源增加白蟻群體數量、卵量 2.滅菌的土壤可以降低土壤中的寄生真菌或是寄生蟲，對於蟻巢有一定的影響。3.不同土壤的特性對於蟻巢傘菌萌發率有一定影響。

結果/結論/應用啟示

在這七種不同的土壤中，均可以看到白蟻築巢、產卵、工蟻孵化、工蟻建築蟻道。在不同土壤的蟻巢生存率：泥黃土、滅菌紅土、滅菌半紅黃、椰纖土生存率有 70% 以上。蟻道出現的時間：滅菌紅土、滅菌椰纖土、滅菌半紅黃土出現的時間較早，平均天數為 93 天。蟻道建築率最高的為滅菌紅土。這些研究資料可以看出土壤的特性可能會影響蟻巢的發育階段，這可以提供在實驗室大規模養殖黑翅土白蟻的先備實驗。

關鍵詞（Keywords）：蟻道（ant channel）、黑翅土白蟻（*Odontotermes formosanus*）、土壤（soil）、生存率（survival rate）

PB_02

探討台中市區國、高中生對食用昆蟲的態度現況
To explore the situation of attitudes towards edible insects among junior and senior high school students in Taichung City

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背景/研究問題/材料方法

本文研究重點是了解國高中生對食用昆蟲態度的現況並加以探討。氣候變遷及土地汙染使得全球都面臨糧食資源的缺乏，為了解決這個問題，尋找替代食品成為重要的議題。其中，昆蟲因其種類多樣且數量龐大，成為替代食品中的熱門選項。昆蟲是許多動植物的蛋白質來源，在許多地方的傳統飲食中人類也同樣會食蟲。昆蟲的飼養不會占用大面積土地及過多水資源。就營養價值來看，除了蛋白質含量高，昆蟲亦富含多樣營養。在臺灣，食用昆蟲並不普遍，本研究以問卷調查的方式，了解國、高中生對食用昆蟲的態度。在問卷的設計上，本文對食用昆蟲的態度使用「知識-行為-態度」模型，將態度分成「對食用昆蟲的情感」、「對食用昆蟲的認知」，以及「對食用昆蟲的行為傾向」進行分析並了解食用昆蟲在推廣上的困境及可能的解決方法。

結果/結論/應用啟示

根據本研究的前測結果，情感與行為傾向態度中，有嘗試過食用昆蟲者對情感態度有顯著性的影響，且大部分受試者對食蟲還是會感到不適。然而前測結果亦顯示，男性及偏愛海鮮或羊肉的民眾對食用昆蟲有較正向的態度。受測者對於昆蟲食品的偏好方面，鹹甜味覺並沒有顯著影響態度，而以食品中昆蟲完整性來說受試者對放入完整昆蟲的食品態度沒有昆蟲麵粉製作的食品正向。

關鍵詞（Keywords）：食用昆蟲（Edible insect）、替代蛋白質（Alternative proteins）、ABC 態度模型（The ABC Model of Attitude）、問卷研究（Questionnaire research）

PB_03

暖化及土壤水分境況對蘿蔔苗 (*Raphanus sativus*) 與桃蚜 (*Myzus persicae*) 之影響

Effect of warming and soil water regime on radish seedlings *Raphanus sativus* and green peach aphid *Myzus persicae*

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背景/研究問題/材料方法

熱壓力與給水壓力，兩者經常是隨之發生的。但有關此二壓力的結合對植食昆蟲之影響的研究卻不常見。因此本次試驗以活株植物替代浮葉，並透過以日溫相同波動之變溫作為研究方法，試圖評估四種不同級別的夏季氣候暖化：夏季氣候均溫 28.6°C、輕度暖化 (上升 1.4°C；均溫 30.0°C)、中度暖化 (上升 3.9°C；均溫 32.5°C) 及重度暖化 (上升 6.4°C；均溫 35.0°C)，以及兩種土壤含水量 (100% 以及 35%)，共 8 種處理下進行在蘿蔔苗 (*Raphanus sativus*) 上桃蚜 (*Myzus persicae*) 的生命表試驗並測量植物生理特性 (包含葉綠素相對量、氣孔導度、地上部乾重、葉片相對含水量)，觀察兩壓力結合下對昆蟲-植物交互作用的影響。

結果/結論/應用啟示

預測 21 世紀末不同級別的夏季氣候暖化情境，對桃蚜族群表現主要隨暖化程度的提升而顯著下降。而植物所受之缺水壓力在平均世代時間上較具顯著影響，在受缺水壓力的蘿蔔上飼養之蚜蟲其平均世代時間較長，且當環境達中度暖化後，缺水壓力會使蚜蟲內在增殖率提升。蘿蔔面對此二壓力的結合，上述植物生理特性主要受土壤含水量影響，乃自於隨暖化程度的提升，蚜蟲族群表現會隨之下降，減少了害蟲侵擾，因此缺水與暖化壓力的結合並未使該植物特性受到顯著影響。

關鍵詞（Keywords）：桃蚜（*Myzus persicae*）、生命表（life table）、暖化及土壤水分境況（warming and soil water regime）

PB_04

氣候變遷對濁水溪流域膜翅目授粉者棲地變化之影響
Distribution range shift of pollinators (Hymenoptera) under climate change in the Choshui River Basin

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背景/研究問題/材料方法

全球氣候變遷對生態系統造成嚴重影響，也造成膜翅目授粉者族群減少。為了解氣候變遷對不同海拔膜翅目授粉者的影響，挑選 6 種分布於不同海拔高度的標的物種，包括西方蜂 (*Apis mellifera*)、東方蜂 (*Apis cerana*)、精選熊蜂 (*Bombus eximius*)、楚南熊蜂 (*Bombus sonani*)、威氏熊蜂 (*Bombus trifasciatus*) 和銅翼背木蜂 (*Xylocopa tranquebarorum*)等，進行生態棲位模擬 (Ecological niche modeling)，以了解物種適存棲地之變化。為了瞭解生態棲位模型與生理耐熱度是否吻合，本研究探討了西方蜂在不同海拔的 CTmax 和 CTmin，並和分布於高海拔的威氏熊蜂及楚南熊蜂比較，了解不同物種之間的耐熱度差異。

結果/結論/應用啟示

在高排碳 (SSP5-8.5) 情景下，中高海拔之威氏熊蜂及楚南熊蜂有適存棲地縮減的現象；而低海拔西方蜂及銅翼背木蜂適存棲地則有增加的現象；廣佈的東方蜂棲地則明顯增加，但同為廣布種的精選熊蜂則有棲地減少的現象。在生理耐受度的部分，不同海拔分布的西方蜂沒有顯著差異，兩種熊蜂在種間也沒有顯著差異，但西方蜂與兩種熊蜂都有顯著差異，可能因蜜蜂屬和熊蜂屬的生理限制與不同海拔的適應能力有關。由生理耐受度可以看出西方蜂與高海拔物種相比 CTmin 較高，氣候變遷下可以在中高海拔生存；兩種熊蜂的 CTmax 較低，模型顯示其棲息地將侷限於高海拔，雖然兩種熊蜂可以在 40°C的溫度下短暫生存，但在長時間下仍無法穩定族群。

關鍵詞（Keywords）：Hymenoptera, altitude, thermal tolerance, ecological niche modeling, climate change

PB_05

Analyzing possible niche shift in alien populations of the Indochina mantis (*Hierodula patellifera*)

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背景/研究問題/材料方法

The Indochina mantis (*Hierodula patellifera* Serville, 1839) is one of the most common mantis species (order Mantodea) in Asia, including Taiwan. However, it is becoming widespread in other areas too (e.g., Northern Italy, Croatia, France, Hawaii and Seychelles), probably because of incidental introductions of oothecas on imported Asian wood. Interestingly, the Northern Italian records suggest that the species is shifting its niche in Europe, being more present in urbanized areas compared to the tree-dwelling populations in the natural range.

For testing this hypothesis, we decided to build species distribution models (SDMs) for Northern Italian, Hawaiian and Asian records by using Maxent implemented into the R package "ENMeval" and the bioclimatic variables available in the Worldclim website, at 5 arcminutes resolution. We took the mantis presence points from iNaturalist's "Research Grade" observations and literature. We used Schoener's D, PCA and niche equivalency test for comparing native and alien range.

結果/結論/應用啟示

From the preliminary results we have, the species tends to avoid mid- (roughly 1000 meters asl) and high-elevation areas in both alien and native range. However, the Northern Italian range seems to be split in two different areas, hinting on the huge role of accidental introductions in shaping the species's distribution highlighted by previous studies.

This study will be helpful for quantifying the possible shift of this alien mantis, given the lack of data about the ability of Mantodea to spread in other environments and causing possible competition issues with native mantises

關鍵詞（Keywords）：Mantodea, Alien Species, Indochina Mantis, Species Distribution Modeling, Niche shift

PB_06

高溫蒸氣處理對設施土壤內瓜實蠅幼蟲及蛹之影響
Effects of steam treatment on the soil-borne larvae and pupae of *Zeugodacus cucurbitae* (Coquillett) in the greenhouse

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背景/研究問題/材料方法

土壤蒸氣處理為用於去除設施溫室內土壤中有害生物，如微生物、昆蟲、種子的一項消毒技術。現行我國主要採用衛生管理及化學藥劑進行瓜實蠅 (*Zeugodacus cucurbitae* (Coquillett)) 老熟幼蟲及蛹的管理，然為減少農藥使用，物理性防治策略如蒸氣處理應為具發展潛力的技術。為了解瓜實蠅老熟幼蟲及土壤中蟲蛹對高溫蒸氣的反應，本研究探討在土表進行蒸氣處理對於位於不同土壤深度的瓜實蠅幼蟲及蛹所產生的致死效果。試驗模擬溫室中，高溫蒸氣消毒土壤之方式，以高溫蒸氣處理 1 小時後緩慢降溫 2 小時，紀錄此 3 小時高溫處理後位於土表下深度 5、10 及 15 公分幼蟲及蛹之存活情形。共計進行 20 次重複試驗，合計各收集 100 組老熟幼蟲及蛹樣本的死亡率數據。

