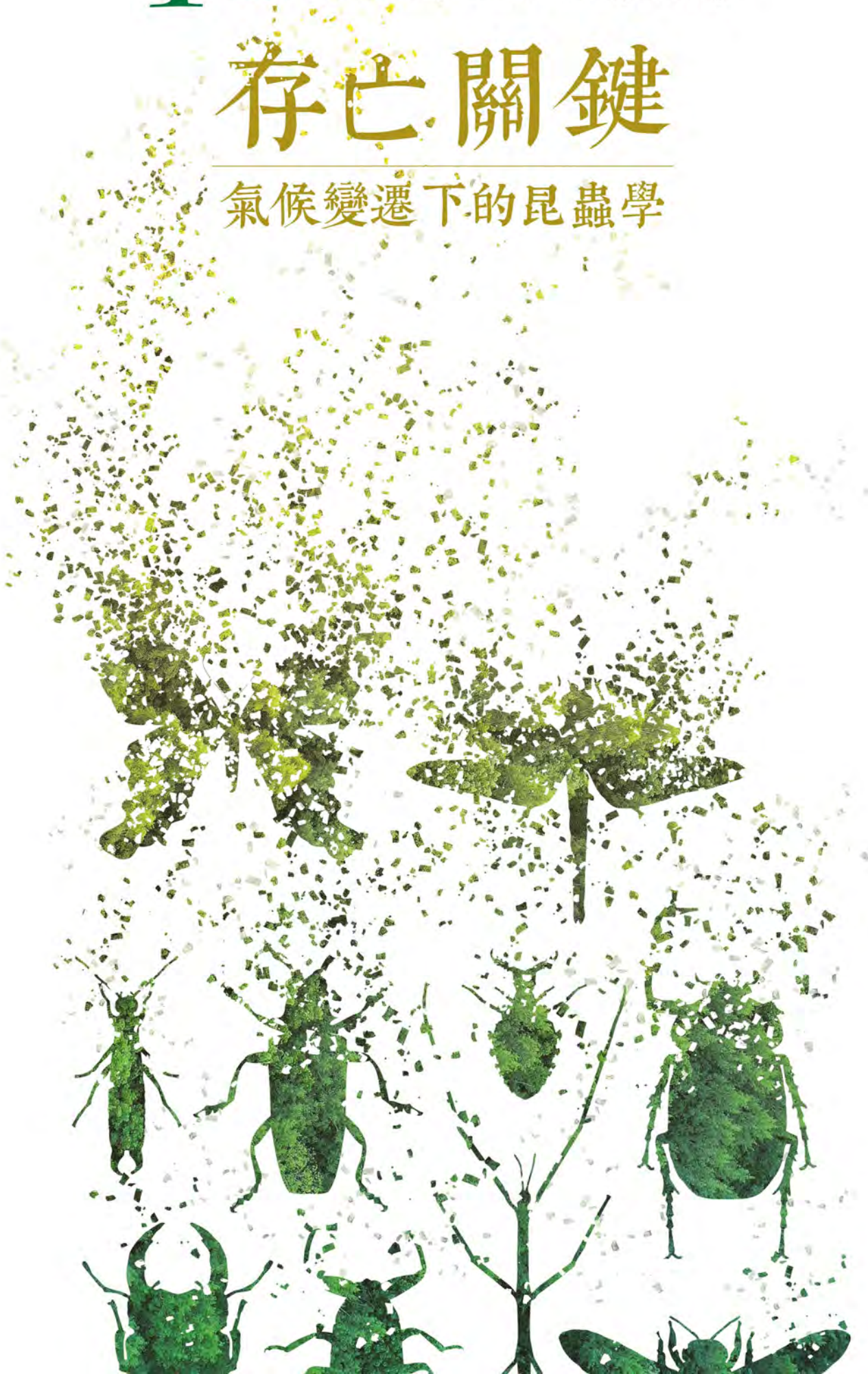
42nd 台灣昆蟲學會年會

Annual Meeting of Taiwan Entomological Society

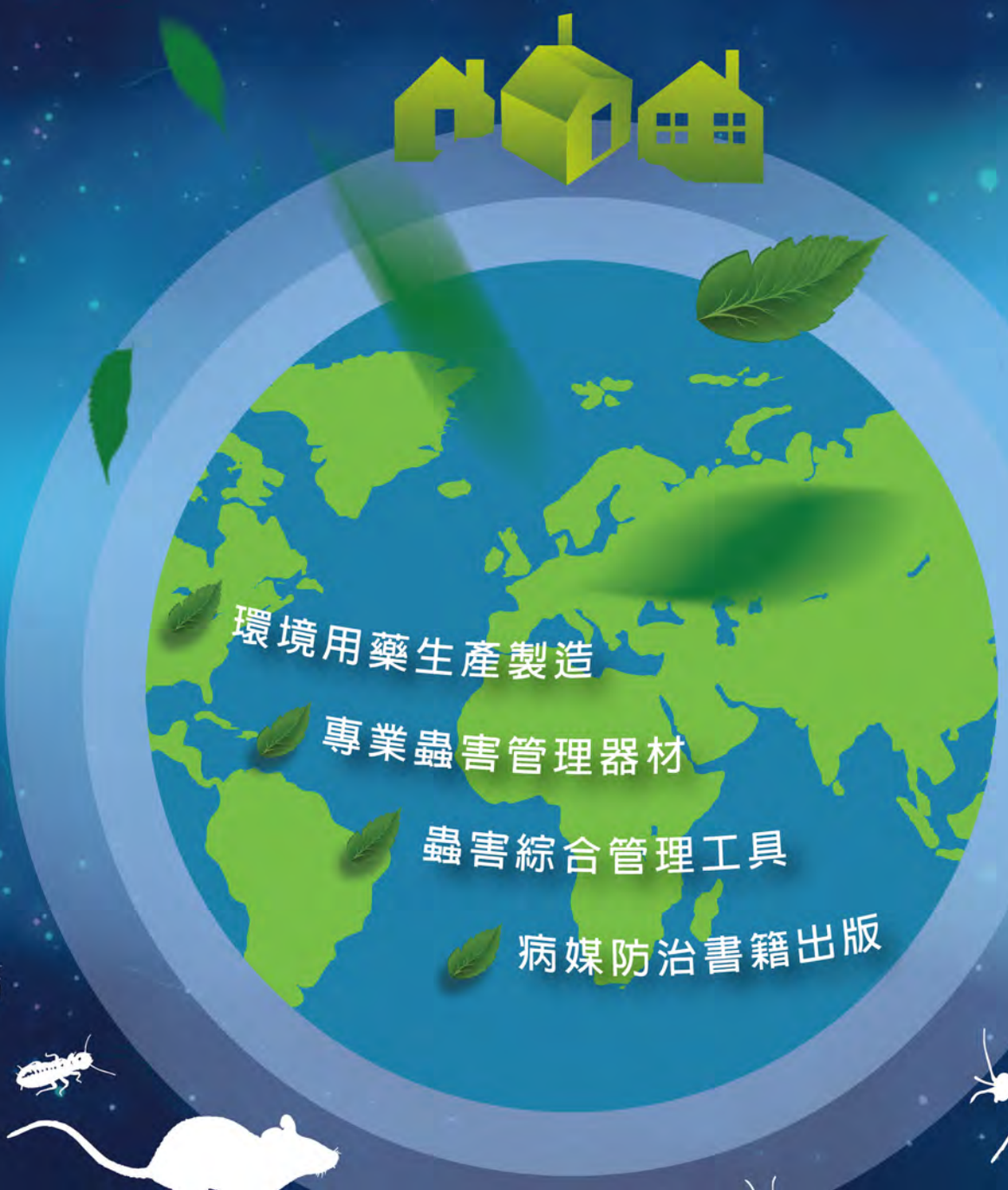
存亡關鍵

氣候變遷下的昆蟲學



超越半世紀蟲害防治

致力維護生態平衡・打造永續自然環境



中西化學工業股份有限公司
CHUNG HSI CHEMICAL PLANT, LTD.

第四十二屆台灣昆蟲學會年會

The 42nd Annual Meeting of Taiwan Entomological Society

2021 年 10 月 23 -24 日

台灣 | 視訊會議

Oct. 23-24, 2021

Online Meeting | Taiwan

合辦單位：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：

首先要感謝各位參與台灣昆蟲學會第 42 屆年會，回想去年在昆蟲年會與前輩和年輕熱情的研究同好們齊聚，竟也只是短短一年前的事情。過去這一年來大大小小的活動、會議都轉為線上或取消，但昆蟲學的研究並未因此停滯，昆蟲學家們仍然持續不懈地在其領域中投注心血。今年我們首次全程以視訊和直播的方式舉行年會，活動和形式或許受到了一些限制，但我們仍期待且盡力將昆蟲年會彼此交流、互相支持的精神延續下去。疫情漸趨和緩，相信在不久的將來，我們就能再次見面。

今年年會的主題為「存亡關鍵－氣候變遷下的昆蟲學」，聚焦在氣候變遷對昆蟲的影響。近年來我們在生活中都深刻感受到了全球氣候變遷對人類、環境帶來的衝擊。今年年會很榮幸邀請到四位優秀的研究學者 Dr. Chow-Yang Lee（University of California, Riverside）、Dr. Louise Ashton (University of Hong Kong) 、莊汶博博士（國立臺灣大學農藝學系）、吳立心博士（國立屏東科技大學植物醫學系）帶來專題演講（Keynote），剖析全球氣候快速變遷對於都市昆蟲和農業昆蟲帶來的變化以及我們的應對方式。

氣候變遷專題將由陳一菁博士(國立成功大學生命科學系)、何傳愷博士(國立臺灣大學生態學與演化生物學研究所)、鄭明倫博士（國立自然科學博物館)、莊汶博博士（國立臺灣大學農藝學系）對談，探討國內氣候變遷與昆蟲相關研究的現狀與展望。閉幕專題演講邀請到今年甫退休的資深教授路光暉博士（國立中興大學昆蟲學系）和唐立正博士（國立中興大學昆蟲學系），帶來昆蟲防檢疫實務上的經驗分享。

而回歸到基本的學習及研究心態的設定和調適，相信同學們常常被詢問也會自問：就讀昆蟲相關科系，未來可以從事哪些工作？做研究是一條漫漫長路，該如何面對迷惘和心魔？在本次昆蟲年會的「職涯發展與企業分享」場次中，我們邀請到五間來自不同領域的成功企業，他們涉足且長期支持台灣的昆蟲學研究，由企業分享他們對昆蟲相關人才的需求，並介紹公司營運方向和提供的服務等，與會者可作為思考未來職涯發展和研究方向的參考。而晚間的「與學生對談：學術傾向與面對未來的焦慮」場次，由顏聖紘博士（國立中山大學生物科學系）主

持，邀請到四位學者：蔡坤憲博士（國立臺灣大學公共衛生學系）、李後鋒博士（國立中興大學昆蟲學系）、林明瑩博士（國立嘉義大學植物醫學系）、黃大益博士（科迪華農業科技），分享研究經歷與心路歷程，協助學生探索專業傾向，降低面對未來的焦慮。

最後我要再次感謝各位的參與、贊助廠商的支持，以及本屆理監事和工作團隊的辛勞。辦理非實體的年會，形式上雖然有其限制性，但內容仍相當紮實豐富，祝福各位與會的朋友們都能有所收穫。