結果/結論/應用啟示

本研究顯示，土壤深度 10 公分以內，以 4bar 壓力所傳遞的蒸氣可達到 50-90°C 之高溫，並維持達 1 小時 (以 4bar 壓力所傳遞的蒸氣溫度最高可達 90°C，並可維持 50°C 以上 1 小時)，因此蛹及幼蟲致死率達 100%。在 15 公分土壤深度經 3 小時的處理，其平均溫度可達 40°C，老熟幼蟲及蛹之平均死亡率分別為 97 及 94%。本研究結果顯示高溫蒸氣處理對存在土壤內的瓜實蠅幼蟲及蛹皆能達到致死的功效，且蒸氣可達到土壤下 15 公分之深度。此項技術不但可用於一般瓜、果栽培溫室設施消毒之用，亦可作為瓜實蠅非疫生產之系統性管理策略或緊急防治措施之一環。

關鍵詞（Keywords）：瓜實蠅（*Zeugodacus cucurbitae*）、致死溫度（lethal temperature）、蒸氣消毒（steam disinfection）、系統性管理（systems approach）

PB_07

台北地區焚燒豬屍之昆蟲相演替初探
Preliminary study on the insect succession of burnt pig carcasses in Taipei

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背景/研究問題/材料方法

法醫昆蟲學在特定狀況中可透過屍體上的昆蟲發育時間及昆蟲相組合來推測死亡時間、死因或地點。但因屍體所處、環境、時間及不同處理方法會導致昆蟲發育與組成有很大的變化。而焚燒是刑事案件中常見的毀屍手法，且北台灣地區較少有相關昆蟲相比較研究。本實驗以兩隻約 15 公斤家豬模擬人類屍體，於 2022 年 7 月 29 日放置於台北市大安區室外，其中實驗組以 95 無鉛汽油澆淋焚燒至體表焦黑、部分表皮龜裂。藉由密集觀察與適量採集從新鮮期至乾燥期之屍體上及周圍出現的昆蟲並加以鑑定。本次主要記錄焚燒組昆蟲相演替及屍體腐敗過程，並與未處理組做初步對照。

結果/結論/應用啟示

本次實驗出現昆蟲主要涵蓋雙翅目、膜翅目、鞘翅目及部分蛛形綱種類。對照組第一批抵達昆蟲為麗蠅科與花蘆蜂屬，焚燒組則為火蟻屬，與預期結果大致相同，其中花蘆蜂的出現較為特殊。焚燒組因腹部龜裂而跳過膨脹期提早進入腐敗期，進入乾燥期的時間也比對照組快 1 至 2 天，昆蟲相變化速度相對快。本研究採集樣本中發現不少在法醫昆蟲學中過去較不被重視的類群，如稈蠅科、廁蠅科等，但目前仍無法得知其重要性與出現於屍體上的原因。本研究是台北地區初次較詳細記錄焚燒屍體昆蟲相演替，並將持續進行後乾燥期的紀錄與比較。

關鍵詞（Keywords）：法醫昆蟲學（forensic entomology）、演替（succession）、腐敗（decomposition）、臺灣（Taiwan）

PB_08

2022 年臺灣登革熱病媒蚊分布調查
Survey on the distribution of dengue vector mosquitoes in Taiwan in 2022

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背景/研究問題/材料方法

臺灣登革熱病媒蚊是埃及斑蚊與白線斑蚊，過去埃及斑蚊分布在嘉義布袋以南，海拔 500 公尺以下地區，白線斑蚊則分布在全台海拔 1,500 公尺以下地區。氣候變遷會影響生物的分布，過去推估節肢動物在溫度上升的情境下，將會往高緯度與高海拔移動。為了瞭解登革熱病媒蚊在臺灣分布是否改變，本調查將臺灣以 10 x 10 km2 畫分成 420 區域進行調查，調查方式主要是利用誘卵桶及誘殺桶兩種工具誘集蚊卵或成蚊 3 週，再進行蚊卵孵化飼養與鑑定，設置及檢查監測工具過程中也同時進行孳生源尋找與成蚊採集，並以 GPS 定位，記錄工具及病媒蚊採集位置、海拔高度及孳生源種類等資訊。

結果/結論/應用啟示

目前完成調查的 280 個區域結果顯示，埃及斑蚊分布與過去相當，而白線斑蚊可在海拔 1,990 m 發現，顯示白線斑蚊有往高海拔分布的趨勢。未來這些結果可與氣候推估資料結合，推測登革熱病媒蚊在臺灣的地理分布與未來的變化，並可藉此提早因應，減少未來國人受重要病媒蚊分布改變的影響。

關鍵詞（Keywords）：登革熱（Dengue）、病媒蚊（Mosquito Vectors）、分布（Distribution）

系統分類、族群遺傳、演化

壁報展示

Posters: Systematics, Population Genetics and Evolution

PS_01

台灣產新紀錄種短尾馬尾繭蜂短記

Notes on *Euurobracon breviterebrae* Watanabe, 1934 (Hymenoptera: Braconidae), a New Record of Taiwan.

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背景/研究問題/材料方法

Euurobracon Ashmead 1900 is a unique genus in the subfamily Braconinae, which plays an important role both in braconine evolution and biological control. The species of *E. breviterebrae* Watanabe, 1934 was previously reported occurring in Eastern Palaearctic regions (Japan, China, Korea). In this study, we confirmed this species is also distributed in Taiwan.

結果/結論/應用啟示

The braconid species *Euurobracon breviterebrae* Watanabe, 1934 is recorded from Taiwan for the first time. Although the biology of *E. breviterebrae* is still unknown, its first host record, *Acalolepta permutans paucipunctata* (Gressitt, 1938) (Coleoptera: Cerambycidae), is reported herein. Two currently recorded *Euurobracon* species of Taiwan, *E. yokahamae* and *E. breviterebrae*, can be divided by the characters of hindwing venation and ovipositor length.

關鍵詞（Keywords）：Hymenoptera, Braconidae, *Euurobracon*, Taiwanese fauna, new record

PS_02

臺灣偽圓跳蟲科 (Dicyrtomidae) 之分類學研究
Taxonomy of Dicyrtomidae (Collembola: Symphypleona) of Taiwan

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背景/研究問題/材料方法

Dicyrtomidae (Collembola: Symphypleona) are globular springtails with the fourth antenna segment shorter than the third one. Due to lack research, our knowledge about Dicyrtomidae of Taiwan has not seen much update for decades. Only a few articles focused on morphological descriptions, while there is no molecular data for comparative studies. So far, seven dicyrtomid species were recorded in Taiwan. This study aims to explore the diversity of Dicyrtomidae in Taiwan using both morphology and DNA (cytochrome *c* oxidase subunit 1, COI). Samples were collected using beating, searching and aspirating, Berlese Funnel after sifting leaf litter, Malaise trap, and Flight intercept trap throughout Taiwan. Specimens were either made into slides or used for DNA extraction. We compared the morphological and molecular data to uncover cryptic diversity within previously recognized morphospecies, and compared distinct intraspecific biogeographic patterns among different species.

結果/結論/應用啟示

A total of more than 2000 specimens belonging to 11 species were collected. Four of them are either new records or potential new species. DNA barcode analysis shows that most species we analyzed are monophyletic. Additionally, *Papirioides jacobsoni*, *Ptenothrix denticulata*, and *Ptenothrix corynophora* have relatively high intraspecific genetic variation. Among them, *Papirioides jacobsoni* shows differentiation among population around 8% for COI. In addition, we re-examined the morphological descriptions of *Ptenothrix denticulata* Folsom, 1899 in the literature and found morphological variations among different descriptions, suggesting the existence of multiple forms or even cryptic species. Future work will focus on exploring the diversity of Collembola of Taiwan and investigating the potential mechanisms leading to intraspecific genetic variations in Dicyrtomidae.

關鍵詞（Keywords）：彈尾綱（Collembola）、偽圓跳蟲科（Dicyrtomidae）、*Ptenothrix denticulata*

PS_03

斑蛾科螢斑蛾亞科的首個分子親緣關係假說以及對分類體系及特徵演化推測的影響

The first molecular phylogeny of Chalcosiinae (Zygaenidae) and its influence on classification and inference of character evolution

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背景/研究問題/材料方法

Amongst the zygaenid subfamilies, the Chalcosiinae are a diverse group. Second only in size to the Procridinae, they probably exhibit the highest diversity in morphology and ecology both within the Zygaenoidea and within the non-obtectomeran apoditrysian Lepidoptera. Owing to their often brilliant coloration, high level of sexual dimorphism, complicated mimetic patterns, little-known biology and rarity in museum collections, they have received the attention of many researchers and insect collectors. The group's taxonomy has remained confusing since its initial documentation in the 18th century. Although Yen et al. (2004) reconstructed a huge phylogeny by using 414 morphological characters obtained from 411 species representing 73 genera, some internal relationships of the subfamily remain unclear. In the present study, we used 4 markers, viz. COI (mtDNA 1470 b.p.) + 28S (nuDNA 749 b.p.) + ef1a (nuDNA 1202 b.p.) + RpS5 (nuDNA 600 b.p.) to reconstruct the first molecular phylogeny of this group and Limacodidae, Lacturidae and Phaudidae were selected as the outgroups.

結果/結論/應用啟示

The phylogenetic analysis shows that the Chalcosiinae with the current contents is not monophyletic. The genus *Chalcosiopsis* should be placed in its own subfamily, and Inouelinae, which was placed in Chalcosiinae, is found sister to Zygaeninae in some analyses. All the tribes of Chalcosiinae are not monophyletic due to convergence and mimicry so that many new tribes are supposed to be erected to stabilize the classification. The new phylogeny also reveals that the evolutionary trends of complexity of androconial system, reduction of genitalia and specialization of the male 8th tergite and sternite.

關鍵詞（Keywords）：Mimicry, Phenotypic evolution, Chemical defense, Aposematism, Convergence

PS_04

尺蛾科枝尺蛾亞科潔尺蛾屬的整合分類學揭示台灣與東南亞產五個新物種的發現

Integrated taxonomy of the genus *Genusa* (Geometridae, Ennominae) reveals discovery of 5 new species from Taiwan and southeast Asia

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背景/研究問題/材料方法

Genusa Walker, 1855 is a small geometric genus currently placed in Hypochrosini. After the erection of the genus in 1855, only Holloway (1994) and Cui et al. (2014) paid attention to the taxonomy and the species number was five prior to the present study. The adult wing pattern and shape of the genus is almost identical among species and the fact that most specimens deposited in museum collections are very worn so that identification and matching between sexes based on external characters was unlikely. The adults of this genus strongly associated with the host trees, *Gonocaryum* and they release distasteful fluid when disturbed by predators. The larvae possess unique color pattern and hanging behavior to deter predators. In order to investigate the origin of the aposematism and behavior of both the immature and adult stages, we employed morphological, molecular and behavior approaches. A *Celenna* species was selected as an outgroup and the COI, COII and EF1a sequences were obtained from 51 *Genusa* specimens collected from 8 countries. Both Maximum Likelihood and Bayesian Inferences were used to reconstruct the phylogenetic trees.

結果/結論/應用啟示

Our analysis suggests existence of 5 new species from southern Vietnam, Malaysia/Singapore, Taiwan/Philippines, Mindanao and northwest Sabah. The abdominal pattern, larval and pupal coloration seems to be more reliable characters than wing patter for identification. This discovery may also suggest that aposematic species might not undergo phenotypic shift during speciation in order to maintain benefit in adult stage.

關鍵詞（Keywords）：Cryptics species, Sympatric speciation, Sundaland, Biogeography, Chemical defense

PS_05

原生種短斑偽菜蛾以及入侵種札幌偽菜蛾在台灣的發現以及在珠蔥害蟲防治上的意義

Discoveries of the indigenous *Acrolepiopsis brevipenella* (Moriuti, 1972) and the invasive *A. sapporensis* (Matsumura, 1931) in Taiwan and the implication for pest control of leek

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背景/研究問題/材料方法

In May of 2022, an unfamiliar micromoth was detected from leek (*Allium cepa* var. *aggregatum*) in Xindian, New Taipei City, by Y.R. Chang, a famous insect photographer. The larvae were immediately brought to us and it was provinsionally identified as an *Acrolepiopsis* species (Glyphipterigidae). According to the checklist of the Lepidoptera of Taiwan, a species, namely *Acrolepiopsis brevipenella*, was described by Moriuti in 1972 based on one specimen collected from Xindian. We therefore suspected that the leek-feeding species might represent the species, that has never been seen after its discovery. However, one of our co-author (Lin) found another *Acrolepiopsis* species of which the larvae feed on *Discorea* in Xindian. We therefore found it is necessary to clarify the taxonomic identity of these two species and their origins. The COI sequence (658 bp) were obtained from 34 specimens of 8 species plus *Digitivalva reticulella*as the outgroup. Maximum likelihood method was used to reconstruct and tree and nodel supported was evaluated by 1000 bootstrap replicates.

結果/結論/應用啟示

Our analysis reveals that the leek-feeding species is *A. sapporensis* (= *Acrolepia salliella*), a new invasive species in Taiwan, and the *Discorea*-feeding one is *A. brevipenella*, an extremely rare indigenous species which has never been found again since 1972. Since *A. sapporensis*is considered as a serious pest of leek from Japan, Russia, Korea and China, the pathway of introduction of this new pest in Taiwan requires further investigation. We also wish to call the need of collecting genetic information of indigenous species that are related to alien pests in order to prompt early detection.

關鍵詞（Keywords）：Leaf-miner, Skeletonizer, Pest management, Hostplant utilization, Oligophagy

PS_06

臺灣巨波眼蝶亞種間之系統分類問題探討
Discussion on systematic problems between two subspecies of *Ypthima praenubila* in Taiwan

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背景/研究問題/材料方法

臺灣的蛺蝶科 (Nymphalidae) 內截至目前已記錄 12 個波眼蝶屬 (*Ypthima*) 物種 (Hsu et al., 2022)，其中巨波眼蝶 (*Ypthima praenubila*) 為體型最大且唯一一年一化 (Univoltine in occurrence) 的物種。本種過去被依體型大小分為臺灣北部亞種 ssp. *kanonis* 以及臺灣中南部亞種 ssp. *neobilia*，然而除體型外，兩者間的生活史、交尾器構造差異與分子生物學等相關證據尚未被進一步探討比較。本實驗分別以野外捕獲雌蝶進行人工採卵飼養、檢視不同地區成蟲之交尾器以及分析不同地區族群間粒線體 DNA*cox1* 片段是否存在不同結構組成，以探討兩亞種現行之分類處理是否適當。

結果/結論/應用啟示

初步檢視兩亞種間之交尾器顯示並無顯著構造差異，在粒線體 DNA*cox1* 片段分析之結果中亦顯示不同棲地之巨波眼蝶可能不存在明顯之隔離與遺傳分化。而生活史實驗方面以竹葉草 (*Oplismenus compositus*) 飼育之北中南三地族群所羽化的成蟲體型及幼期生物學特徵並無二致，將進一步分析成蟲翅紋組成是否存在分化。

關鍵詞（Keywords）：巨波眼蝶（*Ypthima praenubila*）、亞種（subspecies）、系統分類（systematic）、生活史（life history）

PS_07

應用 DNA 分子證據台灣地區長肛屬竹節蟲的分類地位與地理變異

Using DNA molecular evidence to analysis the phylogenetic and taxonomic status of *Entoria* stick insects (Phasmida: Phasmatidae: Clitumninae) in Taiwan

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背景/研究問題/材料方法

長肛竹節蟲主要分布在中國、台灣、日本、越南與菲律賓之沿海至淺山地區，共有 33 種，台灣有 12 種，皆為 1935 年之前發表，為台灣竹節蟲目中種數最多的一屬。雖多位學者質疑，許多物種僅根據少數或局部地區樣本而命名，可能有同物異名的分類疑慮，但至今尚未有學者對長肛屬進行更新或整理。

本研究根據學者提出的分類特徵及全台調查的形態變異特性，發現部份分類特徵在各地區有連續性的特徵變異，顯示各地族群處於不同程度的種化階段，長肛竹節蟲無飛行能力，在眾多高山分隔的台灣，極有可能產生地理隔離的形態變異，遂提出假說，認為長肛竹節蟲遷移特性弱及更新世週期性冰河期的族群隔離，與各地區長肛竹節蟲的不同形態變異程度有關。

本研究採集台灣各地的長肛竹節蟲成蟲，進行形態鑑定與分類特徵建檔分析，應用 DNA 序列分析其親緣關係，界定各物種單源群的特性，比較親緣關係結果後，分析各地區形態特徵的變異特性，尋找穩定的形態特徵應用於各物種的鑑定。

結果/結論/應用啟示

比較分析結果顯示親緣關係結果不支持形態鑑定結果，且各地族群在親緣關係分析上有明顯分化，可將族群依照地區區分為北部丘稜族群、中部山區族群、南部淺山族群、恆春半島族群、花蓮北部族群、台東南部族群等六大族群，其中北部族群與中部族群亦有出現依海拔高度分化的現象，結果顯示目前使用之鑑定特徵不適用，並在特徵統整上發現頭角、腿節與脛節的葉狀突起等主要的分類特徵已觀察到連續性變化，有重建形態特徵之必要。

關鍵詞（Keywords）：竹節蟲目（Phasmatodea）、長肛屬（*Entoria*）、親緣分析（Phylogenetic analysis）、DNA 分子證據（DNA molecular evidence）

PS_08

食孢展足蛾亞科 (Cuprininae) 之系統分類學研究及蕨類昆蟲演化關係之探討

Systematics and evolution dynamics of insect-fern interaction in the specialized fern-spore feeding Cuprininae (Lepidoptera, Stathmopodidae)

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背景/研究問題/材料方法

Fern feeding is rare in insects and restricted to only few groups of Lepidoptera. An even rarer phenomenon, fern-spores-feeding (FSF), can only be found in three families of moths. Stathmopodidae Meyrick, 1913 is the most speciose family that contains FSF species, where a subfamily, Cuprininae Sinev, 2015, exclusively specializes on FSF. Additionally, there are three species from subfamily Stathmopodinae Meyrick, 1913 that also specialize on FSF. To better understand the evolution of FSF, a systematics and taxonomic revision is necessary. We asked the following questions in this study: (1) does speciation/extinction rate differ between FSF and non-FSF groups? (2) how specialized is the host preference? and (3) does larval shelter type evolve in response to the association with different fern hosts?

結果/結論/應用啟示

We included representatives from all named genera in Cuprininae. We also included selected species the other two subfamilies, Stathmopodinae and Atkinsoniinae, for molecular systematics. Specifically, one mitochondria locus and four nuclear loci were used to reconstruct the phylogeny. We further argued that FSF evolved more than once in Stathmopodidae based on our reconstructed phylogeny. Our results also suggested that (1) speciation/extinction rates are not significantly different between FSF and non-FSF groups, (2) oligophage could be the ancestral state for Cuprininae, while lineages of specialist accumulated faster than oligophagous lineages through time, and (3) oval shaped shelter could be the ancestral state, while lineages of tunnel-shaped shelters builder accumulated with a faster rate through time. Nevertheless, there seems to be no association between shelter type and FSF.

關鍵詞（Keywords）：親源分析（Phylogenetic analysis）、昆蟲蕨類交互作用（Fern-insect interactions）、食蕨孢子（Fern-spore feeding）、祖徵重建（ancestral state reconstruction）、分子系統分類學（molecular systematics）

PS_09

台灣產霜天蛾屬的分類訂正

Taxonomic revision of *Psilogramma* Rothschild & Jordan, 1903 (Sphingidae) of Taiwan

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背景/研究問題/材料方法

The genus *Psilogramma* Rothschild & Jordan, 1903 (Type species: *Sphinx menephron* Cramer, 1780) is a genus of hawkmoth that is widely distributed from the Indian subcontinent, Indo-China, east Asia, Sunda islands, and Wallacea. In Taiwan, the genus was previously only known from a single species, *P. increta* (Walker, 1865). In 1994, Y.H. Chen reported "*Psilogramma menephron*" from Lanyu (Orchid Island) as a new addition to the sphingid fauna of Taiwan. This species was later also discovered from Green Island. In 1995, a congeneric moth collected from I-Lan was barcoded in 2022 and identified as *P. discistriga*. In addition, a *Psilogramma* species with extremely dark wing color was found in Taipei and Taichung, respectively. These findings suggest that a revision of this genus based on both morphological and molecular evidence is necessary. In order to clarify these taxonomic problems, we extracted COI sequence data from 68 individuals representing 32 *Psilogramma* species plus a *Macropollana gessi* as the outgroup. Both Maximum Likelihood and Bayesian inference were used to reconstruct the phylogeny and the species divergence was estimated following the general protocol for species delimitation based on COI fragment.