理事長

蕭旭峰

敬上

2021 年 10 月 23 日

第 42 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
秘書組 Secretary section	吳岳隆 Yueh-Lung Wu	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
	羅意瑜 Yi-Yu Luo	台灣昆蟲學會 Taiwan Entomological Society
學術組 Academic section	曾惠芸 Hui-Yun Tseng	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
	林育脩 Yu-Hsiu Lin	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
活動組 Activities section	謝佳宏 Chia-Hung Hsieh	中國文化大學森林暨自然保育學系 Department of Forestry and Nature Conservation, Chinese Culture University
資訊組 Information section	莊士欣 Shih-hsin Chuang	尼奧梵科學藝術有限公司 NEOPHOEN Science & Art Co., Ltd
會計組 Accounting section	黎瑞鈴 Jui-Ling Lee	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
國際組 International affair section	樂大春 David Redei	國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
公關組 Public relations section	林韋宏 Peter Lin	艾爾生態有限公司 A.I.R Ecological Education
企劃組 Project planning section	吳加雄 Chia-Hsiung Wu	台灣生態樹藝協會 Taiwan Ecological Arboriculture Society
總務組 General affair section	王詩儀 Shih-Yi Wang	國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
出版組 Editing and publication section	吳明城 Ming-Cheng Wu	國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
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

目錄 Table of contents

大會專題演講 Keynote Speech

時間：10 月 23 日 9:10-10:10

會議代碼：zpx-rqcz-zhr

直播：https://youtu.be/JsCDadBgCbA

Climate change impact on insect pests in the urban environment

Dr. Chow-Yang Lee

Professor and Endowed Presidential Chair in Urban Entomology
Board Certified Entomologist (Urban & Industrial)

University of California, Riverside, USA

大會專題演講 Keynote Speech

時間：10 月 23 日 10:10-11:10

會議代碼：zpx-rqcz-zhr

直播：https://youtu.be/JsCDadBgCbA

Host plant resistance in rice: new discovery and climate change impact

Dr. Wen-Po Chuang 莊汶博 博士

Associate Professor

Department of Agronomy,
National Taiwan University, Taiwan

國立臺灣大學農藝學系 副教授

大會專題演講 Keynote Speech

時間：10 月 23 日 16:30-17:30

會議代碼：zpx-rqcz-zhr

直播：https://youtu.be/5p73rP-VLIY

極端氣候影響天敵寄主與其共生物間的互動與適應

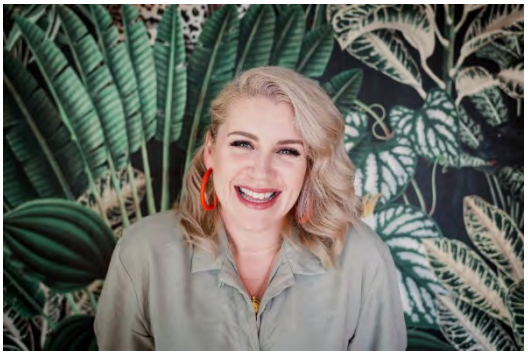
Dr. Li-Hsin Wu 吳立心 博士

Assistant Professor

Department of Plant Medicine,
National Pingtung University of Science and Technology,
Taiwan

國立屏東科技大學植物醫學系 助理教授

大會專題演講 Keynote Speech



時間：10 月 24 日 9:00-10:00

會議代碼：ukh-fpwd-fmy

直播：https://youtu.be/5Rgp_LTSiY4

Insects in the Anthropocene – how insects can help us understand our changing world

Dr. Louise Ashton

Assistant Professor

School of Biological Sciences, Faculty of Science,
The University of Hong Kong, Hong Kong

大會專題演講 Keynote Speech

時間：10 月 24 日 14:40-15:40

直播：https://youtu.be/WIqIBvJAbtM

輻射照射在植物檢疫上的應用與安全性

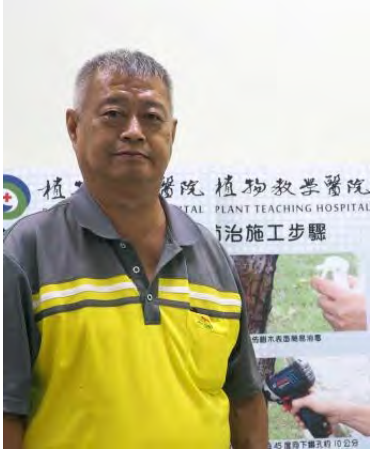
Dr. Kuang-Hui Lu 路光暉 博士

Retired Professor

Department of Entomology,
National Chung-Hsin University, Taiwan

國立中興大學昆蟲學系 退休教授

大會專題演講 Keynote Speech



時間：10 月 24 日 15:40-16:40

直播：https://youtu.be/WIqIBvJAbtM

植醫甘苦談

Dr. Li-Cheng Tang 唐立正 博士

Retired Professor

Department of Entomology,
National Chung-Hsin University, Taiwan

國立中興大學昆蟲學系 退休教授

議程大綱

Program at a glance

Oct. 23, 2021（Sat.）				
時間/地點	-			
9:00-9:10	開幕直播			
9:10-10:10	大會專題演講 Climate change impact on insect pests in the urban environment **Dr. Chow-Yang Lee**			
10:10-11:10	大會專題演講 Host plant resistance in rice: new discovery and climate change impact **Dr. 莊汶博**			
11:10-11:20	換場			
時間/地點	生物多樣性、族群與群聚生態學	系統分類、族群遺傳、演化	行為、生理、個體生物學	農業昆蟲學
11:20-12:20	OB_01-04	OS_01-03	OE_01-04	OA_01-04
12:20-13:40	休息用餐／12:25-13:00 會員大會			
時間/地點	生物多樣性、族群與群聚生態學	系統分類、族群遺傳、演化	行為、生理、個體生物學	農業昆蟲學
13:40-15:10	OB_05-10	OS_04-09	OE_05-10	OA_05-10
15:10-15:25	換場			
時間/地點	蝴蝶紅皮書工作坊	職涯發展與企業分享	農業昆蟲學	農業昆蟲學
15:25-16:20		中西化學工業股份有限公司 安農股份有限公司 美嘉儀器股份有限公司 頂響能多潔股份有限公司	OA_11-13	OA_14-16
16:20-16:30	換場			
16:30-17:30	大會專題演講 極端氣候影響天敵寄主與其共生物間的互動與適應 **Dr. 吳立心**			
17:30-19:00	用餐			
19:00-20:00	與學生對談：學術傾向與面對未來的焦慮			

Oct. 24, 2021（Sun.）				
時間/地點	-			
9:00-10:00	大會專題演講 Insects in the Anthropocene – how insects can help us understand our changing world **Dr. Louise Ashton**			
10:00-10:10	換場			
時間/地點	氣候變遷專題	海外昆蟲學者	行為、生理、個體生物學	醫學昆蟲/都市昆蟲
10:10-11:55	專家座談：Dr. 陳一菁 Dr. 何傳愷 Dr. 鄭明倫 Dr. 莊汶博	Oversea_01-06	OE_11-17	OM_01- 06
11:55-13:10	休息用餐			
13:10-14:30	海報時間			
14:30-14:40	換場			
14:40-15:40	大會專題演講 輻射照射在植物檢疫上的應用與安全性 **Dr. 路光暉**			
15:40-16:40	大會專題演講 植醫甘苦談 **Dr. 唐立正**			
16:40-17:30	閉幕暨頒獎典禮／抽獎			

Oct. 23, 2021（Sat.）				
Time/Place	-			
9:00-9:10	Opening Welcome			
9:10-10:10	Keynote Speech Climate change impact on insect pests in the urban environment **Dr. Chow-Yang Lee**			
10:10-11:10	Keynote Speech Host plant resistance in rice: new discovery and climate change impact **Dr. Wen-Po Chuang**			
11:10-11:20	Room Switching			
Time/Place	Biodiversity, Population and Community Ecology	Systematics, Population Genetics and Evolution	Ethology, Physiology and Organismic Biology	Agricultural Entomology
11:20-12:20	OB_01-04	OS_01-03	OE_01-04	OA_01-04
12:20-13:40	Lunch Break / 12:25-13:00 General Assembly			
Time/Place	Biodiversity, Population and Community Ecology	Systematics, Population Genetics and Evolution	Ethology, Physiology and Organismic Biology	Agricultural Entomology
13:40-15:10	OB_05-10	OS_04-09	OE_05-10	OA_05-10
15:10-15:25	Room Switching			
Time/Place	Workshop on IUCN Red List	Career Development and Product Sharing	Agricultural Entomology	Agricultural Entomology
15:25-16:20		Chung Hsi Chemical Plant, Ltd. Agro Chemical Corporation Major Instruments Co., Ltd Rentokil Ding Sharn Co., Ltd	OA_11-13	OA_14-16
16:20-16:30	Room Switching			
16:30-17:30	Keynote Speech The consequences and adaptations of extreme climate events on host-parasitoid and its symbionts interactions **Dr. Li-Hsin Wu**			
17:30-19:00	Dinner Break			
19:00-21:00	Career counseling for students: Academic suitability and future anxiety			

Oct. 24, 2021（Sun.）				
Time/Place	-			
9:00-10:00	Keynote Speech Insects in the Anthropocene – how insects can help us understand our changing world **Dr. Louise Ashton**			
10:00-10:10	Room Switching			
Time/Place	Workshop on Climate Change	Oversea Scholar	Ethology, Physiology and Organismic Biology	Medical Entomology/Urban Entomology
10:10-11:55	Experts discussion Dr. I-Ching Chen Dr. Chuan-Kai Ho Dr. Ming-Luen Jeng Dr. Wen-Po Chuang	Oversea_01-06	OE_11-17	OM_01- 06
11:55-13:10	Lunch Break			
13:10-14:30	Poster Time			
14:30-14:40	Room Switching			
14:40-15:40	Keynote Speech 輻射照射在植物檢疫上的應用與安全性 **Dr. Kuang-Hui Lu**			
15:40-16:40	Keynote Speech 植醫甘苦談 **Dr. Li-Cheng Tang**			
16:40-17:30	Award Ceremony & Farewell / Raffle			