結果/結論/應用啟示

The phylogeny recovered from the present study suggests that: (1) the very dark *Psilogramma* found in Taipei and Taichung is a dark form of *P. increta* and such form has only been found in Taiwan and Japan; (2) the real *P. menephron* is endemic to Maluku of Indonesia, and not present in Taiwan; (3) all the previous records of *P. menephron* are *P. discistriga*, while the record of *P. discistriga* in I-Lan needs further confirmation. Our study shows that COI information is useful for species discrimination for the species complex that is almost indistinguishable based on morphology alone.

關鍵詞（Keywords）：Cryptic species, Wallacea, Barcoding, Biogeography, Taxonomy

行為、生理、個體生物學

壁報展示

Posters: Ethology, Physiology and Organismic Biology

PE_01

使用鳥類掠食者檢驗鱗翅目身體與翅膀斑紋在警戒性產生上之相對貢獻
Relative contribution between body and wing patterns in formation of aposematism of the Lepidoptera by using birds in predation experiment

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背景/研究問題/材料方法

動物身上的斑紋具有多種功能，包括熱能調節、性擇、禦敵以及種內競爭等，而體色斑紋在防禦的作用機制大致上可區分為警戒與隱蔽兩大類。以昆蟲警戒性研究來說，先前研究通常聚焦於翅膀，也就是佔身體面積最大的器官，卻鮮少觸及體色與身體斑紋所扮演的角色。然而根據我們的觀察，有相當比例的鱗翅目成蟲具有不醒目或相對不醒目的翅色花紋，但確具有相對醒目的身體花紋與顏色。由於降低掠食者直接攻擊身體似乎是警戒性形成與維繫的鐵律，因此為何部份物種的身體具有相對醒目的顏色與花紋便吸引了我們的注意。為了釐清身體與翅膀的斑紋顏色在警戒性形成所扮演的相對角色，本研究使用軟體設計出其花紋不存在於台灣的假想物種，並調控翅膀與身體顏色與花紋的相對醒目性，並比較無經驗小雞 (*Gallus gallus domesticus*) 對四組不同翅-身體組合的假餌之觀察與攻擊的反應，及其挑選之順序與取食量，並進行分析。

結果/結論/應用啟示

根據實驗結果表明，身體上的斑紋能作為掠食者所記憶的警戒訊號，且與翅膀所扮演的腳色可能不一致。像是金星尺蛾屬 (*Abraxas*) 的翅膀上被認為有擬鳥糞的斑紋，因此被認為是隱蔽性。但是他們的身體大多都有黃底黑點的高對比圖案，與隱蔽性的原則相互牴觸。因此當身體與翅膀扮演不同的腳色時，他們之間的關聯性為何與掠食者是如何判斷警戒與擬態的差異需要再進行更多的探究。

關鍵詞（Keywords）：行為學（Ethology）、警戒性（Aposematism）、迴避反應（Avoidance）、掠食者認知（Cognition of predator）

PE_02

球背象鼻蟲鱗片發育相關轉錄組分析
Transcriptome analysis of scale development in *Pachyrhynchus* weevils

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背景/研究問題/材料方法

許多昆蟲身上的鮮豔斑紋扮演重要的角色，提供交配辨識、警戒、求偶等功能。球背象鼻蟲身上的斑紋為結構色，透過不同晶體結構在不同角度的旋轉，形成多樣化的斑紋顏色。然而相關調節球背象鼻蟲斑紋的基因仍然未知。袖蝶屬蝴蝶 (*Heliconius* butterfly) 的研究中證實色素基因的改變會影響蝴蝶色彩斑紋，亦會影響鱗片的型態。本研究透過解剖羽化後 6 小時及 24 小時的斷紋球背象鼻蟲 (*Pachyrhynchus nobilis*) 翅鞘上有鱗片及無鱗片的位置進行比較，利用 RNA-seq 轉錄組分析鱗片及無鱗片翅鞘位置的差異表現基因 (Differentially expressed genes, DEGs) (foldchange>2, <-2)，找出可能調控鱗片的基因。

結果/結論/應用啟示

轉錄組分析羽化後 6 小時及 24 小時不同部位的 DEGs，分別有 3172 個及 2890 個。其中 1200 個基因於兩個不同羽化階段的鱗片及翅鞘均表現差異，且翅鞘跟鱗片基因表現的數量與羽化時間呈現正相關。從轉錄組基因中篩選鱗片發育相關基因如 Wnt、cortex、tyrosine 等進一步分析，同一階段鱗片或翅鞘會在某一相關的調控基因有較高的表現量。以相關調控路徑進行分析，發現不論羽化 6 小時及 24 小時，皆有較多的 DEGs 參與 Wnt signaling pathway、Ras signaling pathway、Calcium signaling pathway。本研究提供羽化後不同階段轉錄組分析的資訊，利用相關調控路徑分析基因表現數量，針對鱗片發育共篩選 25 及 28 個候選基因供未來進行 qPCR 檢測的參考依據。

關鍵詞（Keywords）：球背象鼻蟲（*Pachyrhynchus* weevils）、次世代定序（NGS）、RNA 序列（RNA-seq）、轉錄組分析（Transcriptome profiling）

PE_03

穀蠹（鞘翅目：長蠹蟲科）α-澱粉酶的基因選殖與轉錄表現
cDNA cloning and transcriptional expression of α-amylase in *Rhyzopertha dominica* (F.) (Coleoptera: Bostrichidae)

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背景/研究問題/材料方法

穀蠹 (*Rhyzopertha dominica* (Fabricius)) (Coleoptera: Bostrichidae) 是廣布全球的重要積穀害蟲之一。屬於初級害蟲的穀蠹，其危害後的破碎穀物易導致次級害蟲的發生，使倉儲損失更加嚴重。化學防治方面，穀蠹已被記錄對多種藥劑出現抗藥性，如磷化氫、第滅寧與馬拉松……等。為解決上述問題，了解穀蠹生理活動，並以此開發有效且環保的防治策略，對於現今社會十分重要。有鑑於穀蠹危害如稻穀、小麥等富含澱粉的穀物，故選殖其澱粉酶基因與檢測表現量，以初步了解穀蠹澱粉酶的特性，可提供資訊於研發破壞穀蠹營養攝取途徑的方法，進而達到防治之目的。

結果/結論/應用啟示

完成穀蠹 α-澱粉酶 cDNA 之選殖，全長為 1,572 bp，可轉譯出含 492 個胺基酸的蛋白質，其中包含與酵素結構完整性有關的鈣離子結合位，以及與酵素活化有關的氯離子結合位。表現量分析方面，雌成蟲與雄成蟲有顯著高於其他發育時期的表現量，其次為幼蟲，卵與蛹則最低。成蟲不同的組織中，中腸與前腸的表現量顯著高於其他組織，其次為後腸與馬氏管，精巢與卵巢則最低。有鑑於在中腸的表現量最高，推測所選殖的 α-澱粉酶基因應與穀蠹的消化生理較為密切，未來將嘗試透過基因默化來探討 α-澱粉酶於穀蠹消化與營養的功能，例如對於進食、生長、繁殖等方面的影響，期許能獲得更多有助於穀蠹防治方案開發的資訊。

關鍵詞（Keywords）：穀蠹（*Rhyzopertha dominica*）、α-澱粉酶（α-amylase）、消化（Digestion）、轉錄調節（Transcriptional regulation）

PE_04

Mass production and purification of GAL1-Melittin fusion protein in a baculovirus expressing vector system

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背景/研究問題/材料方法

Galectin-1 (GAL1) is a mammalian extracellular protein with binding specificity for β-galactoside. Recent studies suggest 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. Melittin is the main components of bee venom peptides with valuable therapeutic functions, such as anti-inflammatory and anti-fibrotic properties. Despite the pharmacologic efficacy of melittin, the cost of production is an issue need to resolve for its therapeutic application. Our research aims to develop a mass production strategy to increase melittin’s therapeutic value. The melittin will be overexpressed in *E. coli*as well as baculovirus in fusion with GAL1 which could be further purified with chitin-based affinity matrix. In a preliminary study, both melittin and GAL1 were cloned into the triex4 plasmid by using *Eco*RI and *Not*I and In-Fusion colony technology to overexpress in *E. coli.*

結果/結論/應用啟示

The results showed the plasmid with the fusion gene were successfully transformed and overexpressed in *E. coli* after IPTG induction, as indicated by SDS-PAGE and western blotting. Moreover, the GAL1-melittin fusion protein expressed in *E. coli* also could be pull-down by chitin powder, indicating the feasibility of mass production of melittin in a fusion protein. Future studies will be focused on the construction of recombinant baculovirus carrying both melittin and GAL1 genes for producing functional melittin, followed by the purification of recombinant products by using chitin matrix as the affinity ligand. These strategies could only efficiently generate adequate bee venom, but also economically purify the recombinant melittin by using a single chitin-based affinity column to enhance the medicinal value of melittin.