編碼對照表

K	大會專題演講
	Keynote Speech
Oversea	海外昆蟲學者論文宣讀
	Oral Session: Oversea Entomologists
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
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/都市昆蟲學論文宣讀
	Oral Session: Medical Entomology/ 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
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. 23, 2021（Sat.）				
時間/地點	-			
9:00-9:10	開幕直播			
9:10-10:10	大會專題演講 Climate change impact on insect pests in the urban environment **Dr. Chow-Yang Lee** 【主持人：蕭旭峰博士】			
10:10-11:10	大會專題演講 Host plant resistance in rice: new discovery and climate change impact **Dr. 莊汶博** 【主持人：趙裕展博士】			
11:10-11:20	換場			
時間/地點	生物多樣性、族群與群聚生態學 【主持人：宋一鑫博士】	系統分類、族群遺傳、演化 【主持人：廖一璋博士】	行為、生理、個體生物學 【主持人：姚美吉博士】	農業昆蟲學 【主持人：黃榮南博士、曾慶慈博士】
11:20-11:35	OB_01 Global pattern and climatic predictor of eyespot traits in nymphalid butterfly 韋家軒，姜信宏，陳一菁	OS_01 臺灣產蠟蟬科(半翅目：蠟蟬總科)分類學研究現況 林佑昇，廖治榮，柯俊成，蕭旭峰	OE_01 尼泊爾埋葬蟲(*Nicrophorus nepalensis* Hope) (Coleoptera: Silphidae)之幼蟲回巢定位 永政澤，黃文伯	**OA_01** **彰化與雲林地區之黃條葉蚤對藥劑感受性之探討** **洪欽麟，魏紹華，林明瑩**
11:35-11:50	OB_02 What is the effect of *Wolbachia* in sib-mating ambrosia beetles of the *Euwallacea fornicatus* Eichhoff (Coleoptera: Curculionidae) species complex? 劉芳綾，Paul Rugman-Jones，Richard Stouthamer，段淑人	OS_02 一種出乎意料之外的荔枝細蛾新種在台灣的發現及其對荔枝與龍眼害蟲管理策略的意涵 顏聖紘，王崇羽，廖士睿，賴柏羽，劉耕樵，許如君	OE_02 稻穀倉庫主要害蟲穀蠹對第滅寧抗藥性之探討 姚美吉，李啟陽，王泰權，馮文斌	**OA_02** **光敏劑對菸草粉蝨 (*Bemesia tabaci*) 之光活化致死效果及殺蟲機制** **黃玉媛，李威樺，宋一鑫，蔡志偉**

11:50-12:05	OB_03 農業長期生態園區指標昆蟲-瓢蟲之調查 許北辰，楊婉秀，余志儒，董耀仁，陳琦玲，石憲宗	OS_03 社會性蚜蟲短角綿蚜之生殖限制：胎生昆蟲兵蚜階級不孕之調控 鍾成侑，重信秀治	OE_03 進口糙米倉庫主要積穀害蟲對磷化氫抗藥性之探討 姚美吉，李啟陽，王泰權，馮文斌	**OA_03** **不同定溫下伊凡氏葉蟎在龍葵上之生活史** **葉千榕，林明瑩**
12:05-12:20	OB_04 訪花膜翅目昆蟲多樣性與蜜源植被營造關聯性之研究 徐培修，吳姿嫻		OE_04 Biological control of *Forcipomyia taiwana* Shiraki by entomopathogenic fungi Nian-tong Ni, Chuen-Fu Lin, Yu-Shin Nai	**OA_04** **甜菜夜蛾 (鱗翅目: 夜蛾科) 在青蔥上之生命表與取食量** **阮韞澔，林明瑩**
12:20-13:40	休息用餐／12:25-13:00 會員大會			
時間/地點	生物多樣性、族群與群聚生態學 【主持人：陸聲山博士、顏聖紘博士】	系統分類、族群遺傳、演化 【主持人：李奇峯博士、吳立偉博士】	行為、生理、個體生物學 【主持人：陳美娥博士、乃育昕博士】	農業昆蟲學 【主持人：楊恩誠博士、林明瑩博士】
13:40-13:55	**OB_05** **入侵小蜜蜂之畸翅病毒分離株研究** **田謹萱，蔡文錫，宋一鑫**	**OS_04** **台灣家白蟻與格斯特家白蟻的種間隔離** **陳冠豫，黃詩穎，靖永皓，李後鋒**	**OE_05** **大蠟蛾對 *Fusarium solani* 及 *F. rubicola* 病原菌之致病影響觀察** **余品臻，傅于珊，黃健瑞，宋一鑫**	**OA_05** **乙基或甲基取代的呋喃和噻吩作為控制昆蟲的新型燻蒸劑的潛力** **黃勝，姚美吉，李成正，呂維茗，戴淑美，孟孟孝**
13:55-14:10	**OB_06** **一種於臺灣寄生六條瓢蟲 (*Cheilomenes semaculata*)的寄生蜂之分類與生活史研究** **鄭中涵，黃紹毅**	**OS_05** **台灣產新白蟻屬的分類學研究** **吳佳倩 ，蔡經甫 ，李後鋒**	**OE_06** **Analysis of germline development under heat stress in the asexual viviparous pea aphid** **蔡沐慈，張俊哲**	**OA_06** **桿狀病毒表現醣類結合蛋白提升殺蟲活性之研究** **林家揚，吳岳隆，黃榮南**
14:10-14:25	**OB_07** **漂海性白蟻之雙重巢群拓殖策略** **邱奕寧，邱俊禕，劉佳穎，林明德，李後鋒**	**OS_06** **探討長毛跗蟎屬 (*Sennertia*) 蜂蟎種群於木蜂體上之分布** **趙家慧，陸聲山，宋一鑫**	**OE_07** **以 micro-CT 技術探討蜜蜂工蜂大腦的結構** **扶尚睿，楊恩誠**	**OA_07** **The interaction of two tomato-infecting begomoviruses in *Bemisia tabaci* and its effect on virus transmission** **李威樺，蔡志偉**

14:25-14:40	**OB_08** **都市湧泉型溪流水棲昆蟲之生態初探：以台中南勢溪為例** **鍾濬宇，張依潔，黃彩瑜，徐崇斌**	**OS_07** **臺灣產擬瘦姬蜂屬 (膜翅目：姬蜂科：柄卵姬蜂亞科)之分類學回顧** **陳玄樸，蕭旭峰**	**OE_08** **優化以氣相色譜質譜儀分析西洋蜂青春激素之方法** **陳琬鎰，楊恩誠**	OA_08 The emerging pest of tea plants, *Euwallacea fornicatus* (Coleoptera: Curculionidae), in Taiwan Liao, Yi-Chang, Paul Rugman-Jones, Fan-Ling Liu, Hui-Hung Liang, Chun-Yen Lee, Lan-Yu Liu, Shu-Jen Tuan, Richard Stouthamer
14:40-14:55	**OB_09** **A study on Taiwanese Erotylinae (Coleoptera: Erotylidae) species richness reveals conflicts morphological and genetic data** **彭冠傑，黃仁磐**	**OS_08** **台灣產背寡毛實蠅屬形態與分類學研究** **黃千育，蕭旭峰**	**OE_09** **氣候變遷對熊蜂震動授粉 (buzz pollination) 的影響** **郭耘，吳岳隆**	OA_09 旋轉式避蛾燈開發及防治水蜜桃吸果夜蛾之效果評估 陳巧燕，莊國鴻，李汪盛，施錫彬
14:55-15:10	**OB_10** **What makes a nasty pest? - Unveiling the intestinal microbial profile of coconut rhinoceros beetles (*Oryctes rhinoceros*) in Taiwan** **韓喬融，薛馬坦**	**OS_09** **臺灣產白斑翅野螟(鱗翅目：草螟科，斑野螟亞科)的分類檢討** **蔡岳承，王崇羽，顏聖紘**	**OE_10** **溫度影響紋白蝶翅黑化面積** **陳柏凱，朱清麟，賴慶庭，吳立心**	OA_10 荔枝椿象蟲生真菌淡紫菌(*Purpureocillium takamizusanense*)之寄主範圍與固態發酵條件初步研究 陳盈丞，陳奐宇，林慧婷，黃慈閔，蔡孟旅
15:10-15:25	換場			
時間/地點	蝴蝶紅皮書工作坊 【主持人：陳一菁博士】	職涯發展與企業分享 【主持人：謝佳宏博士】	農業昆蟲學 【主持人：石憲宗博士】	農業昆蟲學 【主持人：蔡志偉博士】
15:25-15:40	台灣蝶類紅皮書名錄資訊彙整與評估 林承昊，韋家軒，徐堉峰，顏聖紘，黃行七，呂晟智，朱汶偵，楊曼妙，趙榮台，陳一菁	中西化學工業股份有限公司 安農股份有限公司 美嘉儀器股份有限公司 頂響能多潔股份有限公司	OA_11 淡紫菌液態發酵初探及化學藥劑之抑制效果 林慧婷，陳盈丞，陳奐宇，蔡孟旅	OA_14 以不同介質飼育外米綴蛾生長表現比較 潘光琦，林立
15:40-15:55			OA_12 無人植保機防治蓮花小黃薊馬之研究 陳盈丞，黃美靜，張淳淳	OA_15 Interaction of two host-specific begomoviruses in *Bemisia tabaci* and its effect on virus transmission 蘇珊媞，李威樺，黃玉媛，蔡文錫，蔡志偉

15:55-16:10			OA_13 蓮花小黃薊馬之空間分布與最適取樣數估算 陳盈丞，黃美靜，林金樹	OA_16 臺灣荔枝害蟲(蟎)名錄之修訂 王泰權，李啟陽，賴柏羽
16:10-16:20				
16:20-16:30	換場			
16:30-17:30	大會專題演講 極端氣候影響天敵寄主與其共生物間的互動與適應 **Dr. 吳立心** 【主持人：吳文哲博士】			
17:30-19:00	用餐			
19:00-20:00	與學生對談：學術傾向與面對未來的焦慮（主持人：顏聖紘博士） 與談人： 臺灣大學公共衛生學系 蔡坤憲博士 中興大學昆蟲學系 李後鋒博士 嘉義大學植物醫學系 林明瑩博士 科迪華農業科技 黃大益博士			

Oct. 24, 2021（Sun.）				
時間/地點	-			
9:00-10:00	大會專題演講 Insects in the Anthropocene – how insects can help us understand our changing world **Dr. Louise Ashton** 【主持人：李後鋒博士】			
10:00-10:10	換場			
時間/地點	氣候變遷專題 【主持人：陳一菁博士】	海外昆蟲學者 【主持人：吳明城博士】	行為、生理、個體生物學 【主持人：呂曉鈴博士、 黃佳欣博士】	醫學昆蟲/都市昆蟲 【主持人：李後鋒博士、 黃旌集博士】
10:10-10:25	專家座談 Dr. 陳一菁 Dr. 何傳愷 Dr. 鄭明倫 Dr. 莊汶博	Oversea_01 探討長腳捷山蟻與沃爾巴克氏菌之共演化及全球入侵 李志琦，楊景程	**OE_11** **穀蠹(鞘翅目：長蠹蟲科)Prip 水通道蛋白之表現調節及生理功能** **陳覽繽，雷喬安，陳美娥**	**OM_01** **遠紫外光 (222 nm) 對白線斑蚊生長的影響** **陳盈瑄，蕭旭峰，蔡坤憲**
10:25-10:40		Oversea_02 Insect vector of palm-infecting phytoplasma disease 牟德芬，Brian Bahder	**OE_12** **蟲生真菌防治偽菜蚜 (*Lipaphis erysimi* Kaltenbach) 及寄主免應反應探討** **楊承儒，乃育昕**	**OM_02** **利用體腔真菌防治白線斑蚊** **林芳伶，蕭旭峰，蔡坤憲**
10:40-10:55		Oversea_03 植物氣孔與植食性昆蟲之交互作用 林柏安	**OE_13** **馬尼拉小繭蜂共生病毒調控斜紋夜蛾營養代謝之研究** **林鈺淳，吳岳隆**	OM_03 Detection of *Rickettsia* spp. and *Bartonella* spp. in fleas and small mammals in Chiayi and Tainan area in Taiwan Pei-Yun Deng, Chuen-Fu Lin, Kun-Hsien Tsai
10:55-11:10		Oversea_04 Phytochemicals mediated interactions among aphids *Aphis nerii* and *Myzocallis asclepiadis* and a shared predator 李志中，Brigitte Tenhumberg	**OE_14** **雌性遭遇密度對尼泊爾埋葬蟲 (*Nicrophorus nepalensis* Hope) (Coleoptera: Silphidae)繁殖策略的影響** **鄭新翰，黃文伯**	OM_04 Neglected phthiriasis in Taiwan: a case of *Pthirus pubis* hyperinfestation, comparative morphological and molecular identification, and retrospective clinical case series Yu-Feng Tsai, Chia-Wen Lee, Wen-Jer Wu, Kun-Hsien Tsai

11:10-11:25		Oversea_05 步行蟲 (鞘翅目:步行蟲科) 翅鞘金屬光澤遺傳機制初探 翁逸明，Sean Schoville	**OE_15** **為何昆蟲無法叮咬斑馬？以蜜蜂著陸行為為例** **謝祥文，楊恩誠**	OM_05 六伏隆白蟻餌劑在養菌白蟻防治上的應用 邱俊禕，莊雅惠， 梁維仁，葉信廷， 楊小瑩，蔡明哲，Neil A. Spomer，李後鋒
11:25-11:40		Oversea_06 蟲害誘導的梨樹揮發性成分對於桃折心蟲的產卵及其天敵昆蟲搜尋寄主行為之影響 劉家銘，松山茂，戒能洋一	OE_16 台灣秋行軍蟲(*Spodoptera frugiperda* J.E. Smith)腸道菌相宏基因體調查(metagenomics) 劉曜嘉，乃育昕	OM_06 熏香對埃及伊蚊影響的初步研究 Ching-Yu Shu, Hsueh-Lien Lai, Pei-Yin Lin, Kevin Chi-Chung Chou, Matan Shelomi
11:40-11:55			OE_17 亞致死劑量益達胺對蜂后幼蟲發育之影響 陳韻如，林詩舜，楊恩誠	
11:55-13:10	休息用餐			
13:10-14:30	海報時間			
14:30-14:40	換場			
14:40-15:40	大會專題演講 輻射照射在植物檢疫上的應用與安全性 **Dr. 路光暉** 【主持人：蕭旭峰博士】			
15:40-16:40	大會專題演講 植醫甘苦談 **Dr. 唐立正** 【主持人：蕭旭峰博士】			
16:40-17:30	閉幕暨頒獎典禮／抽獎			

Conference Agenda

Underline denotes speakers, Bold denotes competition

Oct. 23, 2021（Sat.）				
Time/Place	-			
9:00-9:10	Opening Welcome			
9:10-10:10	Keynote Speech Climate change impact on insect pests in the urban environment **Dr. Chow-Yang Lee** 【Host: Dr. Shiuh-Feng Shiao】			
10:10-11:10	Keynote Speech Host plant resistance in rice: new discovery and climate change impact **Dr. Wen-Po Chuang** 【Host: Dr. Yu-Chan Chao】			
11:10-11:20	Room Switching			
Time/Place	Biodiversity, Population and Community Ecology 【Host: Dr. I-Hsin Sung】	Systematics, Population Genetics and Evolution 【Host: Dr. Yi-Chang Liao】	Ethology, Physiology and Organismic Biology 【Host: Dr. Me-Chi Yao】	Agricultural Entomology 【Hosts: Dr. Rong-Nan Huang, Dr. Ching-Tzu Tseng】
11:20-11:35	OB_01 Global pattern and climatic predictor of eyespot traits in nymphalid butterfly Chia-Hsuan Wei, Shin-Hung Jiang, I-Ching Chen	OS_01 Taxonomic study of the Family Fulgoridae (Hemiptera: Fulgoroidea) of Taiwan You-Sheng Lin, Jhih-Rong Liao, Chun-Cheng Ko, Shiuh-Feng Shiao	OE_01 Larva homing positioning of Burying beetle *Nicrophorus nepalensis* Hope (Coleoptera: Silphidae) Zheng-Tsu Yung, Wenbe Hwang	**OA_01** **Research on the insecticides susceptibility of *Phyllotreta striolata* (Fabricius) from Changhua and Yunlin districts** **Chin-Lin Hung, Shao-Hua Wei, Ming-Ying Lin**
11:35-11:50	OB_02 What is the effect of *Wolbachia* in sib-mating ambrosia beetles of the *Euwallacea fornicatus* Eichhoff (Coleoptera:	OS_02 Discovery of an unexpected new species of *Conopomorpha* (Gracillariidae) in Taiwan and its	OE_02 Deltamethrin resistance in major pest *Rhyzopertha dominica* in paddy rice warehouse	**OA_02** **Light-activated lethal effect and killing mechanism of photosensitizer on *Bemesia tabaci***

	Curculionidae) species complex? Fang-Ling Liu, Paul Rugman-Jones, Richard Stouthamer, Shu-Jen Tuan	implications on pest management for lychee and longan orchards Shen-Horn Yen, Chung-Yu Wang, Shi-Rei Liao, Keng-Chiao Liu, Ju-Chun Hsu	Me-Chi Yao, Chi-Yang Lee, Tai-Chuan Wang, Wen-Bin Feng	**Yu-Yuan Huang, Wei-Hua Li, I-Hsin Sung, Chi-Wei Tsai**
11:50-12:05	OB_03 Surveys of insect as the indicator in experiment fields of long-term ecological research for agriculture - coccinellids Pei-Chen Hsu, Wan-Shiou Yang, Jih-Zu Yu, Yew-Jen Dong, Chi-Ling Chen, Hsien-Tzung Shih	OS_03 Reproductive constraint in the social aphid *Ceratovacuna japonica*: sterility regulation in the soldier caste of a viviparous insect Chen-yo Chung, Shuji Shigenobu	OE_03 Phosphine resistance in major pests of stored-product insect in imported brown rice warehouse Me-Chi Yao, Chi-Yang Lee, Tai-Chuan Wang, Wen-Bin Feng	**OA_03** **The life history of *Tetranychus evansi* (Acari: Tetranychidae) on *Solanum nigrum* at varied temperatures** **Chien-Yong Yeh, Ming-Ying Lin**
12:05-12:20	OB_04 The study of relationship between bee (Hymenoptera) diversity and nectar vegetation planting Pei-Shou Hsu, Tzu-Hsien Wu		OE_04 Biological control of *Forcipomyia taiwana* Shiraki by entomopathogenic fungi Nian-tong Ni, Chuen-Fu Lin, Yu-Shin Nai	**OA_04** **Life table and consumption of *Spodoptera exigua* (Lepidoptera: Noctuidae) on green onion** **Yun-Hao Juan, Ming-Ying Lin**
12:20-13:40	Lunch Break / 12:25-13:00 General Assembly			
Time/Place	Biodiversity, Population and Community Ecology【Hosts: Dr. Sheng-Shan Lu, Dr. Shen-Horn Yen】	Systematics, Population Genetics and Evolution【Hosts: Dr. Chi-Feng Lee, Dr. Li-Wei Wu】	Ethology, Physiology and Organismic Biology【Hosts: Dr. Mei-Er Chen, Dr. Yu-Shin Nai】	Agricultural Entomology【Hosts: Dr. En-Cheng Yang, Dr. Ming-Ying Lin】
13:40-13:55	**OB_05** **Deformed wing virus isolates of invasive dwarf honeybee *Apis florea*** **Jin-Xuan Tian, Wen-Shi Tsai, I-Hsin Sung**	**OS_04** **Species barrier between Formosan and Asian subterranean termites** **Guan-Yu Chen, Shih-Ying Huang, Yung-Hao Ching, Hou-Feng Li**	**OE_05** **Pathogenic effect of *Fusarium solani* and *F. rubicola* on greater wax moth (*Galleria mellonella*)** **Pin-Chen Yu, Yu-Shan Fu, Chien-Jui Huang, I-Hsin Sung**	**OA_05** **Potential of ethyl- or methyl-substituted furan and thiophene as novel fumigants for insect control** **Joey Huang, Me-Chi Yao, Cheng-Cheng Lee, Wei-Ming Leu, Shu-Mei Dai, Menghsiao Meng**

13:55-14:10	**OB_06** **The Study of Taxonomy and Life History of a Parasitic Wasp on *Cheilomenes semaculata* in Taiwan** **Chung-Han Chang, Shaw-Yhi Hwang**	**OS_05** **Taxonomy of *Neotermes* (Blattodea: Kalotermitidae) in Taiwan** **Chia-Chien Wu, Jing-Fu Tsai, Hou-Feng Li**	**OE_06** **Analysis of germline development under heat stress in the asexual viviparous pea aphid** **Mu-tzu Tsai, Chun-che Chang**	**OA_06** **Enhancing the insecticidal potential of baculovirus by overexpressing the mammalian β-galactosyl binding protein galectin-1** **Chia-Yang Lin, Yueh-Lung Wu, Rong-Nan Huang**
14:10-14:25	**OB_07** **Dual-dispersal strategy of oceanic termite** **Yi-Ning Chiu, Chun-I Chiu, Chia-Ying Liu, Ming-Der Lin, Hou-Feng Li**	**OS_06** **Exploratory on *Sennertia* bee mites (Sarcoptiformes: Chaetodactylidae) phoretic on *Xylocopa* bees (Hymenoptera: Apidae)** **Chia-Hui Chao, Sheng-Shan Lu, I-Hsin Sung**	**OE_07** **Study of anatomical of honey bee worker's brain by micro-CT** **Shang-Jui Fu, En-Cheng Yang**	**OA_07** **The interaction of two tomato-infecting begomoviruses in *Bemisia tabaci* and its effect on virus transmission** **Wei-Hua Li, Chi-Wei Tsai**
14:25-14:40	**OB_08** **A preliminary study of the ecology of aquatic insects in a spring originated stream in urban areas: The case of Nan-Shih Stream in Salu District, Taichung City** **Chun-Yu Chung, Yi-Chieh Chang, Tsai-Yu Huang, Chorng-Bin Hsu**	**OS_07** **A taxonomic review of *Netelia* species (Hymenoptera: Ichneumonidae: Tryphoninae) of Taiwan** **Hsuan-Pu Chen, Shiuh-Feng Shiao**	**OE_08** **Optimizing the GC-MS protocol for juvenile hormone analysis of *Apis mellifera* L.** **Wan-Yi Chen, En-Cheng Yang**	OA_08 The emerging pest of tea plants, *Euwallacea fornicatus* (Coleoptera: Curculionidae), in Taiwan Liao, Yi-Chang, Paul Rugman-Jones, Fan-Ling Liu, Hui-Hung Liang, Chun-Yen Lee, Lan-Yu Liu, Shu-Jen Tuan, Richard Stouthamer
14:40-14:55	**OB_09** **A study on Taiwanese Erotylinae (Coleoptera: Erotylidae) species richness reveals conflicts morphological and genetic data** **Guan Jie Phang, Jen-Pan Huang**	**OS_08** **Morphological and taxonomic study of genus *Bactrocera* (Diptera: Tephritidae) in Taiwan** **Chien-Yu Huang, Shiuh-Feng Shiao**	**OE_09** **Effect of climate change on buzz pollination** **Yun Kuo, Yueh-Lung Wu**	OA_09 Development of rotary moth-repellent lamps and evaluation of the effectiveness of controlling the fruit-piercing moths on peach Chiao-Yen Chen, Kuo-Hung Chuang, Wang-Sheng Li, His-Pin Shih