關鍵詞（Keywords）：（Galectin-1）、蜂毒肽（Melittin）、幾丁質（Chitin）、桿狀病毒表現載體系統（Baculovirus expressing vector system）、蛋白質純化（Protein purification）

PE_05

doublesex 在咖啡果小蠹的選殖及定性
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*) 的族群，雌雄蟲性別比為 10:1，雄蟲的體長 0.99-1.3 mm 小於雌蟲體長約 1.6-1.9 mm。同與咖啡果小蠹類似的小蠹蟲科物種，大多具有兩性異形 (sex dimorphism) 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 (master regulators) 及兩性開關基因 (double-switch genes)，目前仍屬未知。由於兩性開關基因中的 *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 (*in situ* hybridization) 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

我們初步的實驗結果顯示在胚胎發育過程中，偵測到 *dsx* 表現於咖啡果小蠹的胚胎前端位置。未來將藉由基因靜默技術來確認 *dsx* 在咖啡果小蠹的基因功能。本研究結果將可作為小蠹蟲性別決定的基礎資訊，進而瞭解其展現多雌現象之成因。

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

PE_06

黃斑黑蟋蟀 (直翅目：蟋蟀科) 打鬥行為之動作分類與初探
The classification of action and initial exploration of fighting behavior of *Gryllus bimaculatus* (Orthoptera: Gryllidae)

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背景/研究問題/材料方法

某些動物會有領域行為的表現，表現方式包括氣味、聲音或是打鬥等不同方式防止同種或不同種入侵其領域 (楊瑞珍，2002)。黃斑黑蟋蟀 (*Gryllus bimaculatus*) 會進入台灣大蟋蟀的洞穴並與入侵者發生打鬥的行為，獲勝者則占有該領域。本研究主要以黃斑黑蟋蟀成蟲 (雄)、成蟲 (雌)、老熟若蟲 (雄) 、老熟若蟲 (雌) 、初齡若蟲 (無法分辨雄雌) 等 5 種不同發育期與性別的黃斑黑蟋蟀，進行黃斑黑蟋蟀打鬥行為的動作分類與研究。

結果/結論/應用啟示

黃斑黑蟋蟀有領域行為的表現，在觀察與分析不同發育期與性別蟋蟀的打鬥行為後，其打鬥前的動作有：靜止不動、清潔身體、到處走動；打鬥中的動作有：觸鬚快速抖動並相互碰觸、頭部碰撞、身體抬高、後足彎曲、以頭互頂、張顎對峙、以大顎攻擊；打鬥後的動作有：敗者逃離現場、勝者抖動身體或振翅高歌。其中，當成蟲 (雄)遭遇成蟲 (雌)時，除了成蟲 (雄) 比較不會攻擊成蟲 (雌) 外，還會發出求偶的聲音進而與成蟲 (雌) 發生交配的行為；另外，多數初齡若蟲僅在觸鬚碰觸後而未有其他身體接觸，就會表現出打鬥勝負結果的動作。

關鍵詞（Keywords）：黃斑黑蟋蟀（*Gryllus bimaculatus*）、打鬥行為（Fighting Behavior）

PE_07

光源對螞蟻工蟻定向行為的影響
The effect of light source on orientation behavior of worker ants

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背景/研究問題/材料方法

近幾年來許多地區都受到蟻害威脅，尤其是的中南部地區受到了許多物種，包括：入侵紅火蟻 (*Solenopsis invicta*)、白足扁琉璃蟻 (*Technomyrmex albipes*)、褐色扁琉璃蟻 (*Technomyrmex brunneus*)、疣胸琉璃蟻 (*Dolichoderus thoracicus*)、長腳捷蟻 (*Anoplolepis gracilipes*) 等危害。其中琉璃蟻種類因大量婚飛個體因趨光聚集，造成人們生活影響嚴重，扁琉璃蟻在每年六至十月為交配婚飛 (Nuptial flight) 期。有翅型 (Alate) 的雌蟻與雄蟻因具有趨光性會在該季節夜間在人類活動燈光區域大量聚集，影響人們日常生活。而除了婚飛型螞蟻外，也有許多工蟻也常常受燈光聚集，且程度日甚一日，這些螞蟻在過去十年不曾這麼大量聚集，因此對於近年來螞蟻大量的出現，是否為環境變化或人為更換 LED 型路燈有關值得進行探討。昔日研究指出，昆蟲對於不同的光波長會有不同的行為模式。本實驗主要是針對於不同的光波長，紅光、白光、UV 光透過燈光誘集掉落陷阱的方式來吸引無飛行能力工蟻的定向調查。

結果/結論/應用啟示

依據調查的數據中，在實驗地點中主要存在的螞蟻物種為熱帶大頭家蟻 (*Pheidole megacephala*)，在定向行為 (Orientation Behavior) 中熱帶大頭家蟻的工蟻大多會掉落至 UV 光之陷阱，而白光次之，紅光最少，之後將於調查完後分析不同的光波長及環境因子的變化是否對螞蟻定向行為有所影響。而新式的 LED 路燈含有較多的 UV 光，日後進一步探討藉由新路燈中的 LED 光減少誘引工蟻的靠近，以致解決螞蟻對人類環境生活的影響。

關鍵詞（Keywords）：人造光（Artificial light）、光干擾（Light disturbance）、光波長（Light wavelength）、定向行為（Orientation behavior）、工蟻（Worker）

PE_08

Transcriptome of *Nosema ceranae* with the treatment of *Bidens pilosa* phytogenic during its infection of western honey bee (*Apis mellifera*)

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背景/研究問題/材料方法

Nosema ceranae is a fungal parasite causes honey bee (*Apis mellifera*) nosemosis. In this study we discuss the gene expression of *N. ceranae* during its infection process and the *Bidens pilosa* phytogenic (BP) treatment, which can increase the survival rate and survival time of infected honey bees. The transcriptome profile of mature spores at each time point of infection (5, 10 and 20 days post-infection, d.p.i.) during different treatment (DMSO, BP) were investigated, and identified differentially expressed genes (DEGs).

結果/結論/應用啟示

In *N. ceranae* infection group, it showed more downregulated genes during infection process, especially at late period. Moreover, 70 upregulated genes and 340 downregulated genes among common DEGs and 166 stage specific genes at each stage of *N. ceranae* infection group were identified. The Gene Ontology (GO) analysis indicated that the DEGs and common DEGs in *N. ceranae* infection group were involved in the various functions. The seven genes from *N. ceranae* infection group were selected to validation, including four upregulated common DEGs with higher fold-change values; three of the stage specific genes showed high expression at each d.p.i. Interestingly, more upregulated *N. ceranae* genes at early infection stage in DMSO treatment group, while more downregulated *N. ceranae* genes at early infection stage in BP treatment group were found. The KAAS pathway analysis found that the common DEGs in *N. ceranae* infection, DEGs in DMSO and BP treatment group were more involved in metabolism pathway. One gene involve to V-type ATPase, eukaryotes (M00160), which has higher fold-change during the infection process in DMSO and BP treatment group, was selected to validation. Our data provided the gene expression profiling in *N. ceranae*, which could be a reference for the monitoring nosemosis at the genetic level, besides, also regulation of V-type ATPase in *N. ceranae* during BP treatment will be further investigated.

關鍵詞（Keywords）：differentially expressed genes, transcriptome, *Nosema ceranae*, *Apis*

mellifera, *Bidens pilosa* phytogenic

PE_09

藉由溫控微型 RNA 抑雌系統達到控制東方果實蠅雌蟲數量試驗分析
Experimental analysis of temperature-controlled microRNAfemale repressing system to control the female population of *Bactrocera dorsalis*

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背景/研究問題/材料方法

背景

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。

研究問題

通過對東方果實蠅早期胚胎微型 RNA 定序，Peng 等人發現了一個由體染色體來的 miR-1-3p，透過序列比對預期能與雌性性別決定所需的 *transformer* 基因 (*Bdtra*) 結合，並通過體外和體內測試證明 miR-1-3p 能抑制 *Bdtra* 表現 (Peng *et al.,* 2020)。以此為基礎，我們透過轉殖技術置入外源 miR-1-3p 基因，再利用預設的 Heat shock promoter 誘發性表現，觀察是否能經由干擾 *Bdtraf* 的功能，在轉殖蠅中造成抑雌現象及性別比例改變。

材料方法

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 和野生種果實蠅回交，再使用螢光顯微鏡篩選出帶有紅螢光的 G1，G1 再經過 single pair 實驗，篩選出帶有紅螢光的蛹，此為 G2，G2 成蟲先抽取 genomic DNA 經 PCR 分析外源 miR-1-3p 存在後，再經由後續自交產生 G3，G3 將成蟲平均分成 9 組自交，分別進行熱誘發實驗，將 2 小時內採的卵分一半，一半進行 37℃熱處理 3 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，再與經過相同試驗的野生種果實蠅作為對照組比較差異。

結果/結論/應用啟示

結果

在卵的熱誘發實驗中，G3 M4、M5 和 M9 這三組基因轉殖品系成蟲在熱處理組雄性比分別為 66.67%、77.78% 和 62.50%；無熱處理組分別為 42.86%、53.85% 和 55.35%，在熱處理組中基因轉殖品系的雄蟲數量明顯多於雌蟲，而熱誘發實驗中野生種熱處理組和熱處理組雌雄蟲比例分別是 52.44%和 53.78% 雌雄數量相近。

結論

由初步結果推測在胚胎性別決定時期，若果實蠅體內在短時間內誘發大量 miR-1-3p，會影響到雌蟲生理發育甚至導致死亡，因而造成基因轉殖品系在成蟲時期，雄蟲數量會多於雌蟲，另外推測各轉殖雄性比稍低可能與轉殖蠅品系中帶有 miR-1-3p 的比例與插入位置有關。

應用啟示

後續實驗先從 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 *Bdtra*、*Bddsx* 和 miR-1-3p 在卵、幼蟲、蛹和成蟲不同階段的基因表現。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，將在防治上具有潛力及法規容許下，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*, miR-1-3p, *transformer*, *Bdtra*

PE_10

全樣本原位雜合及免疫染色技術於無性生殖豌豆蚜之不同器官下的最佳化策略

The optimization of whole-mount *in situ* hybridization and immunohistochemistry on different organs of the asexual pea aphid, *Acyrthosiphon pisum*

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背景/研究問題/材料方法

The pea aphid, *Acyrthosiphon pisum*, is a productive hemipteran species whose whole-genome had been sequenced in 2010. By convenience accessibility of genetic information, we established protocols of whole-mount *in situ* hybridization (WISH) and whole-mount immunohistochemistry (WIHC) on ovaries of the asexual pea aphid. These techniques could visualize the loci of gene products including gene transcript and protein, which provide the characteristics of a certain gene. To have these techniques work more efficiently, we study two aspects of which. The first one is to study if customized permeabilization strategy on embryos at different stages is required. The second one is to study if there are possible for these techniques to work on other internal tissues. Therefore, we did not only test Proteinase K incubation time on embryos for detecting ApVas1 protein but also tried to apply these techniques on the salivary gland to detect gene products of a salivary gland gene *c002.*

結果/結論/應用啟示

In our results, we found customized PK incubation is necessary when performing WIHC on different embryos. For early-stage embryos, 10 or 20 min incubation of 1 μg/ml Proteinase K was enough for embryo permeabilization; however, for mid and late-stage embryos within the ovary, only 40 or 60 min incubation of 1 μg/ml Proteinase K was enough. On the other hand, we succeeded in detecting transcript and protein of the gene *c002* by using established WISH and WIHC. The protocols of these techniques can be smoothly transferred from the ovary to the salivary gland without significant change. In summary, we had our established techniques work better on embryos at different stages, and found them also workable on the organ salivary gland. These facts show that permeabilization of different samples should always be assessed. Besides, these techniques have the great potential to apply on other internal organs in the asexual pea aphid.