14:55-15:10	**OB_10** **What makes a nasty pest? - Unveiling the intestinal microbial profile of coconut rhinoceros beetles (*Oryctes rhinoceros*) in Taiwan** **Chiao-Jung Han, Matan Shelomi**	**OS_09** **A taxonomic revision of the genus *Bocchoris* Moore, 1885 (Lepidoptera: Crambidae, Spilomeinae) of Taiwan** **Yue-Cheng Tsai, Chung-Yu Wang, Shen-Horn Yen**	**OE_10** **Temperature affects the wing pattern on *Pieris rapae* (Lepidoptera: Pieridae)** **Po-Kai Chen, Ching-Lin Chu, Ching-Ting Lai, Li-Hsin Wu**	OA_10 Preliminary Study on Host Rangeand Solid-State Fermentation of *Purpureocillium takamizusanense*, an Entomogenous Fungi on Litchi Stink Bug (*Tessaratoma papillosa* (Drury)) Ying-Cheng Chen, Huan-Yu Chen, Hui-Ting Lin, Tzu-Min Huang, Meng-Lu Tsai
15:10-15:25	Room Switching			
Time/Place	Workshop on IUCN Red List Assessment of Butterflies in Taiwan【Host: Dr. I-Ching Chen】	Career Development and Product Sharing【Host: Dr. Chia-Hung Hsieh】	Agricultural Entomology【Host: Dr. Hsien-Tzung Shih】	Agricultural Entomology【Host: Dr. Chi-Wei Tsai】
15:25-15:40	IUCN Red List Assessment of Butterflies in Taiwan Cheng-Hao Lin, Chia-Hsuan Wei, Yu-Feng Hsu, Shen-Horn Yen, Hang-Ci Huang, Cheng-Jhih Lyu, Wen-Chen Chu, Man-Miao Yang, Jung-Tai Chao, I-Ching Chen	CHUNG HSI CHEMICAL PLANT, LTD. AGRO CHEMICAL CORPORATION MAJOR INSTRUMENTS CO., LTD. RENTOKIL DING SHARN CO., LTD.	OA_11 Preliminary study on liquid fermentation of *Purpureocillium takamizusanense* and the inhibition effect of pesticides Hui-Ting Lin, Ying-Cheng Chen, Huan-Yu Chen, Meng-Lu Tsai	OA_14 Evaluation of different food substrates for *Corcyra cephalonica* Kuang-Chi Pan, Li Lin
15:40-15:55			OA_12 The study of using Unmanned Plant Protection Machine to control *Scirtothrips dorsalis* Hood on lotus Ying-Cheng Chen, Mei-Jing Huang, Chun-Chun Chang	OA_15 Interaction of two host-specific begomoviruses in *Bemisia tabaci* and its effect on virus transmission Sushanthi Poovendhan, Wei-Hua Li, Yu-Yuan Huang, Wen-Shi Tsai, Chi-Wei Tsai
15:55-16:10			OA_13 Spatial distribution and estimates of optimal sample size for *Scirtothrips dorsalis* Hood on lotus Ying-Cheng Chen, Mei-Jing Huang, Chin-Su Lin	OA_16 The revised checklist of litchi insects and mites in Taiwan Tai-Chuan Wang, Chi-Yang Lee, Po-Yu Lai
16:10-16:20				

16:20-16:30	Room Switching			
16:30-17:30	Keynote Speech The consequences and adaptations of extreme climate events on host-parasitoid and its symbionts interactions **Dr. Li-Hsin Wu** 【Host: Dr. Wen-Jer Wu】			
17:30-19:00	Dinner Break			
19:00-20:00	Career counseling for students: Academic suitability and future anxiety (Host: Dr. Shen-Horn Yen) Panelists: Dr. Kun-Hsien Tsai (College of Public Health, National Taiwan University) Dr. Hou-Feng Li (Department of Entomology, National Chung-Hsing University) Dr. Ming-Ying Lin (Department of Plant Medicine) Dr. Ta-I Huang (Corteva Agriscience)			
Oct. 24, 2021（Sun.）				
Time/Place	-			
9:00-10:00	Keynote Speech Insects in the Anthropocene – how insects can help us understand our changing world **Dr. Louise Ashton** 【Host: Dr. Hou-Feng Li】			
10:00-10:10	Room Switching			
Time/Place	Workshop on Climate Change 【Host: Dr. I-Ching Chen】	Oversea Scholar 【Host: Dr. Ming-Cheng Wu】	Ethology, Physiology and Organismic Biology 【Hosts: Dr. Hsiao-Ling Lu, Dr. Jia-Hsin Huang】	Medical Entomology/Urban Entomology 【Hosts: Dr. Hou-Feng Li, Dr. Chin-Gi Huang】
10:10-10:25	Experts discussion Dr. I-Ching Chen Dr. Chuan-Kai Ho Dr. Ming-Luen Jeng Dr. Wen-Po Chuang	Oversea_01 Global invasion and host-symbiont coevolution: A case study involving *Wolbachia* in the invasive yellow crazy ant Chih-Chi Lee, Chin-Cheng Scotty Yang	**OE_11** **The expression regulation and physiological function of aquaporin Prip in *Rhyzopertha dominica* (Coleoptera: Bostrychidae)** **Lan-Pin Tan, Qiao-An Lei, Mei-Er Chen**	**OM_01** **Effects of far-UVC light (222 nm) on the development of *Aedes albopictus*** **Ying-Hsuan Chen, Shiuh-Feng Shiao, Kun-Hsien Tsai**

10:25-10:40		Oversea_02 Insect vector of palm-infecting phytoplasma disease De-Fen Mou, Brian Bahder	**OE_12** **Controlling of mustard aphid (*Lipaphis erysimi* Kaltenbach) by entomopathogenic fungi and host immune responses to fungal infection** **Cheng-Ju Yang, Yu-Shin Nai**	**OM_02** **Using *Coelomomyces* spp. to control *Aedes albopictus*** **Fang-Ling Lin, Shiuh-Feng Shiao, Kun-Hsien Tsai**
10:40-10:55		Oversea_03 Stomata-mediated interactions between plants, herbivores, and the environment Po-An Lin	**OE_13** ***Snellenius manila* bracovirus-encoded microRNAs as regulators in *Spodoptera litura* nutrition and metabolism** **Yu-Chun Lin, Yueh-Lung Wu**	OM_03 Detection of *Rickettsia* spp. and *Bartonella* spp. in fleas and small mammals in Chiayi and Tainan area in Taiwan Pei Yun Deng, Chuen Fu Lin, Kun Hsien Tsai
10:55-11:10		Oversea_04 Phytochemicals mediated interactions among aphids *Aphis nerii* and *Myzocallis asclepiadis* and a shared predator Chih-Chung Lee, Brigitte Tenhumberg	**OE_14** **The effects of female encountered density on reproductive strategy of *Nicrophorus nepalensis* Hope (Coleoptera: Silphidae)** **Hsin-Han Cheng, Wenbe Hwang**	OM_04 Neglected phthiriasis in Taiwan: a case of *Pthirus pubis* hyperinfestation, comparative morphological and molecular identification, and retrospective clinical case series Yu-Feng Tsai, Chia-Wen Lee, Wen-Jer Wu, Kun-Hsien Tsai
11:10-11:25		Oversea_05 Genetic basis of metallic color of elytra in carabid beetles (Coleoptera: Carabidae) Yi-Ming Weng, Sean Schoville	**OE_15** **Why can't insects bite zebra? Study landing behavior of honey bee as an example** **Hsiang-Wen Hsieh, En-Cheng Yang**	OM_05 Application of hexaflumuron termite bait in controlling fungus-growing termites Chun-I Chiu, Ya-Hui Chuang, Wei-Ren Liang, Hsin-Ting Yeh, Hsiao-Ying Yang, Ming-Jer Tsai, Neil A. Spomer, Hou-Feng Li
11:25-11:40		Oversea_06 Behavioral responses of the oriental fruit moth *Grapholita molesta* and the parasitoid wasp *Lytopylus rufipes* to herbivore induced plant volatiles released from pear leaves Chia-Ming Liu, Shigeru Matsuyama, Yooichi Kainoh	OE_16 Metagenomics investigation on the gut microbiota of fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuoidea) in Taiwan Yao-Chia Liu, Yu-Shin Nai	OM_06 Preliminary studies on the effects of Taiwanese ritual smoke on *Aedes aegypti* Ching-Yu Shu, Hsueh-Lien Lai, Pei-Yin Lin, Kevin Chi-Chung Chou, Matan Shelomi

11:40-11:55			OE_17 The effect of sublethal dosage of imidacloprid on honey bee queen gene expression Yun-Ru Chen, Shih-Shun Lin, En-Cheng Yang	
11:55-13:10	Lunch Break			
13:10-14:30	Poster Time			
14:30-14:40	Room Switching			
14:40-15:40	Keynote Speech 輻射照射在植物檢疫上的應用與安全性 **Dr. Kuang-Hui Lu** 【Host: Dr. Shiuh-Feng Shiao】			
15:40-16:40	Keynote Speech 植醫甘苦談 **Dr. Li-Cheng Tang** 【Host: Dr. Shiuh-Feng Shiao】			
16:40-17:30	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：蔡經甫博士、蔡正隆博士】 【Judges: Dr. Jing-Fu Tsai, Dr. Cheng-Lung Tsai】		
PB_01	**Gut anatomy and micro-anatomy of several beetle species over their life cycle**	**江旻柔, 薛馬坦** **Min-Rou Chiang, Matan Shelomi**
PB_02	**逆襲的象鼻蟲——生態棲位模擬揭示澳洲蘇鐵蛀莖象鼻蟲入侵臺灣的潛在風險** **Weevil attack: niche modelling highlights risks of potential invasion of Australian trunk-boring cycad weevils in Taiwan**	**蕭昀, 廖治榮** **Yun Hsiao, Jhih-Rong Liao**
PB_03	**造癭強度與其寄主植物誘導植化物質之關係: 以長葉楠姬布癭蚋(*Bruggmanniella litseae*)蟲癭為例** **The effect of galling intensity of *Bruggmanniella litseae* on phytochemicals of *Litsea acuminate***	**王克軒, 楊曼妙, 黃盟元** **Charles Ko-Hsuan Wang, Man-Miao Yang, Meng-Yuan Huang**
PB_04	追溯台灣的大燕蛾(鱗翅目：燕蛾科)，一種最大的迷蛾的地理起源 Tracking the geographical origin of *Lyssa zampa* (Lepidoptera: Uraniidae), the largest stray moth in Taiwan	顏聖紘, 王崇羽, 徐碩謙 Shen-Horn Yen, Chung-Yu Wang, Shuo-Chian Shiu
PB_05	校園封閉對病媒蚊族群之影響—以國立中興大學為例 The influence of campus closed on vector mosquitoes population, a case in National Chung Hsing University	鄭中涵, 黃紹毅 Chung-Han Chang, Shaw-Yhi Hwang
系統分類、族群遺傳、演化 Systematics, Population Genetics and Evolution 【評審：蔡經甫博士、蔡正隆博士】 【Judges: Dr. Jing-Fu Tsai, Dr. Cheng-Lung Tsai】		
PS_01	**擬硬象天牛（*Doliops* spp.）與球背象鼻蟲（*Pachyrhynchus* spp.）的擬態相似度與共演化關係** **Mimetic similarities and coevolution between *Pachyrhynchus* weevils and *Doliops* longhorn beetles**	**孫誼, 陳彭珉, 吳立偉, 顏聖紘, 曾惠芸** **Yi Sun, Shan-Min Chen, Li-Wei Wu, Shen-Horn Yen, Hui-Yun Tseng**
PS_02	**利用親緣基因體學探討球背象鼻蟲屬親緣關係與擬態** **Phylogenomics and mimetic relationship of *Pachyrhynchus* weevils**	**陳彭珉, 孫誼, Ace Kevin S. Amarga, Reagan Joseph T. Villanueva, 曾惠芸** **Shan-Min Chen, Yi Sun, Ace Kevin S. Amarga, Reagan Joseph T. Villanueva, Hui-Yun Tseng**
PS_03	利用次世代定序從博物館典藏樣本中獲取粒線體基因體進行譜系關係研究 Two complete mitochondrial genomes of *Papilio* butterflies obtained from historical specimens (Lepidoptera: Papilionidae)	鄭明倫, 陳明玉, 吳立偉 Ming-Luen Jeng, Ming-Yu Chen, Li-Wei Wu
PS_04	DNA 條碼與形態學證據揭露台灣的禾本科作物田間有三種黏夜蛾族昆蟲 DNA barcode and morphology reveal that three species of Leucaniini occur in Poaceae croplands in Taiwan	顏聖紘, 王崇羽, 謝佳宏 Shen-Horn Yen, Chung-Yu Wang, Chia-Hung Hsieh

PS_05	寬肩蝽亞科(半翅目:寬肩蝽科)臺灣首次紀錄 First record of the subfamily Veliinae (Hemiptera: Veliidae) in Taiwan	劉興哲, 胡芳碩 Hsing-Che Liu, Fang-Shuo Hu
PS_06	大紫蛺蝶(鱗翅目：蛺蝶科)亞種間之親緣關係及其在協助鑑識流通於國際貿易中蝶類標本的意涵 Phylogenetic relationship of the subspecies of *Sasakia charonda* (Lepidoptera: Nymphalidae) and its application on identification of the butterfly taxidermy in trade	顏聖紘, 王崇羽 Shen-Horn Yen, Chung-Yu Wang
行為、生理、個體生物學 Ethology, Physiology and Organismic Biology 【評審：陳韻如博士、邱俊禕博士】 【Judges: Dr. Yun-Ru Chen, Dr. Chun-I Chiu】		
PE_01	評估如何利用鳥類掠食者進行昆蟲警戒性與擬態之行為學測試 Evaluation of the uses of avian predators in behavioral tests of insect aposematism and mimicry	陳俊博, 顏聖紘 Jun-Bo Chen, Shen-Horn Yen
PE_02	**畸翅病毒改變能量代謝影響蜜蜂工蜂分工之研究** **Study of the division of labor in honey bee change due to energy metabolic altered under deformed wing virus infection**	**張維展, 吳岳隆** **Wei-Chan Chang, Yueh-Lung Wu**
PE_03	**球背象鼻蟲的物種形成機制：以 *P. moniliferus* 和 *P. orbifer* 兩姐妹種為例** **Speciation mechanism in *Pachyrhynchus* weevil: the case of two sister species *P. moniliferus* and *P. orbifer***	**何芸, 曾惠芸** **Yun Ho, Hui-Yun Tseng**
PE_04	台灣咖啡果小蠹沃爾巴克氏體之檢測分析 Detection of *Wolbachia* infection in the coffee berry borer from Taiwan	吳翊彥, 呂曉鈴 Yea-Yan Wu, Hsiao-Ling Lu
PE_05	龍眼雞 (半翅目：蠟蟬科) 若蟲形態之個體發生學與渡邊氏東方蠟蟬之比較 Ontogenetic changes in the morphology of *Pyrops candelaria* (Hemiptera: Fulgoridae) and comparison with *Pyrops watanabei*	林亞琍, 林佑昇, 廖治榮, 蕭旭峰, 柯俊成 Ya-Li Lin, You-Sheng Lin, Jhih-Rong Liao, Shiuh-Feng Shiao, Chiun-Cheng Ko
農業昆蟲學 Agricultural Entomology 【評審：陳韻如博士、邱俊禕博士】 【Judges: Dr. Yun-Ru Chen, Dr. Chun-I Chiu】		
PA_01	**蕃茄潛旋蛾在多種茄科植物上的產卵偏好與幼蟲發育表現** **Oviposition preference and subsequent larval performance of tomato pinworm *Phthorimaea absoluta*(=*Tuta absoluta*) when offered a wide range of Solanaceous host plants**	**邱柏諺, 魏壇如, 廖士睿, 顏聖紘** **Po-Yen Chiu, Shann-Ru Wei, Shih-Rei Liao, Shen-Horn Yen**
PA_02	馬尼拉小繭蜂對於不同齡期秋行軍蟲之寄生及發育表現 Parasitism and developmental performance of *Snellenius manilae* on different instars of *Spodoptera frugiperda*	劉蕙如, 黃紹毅 Hui-Ru Liu, Shaw-Yhi Hwang
PA_03	蕃茄潛旋蛾，一個新近入侵物種在台灣的快速擴張與遺傳同質性 Rapid expansion and genetic homogeneity of *Tuta absoluta*, a new invasive species in Taiwan	顏聖紘, 王崇羽, 魏壇如, 徐碩謙, 廖士睿 Shen-Horn Yen, Chung-Yu Wang , Shann-Ru Wei, Shuo-Chian Shiu, Shi-Rei Liao

PA_04	新近在台灣被確認的細蛾科害蟲之分類身份 Taxonomic identity of the newly confirmed gracillariid pests in Taiwan	顏聖紘, 王崇羽, 廖士睿 Shen-Horn Yen, Chung-Yu Wang, Shih Rei Liao
PA_05	抗啃食性害蟲大豆品系篩選與相關化學防禦之揮發性代謝物研究 Screening insect-resistant soybean and determine the volatile organic compounds involved in the chemical defensive mechanism against insect herbivores	張淵云, 林禎祥, 陳賢明 Yuan-Yun Zhang, Chen-Hsiang Lin, Hieng-Ming Ting
PA_07	Evaluation of disease resistance of melon plants by insect vector transmission	Yi-Hui Chen, Chi-Wei Tsai
PA_08	四種藥劑對越冬荔枝椿象之藥劑致死劑量測定 Lethal dose analysis of 4 insecticides on *Tessaratoma papillosa* (Drury)	陳盈丞, 黃慈閔, 林慧婷, 張淳淳 Ying-Cheng Chen, Tzu-Min Huang, Hui-Ting Lin, Chun-Chun Chang
PA_09	玉米簇尖蛾(鱗翅目：紋翅蛾科)在台灣的發現以及對倉儲作物的潛在影響 Discovery of *Anatrachyntis rileyi* (Lepidoptera: Cosmopterigidae) in Taiwan and its potential influence on stored products	顏聖紘, 王崇羽, 葉文彬 Shen-Horn Yen, Chung-Yu Wang, Wen-Bin Yeh
醫學昆蟲學 Medical Entomology		
PM_01	Investigation of *Rickettsia* spp. and *Bartonella* spp. in ectoparasites infesting small mammals in Semarang City, Central Java, Indonesia	Chia Hsuan Chen, Martini Martini, Kun HsienTsai
PM_02	花蓮及新北地區伴侶動物外寄生蟲貓蚤攜帶貓蚤立克次體及巴通氏菌之分子檢驗 Molecular detection of *Rickettsia felis* and *Bartonella* spp. in cat fleas (*Ctenocephalides felis*) infesting companion animals from Hualien and New Taipei City	林子玲, 曾俊傑,吳文哲, 蔡坤憲 Tzu-Ling Lin, Chun-Chieh Tseng, Wen-Jer Wu, Kun-Hsien Tsai
PM_03	Development of a scrub typhus diagnostic platform incorporating baculovirus cell-surface display technology	廖至騏, 蔡智瑄, 羅彗如, 林珮如, 林昌棋, 趙裕展 Chih-Chi Liao, Chih-Hsuan Tsai, Huei-Ru Lo, Pey-Ru Lin, Chang-Chi Lin, Yu-Chan Chao

第 42 屆台灣昆蟲學會年會論文摘要集

Abstract Book

摘要集目錄　Content of Abstract Book

大會專題演講

Keynote Speech

K

Climate change impact on insect pests in the urban environment

Prof. Chow-Yang Lee

Department of Entomology, University of California, Riverside

Today climate change not only has become a significant environmental challenge, but also an economic, human livelihood, and even a political challenge. It poses an existential threat to our ecosystems, food security, water resources that could ultimately affect our survival. The latest United Nations IPCC 2021 report has revealed unequivocally that human activity is responsible for what we are experiencing today. The major effects of climate change are elevated atmospheric CO2, increasing temperature, and changing rainfall patterns. Insects are poikilothermic; hence temperature is perhaps the most crucial factor affecting fecundity, development, survival, activity, distribution, and behavior. However, elevated CO2 and changing rainfall pattern will also directly or indirectly affect insect populations. The urban environment is a complex habitat that is wholly or in part created by man from natural or agricultural ecosystems to meet their specific needs. By 2030, it is predicted that much of the world population will live in urban areas. Urban pest insects have unique behavioral, ecological, and physiological adaptations to thrive well in these resource-limited and water-scarce environment. In this keynote lecture, I will discuss how climate change impacts urban insect pests of public health and aesthetic importance and the outcomes that could led to severe pests and disease issues. I will also elaborate on what we must do to prepare for the upcoming consequences of climate change on urban insect pests.

K

Host plant resistance in rice: new discovery and climate change impact

莊汶博

Wen-Po Chuang

國立臺灣大學農藝學系

Department of Agronomy, National Taiwan University

全世界的農藥銷售量逐年升高。降低農藥使用量但還能保有現有的作物產量以及品質是目前全世界最大的挑戰。因此，種植抗蟲品種取代農藥施用為最佳的取代方案之一。水稻為全球最主要的糧食作物之一且為全球超過三分之一人口的主要能量來源。現今水稻抗蟲性的研究主要針對飛蝨類以及葉蟬類害蟲的相關研究，對於鱗翅目害蟲的研究還僅在初期階段。本次演講會對於抗褐飛蝨的水稻品系以及抗瘤野螟的水稻品系加以介紹以及說明近期新的發現。此外，由於工業時代造成人類活動增加而使得空氣中的二氧化碳逐年增加導致了全球暖化。在本次演講中也會針對於氣候變遷如何影響到水稻抗蟲表現以及對於水稻害蟲的影響。

K

極端氣候影響天敵寄主與其共生物間的互動與適應

The consequences and adaptations of extreme climate events on host-parasitoid and its symbionts interactions

吳立心

Li-Hsin Wu

國立屏東科技大學植物醫學系

Dept. of Plant Medicine, National Pingtung University of Science and Technology

As the frequency of extreme climate events increases, there will be different responses among invasive pests and their interactions with natural enemies. The species distribution models, CLIMEX and MAXENT widely adopted to understand the distribution and potential threat of invasive pests, according to the actual distribution of the species and the environmental factors, following the correlation between the occurrence probability and its habitats (niche). Insect pests provided the most well-studied models while inconsistent experimental paradigms and lack of cross-disciplinary expertise might impede the data integration. The current study aims to understand the impacts of extreme climate events on the efficiency of biological control. Assessing distribution points from the Global Biodiversity Information Facility (GBIF) and some distributions of the latest invasion species of Taiwan, we noticed that model applications and their predictive power will be greatly improved if biotic factors could be better integrated by model-based experimental paradigms. To reveal the possible horizontal transfer route of *Wolbachia w*Ccep in *Trichogramma* spp. and the reason for its disappearance in the field of southern Taiwan, we conducted the thermal adaptation tests, stimulated *Trichogramma* spp., induce the heat shock protein 70 (Hsp 70) in its body to adapt to high-temperature treatments and analyze its influence on the fitness of them. The ultimate goal is to understand the impact of symbionts infection on parasitic efficiency and to further provide integrated applied value under the framework of the increasingly extreme climate events.