關鍵詞（Keywords）：豌豆蚜（*Acyrthosiphon pisum*）、全樣本原位雜合（whole-mount

in situ hybridization）、全樣本免疫染色（whole-mount immunohistochemistry）、蛋白酶 K（Proteinase K）、唾腺（salivary gland）

農業昆蟲學

壁報展示

Posters: Agricultural Entomology

PA_01

Evaluation of selected tomato varieties for female oviposition and larval performances of *Phthorimaea absoluta* (= *Tuta absoluta*) in Taiwan and the implications for its control

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背景/研究問題/材料方法

Phthorimaea absoluta (= *Tuta absoluta*) is a cosmopolitan pest that is native to South America and the global expansion in recent years has threatened the production of a wide range of solanaceous crops including tomatoes. When making policy for management, the knowledge of female oviposition and larval feeding performances on plants is essential. Previous studies have shown that the preference for different solanaceous species of this moth varies in different countries. Meanwhile, the bioassay results from different tomato cultivars are also inconsistent. To investigate whether different tomato cultivars are linked to different management policies of this insect in Taiwan, we examined the female oviposition and larval feeding performance on five major tomato cultivars (Micro Tom, Golden Cherry, Cherry, Black Persimmon, and Beef tomatoes). Oviposition preference was assessed using a choice experiment by using 15 pairs of sex-determined moths per replicate (a total of six replicates per tomato cultivar). The hatching success of eggs, pupa emergence, larval period, and larval mortality were recorded on each cultivar. We also employed an integrated approach (Ilastik [pixel classification] and ImageJ) to quantify the density of the glandular trichomes on leaves of each tomato cultivar to assess the correlation between trichome density and female oviposition and larval feeding performances.

結果/結論/應用啟示

One-Way ANOVA test results indicated that oviposition (p-value = 0.561), pupa emergence (p-value = 0.2948), larval period (p-value = 0.941) and larval mortality (p-value = 0.4621) among the cultivars were not significantly different, while the eggs laid on cherry tomatoes showed the highest percentage of hatching. There was no significant difference among adaxial glandular trichome density in all varieties (p-value = 0.068) so proposing different strategies for different cultivars might not necessary, but the combined effect of volatile chemicals with trichomes might play a significant role in the success of a new invasive herbivore.

關鍵詞（Keywords）：Oviposition, Larval performance, Pest management, Herbivory, Oligophagy

PA_02

以野生十字花科植物作為陷阱作物在蟲害管理之評估研究
Evaluation of wild *Brassicaceae* as trap crops in pest management

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背景/研究問題/材料方法

推拉策略 (push-pull strategy) 為病蟲害整合管理 (IPM) 的一部份，現今多應用於非洲地區且效果顯著，目前在臺灣應用此概念作為害蟲防治之例證較少。十字花科植物產生的次級代謝產物對專食性昆蟲具刺激產卵與取食效果，亦有研究指出在野生植物上的次級代謝產物含量較栽培作物高。因此，野生十字花科對專食性昆蟲可能具更高的取食及產卵偏好效果，且或許能削弱植食昆蟲之族群。本研究試驗專食性昆蟲—紋白蝶 (*Pieris rapae crucivora* Boisduval) 與廣食性昆蟲—斜紋夜蛾 (*Spodoptera litura* Fabricius) 在野生十字花科—細葉碎米薺 (*Cardamine flexuosa*) 及栽培作物上的生長表現、幼蟲取食偏好及成蟲產卵偏好，以評估野生十字花科作為陷阱作物 (trap crop) 的潛力。

結果/結論/應用啟示

取食細葉碎米薺，在三齡幼蟲之相對消耗速率 (RCR) 中，紋白蝶 (1.43mg/mg/hr) 高於斜紋夜蛾 (0.22mg/mg/hr)，具極顯著差異；在消耗食物轉換率 (ECI)，斜紋夜蛾 (23.20%) 高於紋白蝶 (3.83%)，具極顯著差異；在幼蟲相對生長速率 (RGR)，斜紋夜蛾 (0.10mg/mg/hr) 高於紋白蝶 (0.04mg/mg/hr)，具極顯著差異。顯示斜紋夜蛾之三齡幼蟲於相同時間內取食雖較紋白蝶幼蟲少，但消耗食物轉換率卻較高，因此短期生長表現較佳，但尚未測試取食偏好，無法確定細葉碎米薺對斜紋夜蛾是否具忌避作用。後續將針對植物中黑芥子酶 (Myrosinase) 含量做檢測，若能進行田間試驗，了解生態系統及環境因子對此實驗之影響，更能評估用於田間之可行性。

關鍵詞（Keywords）：陷阱作物（Trap crop）、次級代謝產物（secondary metabolites）、細葉碎米薺（*Cardamine flexuosa*）、紋白蝶（*Pieris rapae crucivora* Boisduval）、斜紋夜蛾（*Spodoptera litura* Fabricius）

PA_03

咖啡果小蠹生活史及胚胎發育圖譜建立
Research on the life cycle and developmental atlas of the coffee berry borer

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背景/研究問題/材料方法

咖啡果小蠹 *Hypothenemus hampei* (英文俗名為 coffee berry borer, 簡稱 CBB) 是咖啡的重要經濟害蟲。有關 CBB 的防治策略已有許多研究報導，然而，因其體型小且特殊之隱食性行為，導致不易觀察 CBB 的生命週期，且胚胎發育的基礎研究資訊仍付之闕如。為瞭解 CBB 之發育期程，我們專注於建立其胚胎發育圖譜及後胚胎發育時期的生活史紀錄。以未添加抗生素的人工飼料餵食，在 25°C、85％ 相對濕度且全暗的環境條件下飼養，已成功建立實驗品系族群。藉由每日記錄卵期、幼蟲期、蛹期及成蟲期所需天數，瞭解 CBB 的生活史。在建立胚胎發育圖譜的部分，我們取出不同發育時間的卵，藉由核染劑及細胞骨架染劑進行胚胎染色觀察。

結果/結論/應用啟示

我們所觀察到的 CBB 生活史與前人研究相符，包含有卵期、二齡幼蟲期 (雄蟲僅具一齡)、蛹期及成蟲期。由個別飼養 CBB 所統計的生活史資料，初步統計數據顯示卵期至一齡期的死亡率為 50.3%; 從幼蟲期至蛹期的死亡率降為 30.9%; 而蛹期至成蟲期的死亡率則為 4.39%。本研究使用無抗生素人工飼料所建立之實驗品系，減少對 CBB 共生菌的影響，除了可供作基礎發育生物學之試驗材料，亦可作為農藥試驗之用。未來將致力於建構完整胚胎圖譜，以利比較 CBB 與鞘翅目昆蟲模式物種-擬穀盜 *Tribolium castaneum* 在發育模式及生活史上之演化特徵。

關鍵詞（Keywords）：人工飼料（artificial diet）、胚胎發育（embryonic development）、生活週期（life cycle）

PA_04

利用多光譜影像與機器學習偵測瘤野螟於水稻上的危害
Detection of rice leaf folder damage on rice using multispectral images and machine learning

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背景/研究問題/材料方法

蟲害偵測是綜合害物管理 (Integrated Pest Management) 的重要策略之一，可為作物管理提供防治所需之相關資訊，有助於精準用藥並提高防治效率，降低農藥使用量與農產損失，進而保障糧食作物的生產品質與數量。瘤野螟為造成水稻產量損失的重要害蟲之一，以反射率圖譜差異進行的偵測方式在近年被廣泛研究，但瘤野螟在水稻上造成的危害狀光譜特性仍有待持續探究。本試驗擬使用多光譜影像取得並分析瘤野螟危害狀之反射率圖譜，結合機器學習中的支持向量機 (Support Vector Machine, SVM) 以及深度神經網路 (Deep Neural Networks, DNN) 訓練模型，於田間環境下進行蟲害偵測。

結果/結論/應用啟示

受瘤野螟危害區域的可見光波段的反射率圖譜光譜反射率較未受害者高，在近紅外光波段的反射率圖譜光譜反射率則較未受害者低，而比較不同性質的危害狀發現褐斑危害狀的近紅外光反射率圖譜光譜反射率譜較泛白危害狀低。在模型表現中，SVM 及 DNN 的準確率分別為 85.7% 與 86.0%，召回率為 85.7% 與 86.0%，精確率為 85.6%與 86.0%。本試驗結果顯示不同性質的危害狀具有可辨識的差異，利用以多光譜影像中提取出的反射率圖譜所訓練的蟲害偵測模型能辨識並標記危害狀位置，在精準蟲害偵測上具備發展潛力，未來可做為監測瘤野螟的重要策略之一。

關鍵詞（Keywords）：蟲害偵測（Insect infestation detection）、瘤野螟（*Cnaphalocrocis medinalis*）、反射率圖譜（Reflectance profile）、機器學習（Machine learning）

PA_05

小菜蛾抗因滅汀基因之分析與研究
Genes involved in the emamectin benzoate resistance in diamondback moth, *Plutella xylostella*

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背景/研究問題/材料方法

小菜蛾 (*Plutella xylostella* L.) 為菜蛾科菜蛾屬昆蟲，是全世界分布最廣泛的鱗翅目害蟲，每年估計對全世界造成約40-50億美元的經濟損失及防治成本。小菜蛾的防治策略包含生物防治、耕作防治、化學防治等方法，目前主要以施用殺蟲藥劑為主，但由於藥劑使用頻繁促使田間選汰壓力高，再加上小菜蛾生命週期短、繁殖力強，導致抗藥性發展迅速，現今已對 101 種有效成分產生抗性。為了了解台灣小菜蛾對因滅汀的抗藥性機制，我們採用實驗室以因滅汀長期篩選的抗性品系 TTSel 與未接觸藥劑的因滅汀抗性消退品系 TTRx 進行轉錄質體分析，並針對可能的解毒基因進行 qPCR 檢測，分析抗性品系及消退品系間基因表現量的差異。