K

Insects in the Anthropocene – how insects can help us understand our changing world

Dr. Louise Ashton
University of Hong Kong

Biodiversity loss is a global issue, exacerbated by multiple threats from human activities such as habitat loss, landscape transformation and climate change. There has been an increasing global awareness of the important of biodiversity for maintaining functioning ecosystems which provide us with clean air, water and food, however biodiversity loss and climate change continue to accelerate. There is therefore an urgent need for research to understand biodiversity loss and predict future declines under increasing human pressures.

I focus on the biodiversity of a super-diverse and ecologically essential group – tropical insects, including moths and termites, and how they are responding to environmental change. I will present results demonstrating the importance of insect biodiversity for ecosystem function such as nutrient redistribution and decomposition, and how these functions are affected by climate change impacts such as drought. These insects can be used as sensitive indicators of climate change, and I will summarize some current and future research directions using insects as ecological tools to understand our rapidly changing world in ecosystems ranging from undisturbed to agricultural ecosystems.

K

輻射照射在植物檢疫上的應用與安全性

路光暉

Kuang-Hui Lu

國立中興大學昆蟲學系

Department of Entomology, National Chung Hsing University

全球化農產品貿易量持續成長，使得害蟲入侵到新地區的機會亦隨之提高。為避免新害蟲之入侵，多數國家都訂有相當嚴格的植物檢疫處理條件。長久以來，溴化甲烷 (methyl bromide) 被使用於檢疫燻蒸處理，已滅除存在進、出口農產品中的害蟲。惟因溴化甲烷於 1992 年被聯合國列為破壞臭氧層物質而被逐年禁用。為因應實務需求，各國開始開發不同的植物檢疫處理技術，而其中輻射照射 (irradiation) 即為其中一個漸受重視之替代方案。以輻射照射進行植物檢疫處理處理已於國際間施行多年，相關的國際規範包括國際植物防疫檢疫措施標準第 18 號 (ISPM 18)「輻射照射用作植物防疫檢疫措施的準則」及 ISPM 28「管制類有害生物的植物檢疫處理」。本文旨在簡介輻射照射於植物檢疫處理上的原理、特性及各國相關規範與應用現況等。

蝴蝶紅皮書工作坊

Workshop on IUCN Red List

台灣蝶類紅皮書名錄資訊彙整與評估
IUCN Red List Assessment of Butterflies in Taiwan

林承昊[1]，韋家軒[1]，徐堉峰[2]，顏聖紘[3]，黃行七[4]，呂晟智[4]，朱汶偵[5]，楊曼妙[6]，趙榮台[6]，陳一菁[1]

Cheng-Hao Lin[1], Chia-Hsuan Wei[1], Yu-Feng Hsu[2], Shen-Horn Yen[3], Hang-Ci Huang[4], Cheng-Jhih Lyu[4], Wen-Chen Chu[5], Man-Miao Yang[6], Jung-Tai Chao[6] and I-Ching Chen[1]

[1] 國立成功大學生命科學系 Department of Life Sciences, National Cheng Kung University

[2] 國立臺灣師範大學 National Taiwan Normal University

[3] 國立中山大學 National Sun Yat-Sen University

[4] 社團法人台灣蝴蝶保育學會 The Butterfly Conservation Society of Taiwan

[5] 特有生物研究保育中心 Endemic Species Research Institute

[6] 台灣昆蟲學會 Taiwan Entomological Society

背景/研究問題/材料方法

全球昆蟲多樣性因人類活動與氣候變遷面臨嚴重威脅，尤以鱗翅目為最，台灣亟需完整評估協助擬定保育政策。本報告依據世界自然保育聯盟紅皮書名錄(IUCN Red List of Threatened Species)之標準，全面評估台灣蝶類受脅狀況。依據 TaiBNET 台灣物種名錄、台灣蝶類誌與 IUCN 紅皮書評估指南，排除疑問、偶發、外來等物種，正式評估 358 種蝶類。我們蒐集：族群趨勢與物種時空分布點位，以下列判準進行評估，包括『Criteria A-族群量快速下降』、『Criteria B-分布範圍侷限且族群波動』、『Criteria D-極小族群』。族群趨勢來自全台蝶類複查與蝴蝶保育學會長期監測；物種時空分布點位則蒐集自博物館典藏與台灣生物多樣性網(Taiwan Biodiversity Network，TBN)。評估流程含資料初評與專家複評，專家依據自身經驗，獨立檢視物種資料並予以補充，最後整合專家意見、綜合權衡資訊品質完成最終評估。

結果/結論/應用啟示

台灣蝴蝶有 27 種評估為國家受脅(Nationally Theatened)等級，其中 3 種極危(含黃鳳蝶、截脈絹粉蝶、夸父璀灰蝶)、5 種瀕危(含角翅黃蝶、台灣脈弄蝶、南方燕藍灰蝶、大紫蛺蝶、波紋黛眼蝶)、19 種易危；另外有 174 種列於接近受脅等級，150 種暫無危機、7 種資料缺乏。本次評估提供台灣蝴蝶保育所需之關鍵資訊，所建立之決策流程與資料蒐集建議，可提供未來再次評估之具體藍圖。

關鍵詞(Keywords)：IUCN 紅皮書名錄(IUCN Red List)、族群趨勢(population trend)、分布範圍（geographic distribution）、生物多樣性保育（biodiversity conservation）、長期生態監測（long-term ecological monitoring）

海外昆蟲學者

論文宣讀

Oral Session: Oversea Entomologists

Oversea_01

探討長腳捷山蟻與沃爾巴克氏菌之共演化及全球入侵

Global invasion and host-symbiont coevolution: A case study involving *Wolbachia* in the invasive yellow crazy ant

李志琦[1]，楊景程[2]
Chih-Chi Lee[1] and Chin-Cheng Scotty Yang[2]
[1] 以色列海法大學演化學研究所演化與環境生物學系 Department of Evolutionary and Environmental Biology, Institute of Evolution, University of Haifa, Haifa, Israel
[2] 美國維吉尼亞理工學院暨州立大學昆蟲學系 Department of Entomology, Virginia Polytechnic Institute and State University, Blacksburg, VA, USA
Presenting author's email: clee05@campus.haifa.ac.il

背景/研究問題/材料方法

The sporadic spreads of nonindigenous species to novel environments as result of human-mediated jump dispersal offer an excellent opportunity to explore mechanisms underlying rapid adaptation of invasive species to novel environments that they have never experienced. One of working hypotheses is that endosymbionts confer benefits to its host when the host is challenged by new environmental stress. To test this hypothesis, we examined whether any endosymbionts are tightly associated with the yellow crazy ant (*Anoplolepis gracilipes*), one of the global invasive ant species, across the ant's invasive ranges. The strain/isolate identity of endosymbiont was established using multilocus sequence typing (MLST). To assess co-evolutionary history of the endosymbiont and yellow crazy ant, genome-wide SNP makers of the endosymbiont and its host were identified using double digest restriction site-associated DNA sequencing (ddRAD-seq) and were used in subsequent phylogenomic analyses. Additional analyses to characterize the host-symbiont co-evolutionary patterns include mitochondrial DNA variation of the ant and outlier loci approaches.

結果/結論/應用啟示

Our results showed that *Wolbachia* is the sole microorganism found to be highly prevalent (96.25%) across the global populations of *A. gracilipes*. MLST analysis indicated that all infected ants share the same *Wolbachia* strain. Virtually all datasets including nuclear, mitochondrial, and *Wolbachia* phylogenies are congruent with each other in supporting co-divergence of the ant and *Wolbachia*. Using outlier approaches, genomic regions under selection were pinpointed, and one of which is likely associated with *Wolbachia* manipulation. In *Wolbachia*, we also identified a hypothetical protein gene under the positive selection. Altogether, this study showed the coevolution of *Wolbachia* and the yellow crazy ant at a global scale, and also raises a critical question about how the observed host-symbiont system facilitates the colonization of the host ant.

關鍵詞(Keywords)：長腳捷山蟻(*Anoplolepis gracilipes*)、沃爾巴克氏菌(*Wolbachia*)、雙限制酶點位標定序列（ddRAD-seq）、族群結構（Population structure）、共同演化（Coevolution）

Oversea_02

Insect vector of palm-infecting phytoplasma disease

De-Fen Mou[1] and Brian Bahder[1]
[1]Department of Entomology and Nematology, Fort Lauderdale Research and Education Center, University of Florida
Presenting author's email: defenmou@ufl.edu

背景/研究問題/材料方法

Phytoplasmas are plant pathogenic bacteria that affect hundreds of plants worldwide. Lethal Bronzing (LB) is a fatal disease of palms caused by phytoplasma '*Candidatus* Phytoplasma aculeata'. This disease causes significant economic losses to palm industries and landscapes in Mexico and United States. Phytoplasmas are phloem-limited and are transmitted by phloem-feeding insect vectors. Therefore, the vector is undoubtedly one of the critical factors in phytoplasma disease management. This study presents the insect vector identification for '*Ca*. Phytoplasma aculeata' and the potential impacts of LB infection of palm on the vector abundance.

結果/結論/應用啟示

Firstly, planthoppers and leafhoppers that are potentially feeding on palm phloem in areas with active LB spread were collected and screened for phytoplasma to identify potential vector candidates. The results showed a higher abundance of *Haplaxius crudus* (Hemiptera: Cixiidae) than other insects. *Haplaxius crudus* was also the only insect that consistently tested positive for the phytoplasma. These results suggested that *H. crudus* is a potential vector of the LB phytoplasma. Moreover, impacts of a phytoplasma disease in palms on the vector abundance were investigated. Results showed that the abundance of *H. crudus* was higher on phytoplasma-infected relative to non-infected palms. These results indicated the potential preference of *H. crudus* on LB-infected over non-infected palms. Collectively, these results support that *H. crudus* is a vector of LB phytoplasma and provide critical information that will help develop disease management programs in the future.