結果/結論/應用啟示

根據轉錄質體分析結果發現 32 個與表皮相關的基因及 66 個與解毒代謝相關的基因具有顯著性的表達差異，隨後挑選 $|\text{Log2(fold change)}| \geq 1$ 的 P450 6B7、P450 4C1、Juvenile hormone esterase (JHE) 三個基因進行 qPCR 的分析。結果發現 TTSel 的 P450 6B7 表現量高於 TTRx 2.3 倍、JHE 和 P450 4C1 的表現量則為 0.9 及 0.2 倍，其趨勢與轉錄質體分析結果 (4.8 倍、0.1 倍、0.2 倍) 相似。因此推測 P450 6B7 可能與小菜蛾對因滅汀的抗性機制具有正調節相關性，而 P450 4C1 及 JHE 可能具有負調節相關性。本研究提供了因滅汀與小菜蛾抗性機制的基礎，但未來仍需更深入的實驗來探明其中的機制。

關鍵詞（Keywords）：小菜蛾（*Plutella xylostella*）、因滅汀（Emamectin Benzoate）、抗藥性（Insecticide resistance）、轉錄質體分析（Transcriptome analysis）

PA_06

瓜螟對葫蘆科常用藥劑感受性測試
Evaluation of the sensitivity of *Diaphania indica* to pesticides

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背景/研究問題/材料方法

瓜螟的寄主植物包括甜瓜、西瓜、胡瓜、絲瓜、苦瓜、越瓜、南瓜、棉、桑、茶、梧桐等，在瓜類栽培初期，幼蟲以嫩葉為食，進入開花結小果時期則由嫩果皮鑽入為害，果實成熟期則取食果皮或鑽入果實，族群數量大時嚴重影響產量與品質。瓜螟為多世代物種，在日本、臺灣、印度、中國、澳洲、中亞、非洲與美洲均有分布，在臺灣一年可發生 4-5 代以上。在印度近幾年瓜螟對葫蘆科作物為害日漸重要，而日本自 2000 年起亦成為造成葫蘆科作物苗期缺株的主因，顯示在劇烈的氣候變遷之下，此次要害蟲在不預期發生的情況下，有潛力造成作物嚴重被害的情形。然而，目前國內葫蘆科無針對瓜螟登記的化學防治用藥，本研究使用瓜類常用殺蟲劑二福隆、芬化利、因滅汀、剋安勃、賜諾特和鮎澤蘇力菌，對瓜螟進行室內藥劑感受性評估。依已登記殺蟲劑之使用方法稀釋藥劑，採用葉浸法，以甜瓜葉片浸泡藥劑 10 秒鐘，風乾後放入塑膠盒中，每盒放入 3 片葉片，然後放入 15 隻瓜螟 3 齡幼蟲，每處理 3 重複，72 小時後進行幼蟲存活數量調查，並計算死亡率。

結果/結論/應用啟示

試驗結果，二福隆、因滅汀、剋安勃和賜諾特對瓜螟 3 齡幼蟲室內藥效試驗，分別造成 98.2%、100%、100% 和 100% 的死亡率，顯示對瓜螟幼蟲亦有良好防效，可做為田間防治藥劑之選擇。鮎澤蘇力菌則有 69.8% 死亡率，對瓜螟幼蟲尚有防效，但是芬化利則在室內藥效試驗即無法造成瓜螟 3 齡幼蟲死亡 (死亡率為 0%)，故不建議在田間使用芬化利防治瓜螟。

關鍵詞（Keywords）：瓜螟（*Diaphania indica*）、殺蟲劑（insecticide）、化學防治（chemical control）

PA_07

不同施藥方法對蓮花小黃薊馬防治效果之研究
Study on the control effect of different pesticide spraying methods on *Scirtothrips dorsalis* Hood

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背景/研究問題/材料方法

小黃薊馬 (*Scirtothrips dorsalis* Hood) 危害作物廣，於蓮花上常躲藏於葉背及葉柄，蓮葉受到小黃薊馬吸食或產卵後，無法正常展開或出現皺褶與變色，進而影響蓮子及蓮藕產量。近年來，無人植保機因具備省工且可減少藥液使用量之優點，逐漸受到農業重視，廣泛應用於病蟲害防治。本研究探討蓮花小黃薊馬於不同發生密度時，無人植保機與人工噴藥防治效益之差異。本試驗於雲林縣林內鄉進行，蓮花種植後一週於每塊試驗田設置 9 個黏紙板，正反各 2 張黏紙，每週回收並更換黏紙。於蓮花立葉期後 5 週 (7 月中旬)，依照黏紙上小黃薊馬不同密度，將試驗地分為四區，A 區及 B 區應用無人植保機 (佐翼 DX-10) 搭載噴頭 TR8001 進行防治，C 區則應用噴藥車及人工拉管方式進行防治，CK 區不進行防治，防治區以單位面積用藥量之 20%覆滅蟎水溶性粉劑進行防治。

結果/結論/應用啟示

蓮田立葉期後 5 週，每區黏紙上的平均小黃薊馬密度分別為 CK 區 78.3 隻、A 區 60.1 隻、B 區 174.9 隻及 C 區 168.2 隻。第一次防治後，無人植保機防治方式可達到 75% 以上的防治率，而人工防治方式僅造成 9.8% 的防治率。第二次防治後，四區小黃薊馬密度皆有下降，A 區及 B 區密度分別為 20.3 隻及 44.3 隻，防治率分別為 74.5% 及 80.8%；C 區密度則降至 164.0 隻，防治率僅 26.3%。綜合以上結果，蓮花小黃薊馬發生密度於 175 隻/黏紙以下時，以無人植保機防治蓮花小黃薊馬確實能達到成效，且防治效益明顯優於人工拉管噴藥方式。同時小黃薊馬密度低時進行防治，更能維持防治效果達到四週，顯示蓮田於小黃薊馬發生初期以無人植保機噴灑單位面積用藥量之 20% 覆滅蟎水溶性粉劑，能有效控制小黃薊馬密度且維持其藥劑效果。

關鍵詞（Keywords）：小黃薊馬（*Scirtothrips dorsalis* Hood）、無人植保機（Unmanned Plant Protection Machine）、防治率（Control rate）

PA_08

殺蟲劑對蓮花小黃薊馬之室內藥效評估
Laboratory evaluation of the effect of insecticides for controlling *Scirtothrips dorsalis* Hood on lotus

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背景/研究問題/材料方法

小黃薊馬 (*Scirtothrips dorsalis* Hood) 蟲體小又常躲藏於蓮花葉背或葉柄，加上登記藥劑少，導致蓮花小黃薊馬危害日益嚴重。本研究探討殺蟲劑對蓮花小黃薊馬之毒效及致死劑量。藥劑篩選以浮葉法方式進行試驗，測試小黃薊馬二齡幼蟲對藥劑之敏感性，以藥品噴霧塔噴施可用於蓮花上之登記殺蟲劑及其推薦倍數，而對照組噴施 RO (Reverse Osmosis, RO) 水，每處理三重複，噴施藥劑後置於恆溫生長箱 (25℃，55% RH，12L:12D)，並於 12、24 及 48 小時進行觀察，計算死亡蟲數及校正死亡率。致死劑量試驗以相同方法噴施篩選後之 2 種藥劑，分別為 10% 克凡派水懸劑噴施 25、50、75、100、125、150 ppm 及 20% 覆滅蟎水溶性粉劑噴施 50、250、500、750、1000、2500、5000 ppm，每處理三重複，噴施藥劑後 12、24 及 48 小時進行觀察，計算死亡蟲數與校正死亡率，並以軟體 Probit-MSChart program (Chi, 2021) 估算半數致死劑量 (Lethal Dosage 50%, LD_{50}) 及 90% 致死劑量 (LD_{90})。

結果/結論/應用啟示

藥劑篩選結果顯示以 11.7% 賜諾特 8000 倍、2.5% 賜諾殺 1000 倍、20% 覆滅蟎 400 倍及 10% 克凡派 1000 倍噴施小黃薊馬二齡幼蟲，藥劑效果顯著高於其他藥劑，處理後 48 小時之校正死亡率可達 90% 以上，其次為 40% 納乃得 1500 倍，處理後 48 小時之校正死亡率為 57%，其他供試藥劑之登記稀釋倍數效果均不佳。為提供無人植保機噴藥劑量之參考，兩種藥劑依照政府公告之每公頃推薦最低用藥量，並以 10 L 無人植保機藥桶推算有效濃度，20% 覆滅蟎為 7499.06 ppm，10% 克凡派為 750.02 ppm。而本研究之致死劑量試驗結果顯示覆滅蟎 LD_{50} 及 LD_{90} 分別為 223.3 ppm 及 1335.1 ppm，克凡派 LD_{50} 及 LD_{90} 分別為 80.0 ppm 及 316.8 ppm，兩供試藥劑之濃度皆低於公告之每公頃推薦用藥量，未來應可作為田間無人植保機藥劑施灑之濃度參考，以達到藥劑減量之目標。

關鍵詞（Keywords）：殺蟲劑（insecticides）、小黃薊馬（*Scirtothrips dorsalis* Hood）、死亡率（mortality）、半數致死劑量（Lethal Dosage 50%）

PA_09

評估淡紫菌菌株對荔枝椿象之致病力及幾丁質分解能力
Evaluation of chitinolytic activity and virulence of *Purpureocillium takamizusanense* strains against *Tessaratoma papillosa* (Drury)

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背景/研究問題/材料方法

淡紫菌 *Purpureocillium takamizusanense* 為自荔枝椿象 *Tessaratoma papillosa* (Drury) 蟲體分離鑑定的蟲生真菌。本研究將臺南地區所收集之淡紫菌菌株樣本進行編號，依據菌株的形態特徵及分子生物學特性進行鑑定，以荔枝椿象成蟲及若蟲作為供試寄主，進行淡紫菌菌株致病力試驗，並以軟體 Probit-MSChart program (Chi,2021) 估算半數致死時間 (Lethal Time 50%, LT_{50})。另文獻顯示 *Purpureocillium* 屬蟲生真菌之殺蟲機制與幾丁質酶有密切關係，藉由測量淡紫菌菌株於幾丁質培養基所產生的透化圈直徑/菌落直徑之數值來評估菌株之幾丁質分解能力。

結果/結論/應用啟示

致病力試驗結果顯示，自荔枝椿象成蟲分離的 9 株淡紫菌菌株對荔枝椿象若蟲及成蟲皆具致病性，且對荔枝椿象若蟲及成蟲展現不同程度之感染能力。淡紫菌菌株對荔枝椿象若蟲之校正致死率為 60-100%，半數致死時間 (LT_{50}) 為 14-28 天。其中，NH3 菌株及 RM4 菌株對若蟲的校正死亡率皆可達到 100%。而 NH3 菌株及 NH4 菌株對荔枝椿象若蟲之半數致死時間最短，分別為 14.06 及 14.40 天。荔枝椿象成蟲部分，淡紫菌菌株校正致死率為 70-100%，半數致死時間 (LT_{50}) 為 29-50 天。其中，TNZZS6 菌株、RM4 菌株及 RM5 菌株對荔枝椿象成蟲的校正死亡率皆為 100%。另淡紫菌 TNZZS6 菌株及 NH3 菌株對荔枝椿象成蟲之半數致死時間最短，分別為 29.08 及 29.65 天。幾丁質酶活性試驗結果顯示，淡紫菌 ZZS 系列菌株及 NH3 菌株之幾丁質分解能力最強，透化圈直徑/菌落直徑之數值為 1.54-1.47。綜合上述結果，9 株淡紫菌菌株均可造成荔枝椿象成、若蟲死亡，而 TNZZS6 菌株及 NH3 菌株展現強致病力及分解幾丁質之能力，未來應進一步探討作為微生物殺蟲劑的可行性。

關鍵詞（Keywords）：淡紫菌（*Purpureocillium takamizusanense*）、荔枝椿象（*Tessaratoma papillosa*）、致病力、幾丁質酶

都市昆蟲學

壁報展示

Posters: Urban Entomology

PU_01

疣胸琉璃蟻於休閒場域之入侵與防治調查
Investigation on infestation and control of *Dolichoderus thoracicus* terrestris in leisure fields

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背景/研究問題/材料方法

疣胸琉璃蟻 (*Dolichoderus thoracicus*) 為臺灣本土樹棲型蟻類，分佈於海拔 500 - 600 公尺以下樹林、雜樹林、荒廢地及農園等，其蟻巢型態為多蟻后型；近年疣胸琉璃蟻為入侵休閒環境之新興害蟲，危害干擾民眾之日常生活。本研究自臺灣目前病媒防治業者 1324 家，隨機抽樣 332 家，以電話訪問病媒防治業者對疣胸琉璃蟻防治之知識、態度及行為調查，以期對疣胸琉璃蟻入侵、生態習性、防治策略之瞭解及預防。

結果/結論/應用啟示

結果共完成 321 家業者訪問調查 (回收率 96.7 %)，有 12.5 % 病媒防治業者曾防治過疣胸琉璃蟻，其防治地點分佈於臺灣 14 個縣市，從臺北市至屏東縣及延伸東部花蓮縣，防治月份以 5 月至 9 月最多，結合中央氣象局觀測資料得知，該期間亦為月均溫及月平均雨量之高峰，夏季高溫及陣雨等不穩定之氣候因素，增加驚動蟻群、使其遷徒擴散族群的機會；防治地點以民宅、農園及雜木林等休閒場域最高 (27.5 - 17.5 %)；入侵休閒場域之途徑為水管、電氣設備、鋁門窗及園藝植栽等；而病媒防治業者對疣胸琉璃蟻防治之知識、態度及行為調查結果：病媒防治業者對環境管理及一般防治作業態度及行為具基本認知 (100 - 75.4 %)，但對疣胸琉璃蟻生態習性及天然植物保護資材防治相關知識瞭解較少 (41.1 - 38.0 %)，建議可透過教育訓練或製作文宣手冊加強此相關宣導。

關鍵詞（Keywords）：新興害蟲（Emerging pests）、樹棲型（Arboreal）、疣胸琉璃蟻（*Dolichoderus thoracicus*）、入侵（Infestation）、防治（Control）

PU_02

病媒防治業者之企業責任
Corporate Responsibility of Pest Control Operators

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背景/研究問題/材料方法

城鄉快速發展帶來都會區生活品質提升，為維護全體國民健康，特別是管控居住環境免於被有害生物侵害，成為環境衛生維護工作重要的一環，也是城市衛生指標之一。一般而言病媒防治業 (PCO/ Pest Control Operator) 之業務內容包含兩大部分：在短時間內且快速進行防治有害生物之入侵，以控管有害生物數量或殺滅全數量方式為之，另一作業為進行前面性的環境消毒、殺菌等除滅有害微生物/病毒之威脅。

結果/結論/應用啟示

由於當今全球面臨嚴重氣候變遷，氣溫上升，如此激烈變化，攸關到各國永續發展和人類、物種生態的永續生存，消費者或企業在招標時多已要求病媒防治積極回應聯合國永續發展目標，應提出節能減碳並配合防治之具體行動，例如，使用對環境友善之無污染綠色藥劑、參與降低碳排放量等友善環境等行動，本文針對病媒防治業之企業社會責任提出經驗分享。

關鍵詞（Keywords）：病媒防治業（Pest Control Operator）、有害生物（Pest）、企業責任（Corporate Responsibility）

PU_03

紅外線自動相機應用在有害生物監測與防治-以居家鼠類為例
Infrared automatic camera applied in pest monitoring and control: taking house rodent as an example

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背景/研究問題/材料方法

隨著經濟快速發展，交通便利城鄉都市化加速，又加上全球性暖化產生氣候變遷等因素，增加鼠類繁殖與人類之接觸機會，造成環境衛生問題、財物損失。一般鼠類防治之物理方式如: 設置阻隔設施、捕鼠籠、粘鼠板、驅鼠器等，化學則以毒餌等藥劑誘殺。實務上需要靠有經驗的病媒防治人員執行之，一般需要較長時間及更多的捕器成本，才能有效防治鼠類。如果使用毒餌，必須等到老鼠被毒死產生惡臭才能找到鼠屍，因此造成環境衛生隱憂。使用紅外線自動相機監測鼠類活動範圍與密度，同時標定老鼠活動路線、巢穴與繁殖處所方式捕捉之。

結果/結論/應用啟示

使得執行捕鼠作業時更能掌握:投藥、黏鼠板放置點及其使用量能更精準，不造成浪費，也可節省時間、人力，在病媒防治業缺工的情況下，配合有害生物綜合管理 (Integrated Pest Management) 提升其服務品質、達到友善環境目的。

關鍵詞（Keywords）：鼠類防治（Rodent control）、紅外線自動相機（Infrared automatic camera）、有害生物綜合管理（Integrated Pest Management）

醫學昆蟲學

壁報展示

Posters: Medical Entomology

PM_01

溫度與蚊卵儲存方法對埃及斑蚊蚊卵長期儲存孵化率之影響
Influence of temperature and egg storage methods on hatch rate of *Aedes aegypti* eggs in long term storage

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背景/研究問題/材料方法

Rearing and the maintenance of mosquitoes in laboratory are crucial for studying vector-borne diseases. Although eggs of Aedes mosquitoes can be stored in dried state, their viability decreases over time. Periodical hatching of stored batches is required for sustainable passaging of mosquito strain. In this study, the effect of storage duration and different temperature (5℃ to 25℃, 5℃ increment) on hatching rate of *Aedes aegypti* were evaluated. Additionally, two methods for long term storage were compared: conventional dry storage, and water storage. Stored eggs were hatched with degassed RO water for 24 hours before analyzing.

結果/結論/應用啟示

For dry storage, the highest hatching rate is 65.2% after 2 months of storage at 25℃. The rate dropped drastically to 35.3% after 4 months, and 0% after 8 months. The hatching rate at 20℃ and 15℃ were 37.6% and 13.3% respectively for 2 months. Nevertheless, there were minimal number of eggs which remained viable after 8 months of storage. For water storage, the hatch rates at 25℃ and 20℃ were 72.1% to 73.7%, respectively after 4 months of storage. After 8 months of storage, the rate reduced to 37.4% for the former and 53.8% for the latter. After 12 months of storage, none of 25℃ group hatched, while 47.3% of 20℃ group remained viable. For 15℃ group, the highest hatch rate was 66.1% at one month and reduced to 36.9% after 12 months of storage. Regardless of storage methods, almost no eggs hatched for temperature below 10℃. Our results showed increased storage duration for eggs stored in water, with hatch rate closing up to 50% after 12 months of storage at 20℃. Longer storage duration could provide more flexibility to egg management, reducing the time and labor cost for the maintenance of mosquitoes.

關鍵詞（Keywords）：登革熱（Dengue）、埃及斑蚊（*Aedes aegypti*）、蚊蟲飼養（Mosquito rearing）、孵化率（Hatching rate）

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Functional divergence among cecropin paralogs in pharate adult cuticle formation of mosquito *Armigeres subalbatus* during pupal development

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背景/研究問題/材料方法

Antimicrobial peptides (AMPs), are small inducible peptides, provide non-specific killing or growth inhibition of invading microbes. Most AMPs are encoded by multigene families in the genomes of various insects. Recent studies demonstrated mosquito cecropin Bs play a crucial role in the cecropin-prophenoloxidase regulation mechanism in several mosquito species. In this study, double-stranded RNA (dsRNA) silencing analysis and injection of synthetic cecropin peptide were used to elucidate whether cecropin paralogs play a similar role as cecropin B in pharate adult cuticle formation during pupal development.

結果/結論/應用啟示

Although the genome sequence information of *Ar. subalbatus* is not yet available, five cecropin paralogs have been identified in this species, namely *Armigeres subalbatus* cecropin (Ascec) A1, A2, B1, B2, and N. We found that the expression levels of Ascec A1, A2, B1, and N are induced in bacteria-injected mosquitoes, whilst the mRNA levels of Ascec B2 are constitutively expressed in normal mosquitoes and remain almost the same upon subsequent bacterial challenge. Knockdown in the pupae of Ascec B2 using dsRNA resulted in high mortality. Simultaneous injection of Ascec B2 dsRNA and Ascec B2 peptide into pupae significantly reduced this mortality in a dose-dependent manner. On the other hand, other Ascec peptides are unable to buffer the knockdown effects of Ascec B2. These findings suggest that Ascec B2 plays a unique role in cuticle formation during pupal development and other Ascec paralogs retain the roles in mosquito innate immune.

關鍵詞（Keywords）：*Armigeres subalbatus*, cecropin, paralog, knockdown, rescue

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