關鍵詞（Keywords）：菌質體（Phytoplasma）、病媒昆蟲（Vector）、菱飛蝨（Cixiidae）

Oversea_03

植物氣孔與植食性昆蟲之交互作用

Stomata-mediated interactions between plants, herbivores, and the environment

林柏安 [1]
Po-An Lin[1]
[1]Penn State University, Department of Entomology
Presenting author's email: poanlin1@hotmail.com

背景/研究問題/材料方法

Stomata play a central role in plant responses to abiotic and biotic stresses. Existing knowledge regarding the roles of stomata in plant stress is centered on abiotic stresses and plant-pathogen interactions, but how stomata influence plant-herbivore interactions remains largely unclear.

結果/結論/應用啟示

Here, we summarize the functions of stomata in plant-insect interactions and highlight recent discoveries of how herbivores manipulate plant stomata. Because stomata are linked to interrelated physiological processes in plants, herbivory-induced changes in stomatal dynamics might have cellular, organismic, and/or even community-level impacts. This presentation summarizes our current understanding of how stomata mediate plant responses to herbivory and environmental stimuli and how herbivores influence these responses and identifies key knowledge gaps in plant-herbivore interactions.

關鍵詞（Keywords）：植物防禦反應（plant defense）、氣孔（guard cell）、非生物逆境（abiotic stress）、生物逆境（biotic stress）、植食性昆蟲引發之植物芳香物質（herbivore-induced plant volatile）

Oversea_04

Phytochemicals mediated interactions among aphids *Aphis nerii* and *Myzocallis asclepiadis* and a shared predator

Chih-Chung Lee[1] and Brigitte Tenhumberg[1]
[1] 美國內布拉斯加州立大學林肯分校生物科學系 School of Biological Sciences, University of Nebraska-Lincoln, USA
Presenting author's email: cclee@huskers.unl.edu

背景/研究問題/材料方法

Phytochemicals are one of the most essential plant defense mechanisms which have negative impacts (e.g., reduce survival rate, growth rate, and fecundity) on herbivores. Over evolutionary time, some herbivores have coevolved mechanisms to sequester phytochemicals and use them as protection against their predators. As a result, phytochemicals may mediate interactions among the insect community. Although evidence shows that climate change alters the physiology of plants, little is known about the species-specific effect of climate change on plants' phytochemical synthesis and the consequence of phytochemical variation on insect interactions. In this study, common milkweed (*Asclepias syriaca*) has evolved cardenolides as a phytochemical defense against herbivores. Specialist herbivores such as aphid species, *Aphis nerii* and *Myzocallis asclepiadis*, can sequester cardenolides but differ in the concentration of accumulated cardenolides, which provide different levels of protection against aphid predators. At the same time, *A. nerii* and *M. asclepiadis* coexist on common milkweeds and share common predators during the growing season at the study site. In order to understand how cardenolides mediate interactions between *A. nerii* and *M. asclepiadis* under different environmental conditions. We conducted a field experiment and examined the population growth rates of two aphid species under different competition, predation, and warming conditions.

結果/結論/應用啟示

The result showed when the predator was present, *A nerii* reduced predation pressure on *M. asclepiadis*. Because *M. asclepiadis* has higher sequestration of cardenolides than *A nerii*, this result suggests that the predation preference reduces the negative effect on high sequestration aphid species. The result also shows that the warming effect did not alter the interaction outcomes but slightly increased the population growth rate for both aphid species. Currently, we are in the process of analyzing the cardenolide concentration of milkweeds and aphids, which will shed light on the role of phytochemicals in these interactions.

關鍵詞（Keywords）：cardenolides, predator-mediated interactions, indirect interactions, warming effect, sequestration

Oversea_05

步行蟲 (鞘翅目:步行蟲科) 翅鞘金屬光澤遺傳機制初探
Genetic basis of metallic color of elytra in carabid beetles (Coleoptera: Carabidae)

翁逸明 [1]，Sean Schoville[1]
Yi-Ming Weng[1] and Sean Schoville[1]
[1]Department of Entomology, University of Wisconsin-Madison, USA
Presenting author's email: weng22@wisc.edu

背景/研究問題/材料方法

許多鞘翅目昆蟲因具有多種色彩的金屬光澤而長期受到關注。過去超過半世紀以來由於電子顯微鏡的發展與普及，我們得以進一步研究昆蟲表皮的顯微結構並了解此金屬光澤的物理原理。遺傳學方面，許多近親交配實驗發現某些鞘翅目昆蟲其金屬光澤的表型遺傳遵循單基因或少量基因控制之孟德爾遺傳定律，暗示著能夠讓我們利用表型基因型定位法 (association mapping) 來偵測控制金屬光澤基因的契機。在這個研究當中，我們定序 375 件 *Nebria ingens* complex 樣本之全基因組，其中包含翅鞘為綠色金屬光澤的 *N. riversi*、 黑色光澤的 *N. ingens* 及體色為中間型的雜交後代個體。在個體平均定序深度為 3.5 倍的形況下，我們利用已發表之全基因當作參考基準標定出超過五百萬個單核苷酸多態性 (SNP) 做為遺傳標誌。而在移除包含低頻等位基因之基因座之後，我們將保留下來約 120 萬個 SNP 與轉換自 400-700 奈米區間反射光譜的 CIELAB 色彩空間之綠色軸進行潛在因子線性混合模型分析 (LFMM)。

結果/結論/應用啟示

在控制來自遺傳結構的雜訊並使用 Benjamini-Hochberg 校正第一型錯誤後，我們找出 293 個與體色分布相關性最高的基因，並利用基因本體富集分析 (GO enrichment analysis) 找出相關的基因功能。結果發現其中 22 個基因與體表形成、黑色素分泌、幾丁質鞣化有關。未來將利用 phyloGWAS 方法來擴大分類階級以進一步驗證這些金屬光澤之關鍵基因。

關鍵詞（Keywords）：步行蟲（Carabidae）、翅鞘金屬光澤（metallic color of elytra）、表型基因型定位法（association mapping）、基因本體富集分析（GO enrichment analysis）

Oversea_06

蟲害誘導的梨樹揮發性成分對於桃折心蟲的產卵及其天敵昆蟲搜尋寄主行為之影響

Behavioral responses of the oriental fruit moth *Grapholita molesta* and the parasitoid wasp *Lytopylus rufipes* to herbivore induced plant volatiles released from pear leaves

劉家銘[1]，松山茂[2]，戒能洋一[2]
Chia-Ming Liu[1], Shigeru Matsuyama[2] and Yooichi Kainoh[2]
[1] 農研機構生物機能利用部門 The Institute of Agrobiological Sciences, NARO
[2] 筑波大學生命環境系 Faculty of Life and Environmental Sciences, University of Taukuba
Presenting author's email: cobras770920@hotmail.com

背景/研究問題/材料方法

昆蟲能辨識環境中的化學物質並作出適當的反應。其中植食性昆蟲能根據寄主植物的氣味來選擇適合的棲地；天敵昆蟲則是以植物受到植食性昆蟲攻擊後散發出的 Herbivore-induced plant volatiles (HIPVs) 來尋找寄主。有些植食性昆蟲甚至會遠離 HIPVs 以減少遭遇天敵的機率。因此，在田間施用 HIPVs 能夠提高天敵的數量或是當作忌避劑來降低害蟲的密度，但在果園中使用 HIPVs 進行蟲害防治的研究卻毫無進展。本研究以未被害及被害梨樹新芽作為氣味來源，評估梨樹 HIPVs 對於桃折心蟲 (*Grapholita molesta*) 的棲地選擇及其寄生蜂 (*Lytopylus rufipes*) 搜尋寄主行為之影響。

結果/結論/應用啟示

結果顯示，比起未被害新芽，桃折心蟲傾向於在被害新芽附近產卵；*L. rufipes* 也明顯地在被害新芽區域停留較久。氣相層析質譜儀的分析結果顯示，未被害及被害新芽散發的氣味成分非常相似，唯獨 (*E*,*E*)-α-farnesene 的比例在新芽被害後明顯上升。以 HIPVs 成分進行生物檢測結果顯示，無論桃折心蟲或者 *L. rufipes* 皆對於單一成分無顯著偏好，但將所有成分依照比例混合的梨樹 HIPVs 卻能誘發與被害新芽相似的反應。根據以上結果得知，桃折心蟲和 *L. rufipes* 需要利用完整的植物氣味來選擇棲地以及搜尋寄主，這些辨識氣味的機制可能與寄主專一性有關。此外，桃折心蟲沒有逃離 HIPVs，而是選擇將卵產在被害植物附近，此行為可能與梨樹對於蟲害的耐受性(tolerance)有關。

關鍵詞（Keywords）：Tritrophic interaction, *Grapholita molesta*, *Lytopylus rufipes*, Herbivore-induced plant volatiles, (E,E)-α-farnesene

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

Global pattern and climatic predictor of eyespot traits in nymphalid butterfly

韋家軒[1]，姜信宏[1]，陳一菁[1]
Chia-Hsuan Wei[1], Shin-Hung Jiang[1] and I-Ching Chen[1]
[1] 國立成功大學生命科學系 Department of Life Sciences, National Cheng Kung University
Presenting author's email: weich1206@gmail.com

背景/研究問題/材料方法

Eyespot of butterflies plays a crucial role against attacks from predators. Since the traits (i.e. number, size, and contrast) exhibiting considerable variability in varied climatic conditions, drivers promoting ultimate and proximate causation draws many biologists' attention in ecology, evolution and development. Although ecological drivers have been investigated in several model species, the joint effect of environment factors and predation pressure on interspecific variability of eyespots at macroecological scale is yet clear. Here we explored the general response of the traits by employing public digitized specimens of 2560 species of Nymphalidae butterflies. In order to detect and segment eyespots, a supervised deep learning model, SOLOv2 with ResNet50 backbone, was trained to process the images. In total, eyespots are detected in 768 species, which were used to calculate the functional traits. Climatic factors, integrated enhanced vegetation index (iEVI), insectivorous bird richness were used as predictors for environment factors, productivity, and predation pressure. The values were averaged at 0.5 degree resolution. Hierarchical partitioning was applied to test independent contribution.

結果/結論/應用啟示

Geographical distribution of number and size show a similar pattern with higher value in Nearctic than other biogeographical regions, whereas the pattern of color contrast is inconsistent among the regions. The results of hierarchical partitioning show that independent effects of temperature-related factors are higher than predation pressure and iEVI in all tests. The variability of eyespots is better explained by temperature-related factors than predation pressure and iEVI, suggesting environmental factors play a more important role than biotic ones. The present study provides a new insight to the proximate causation of adaptive eyespot patterns in butterflies.

關鍵詞（Keywords）：Macroecology, Eyespot, Deep learning, Predation pressure, Nymphalidae

OB_02

What is the effect of *Wolbachia* in sib-mating ambrosia beetles of the *Euwallacea fornicatus* Eichhoff (Coleoptera: Curculionidae) species complex?

劉芳綾[1]，Paul Rugman-Jones[2]，Richard Stouthamer[2]，段淑人[1]
Fang-Ling Liu[1], Paul Rugman-Jones[2], Richard Stouthamer[2] and Shu-Jen Tuan[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
[2] 美國加州大學河濱分校昆蟲系 Department of Entomology, University of California, Riverside
Presenting author's email: fiveac45@gmail.com

背景/研究問題/材料方法

Wolbachia is an endosymbiont bacterium well-known for influencing the reproduction of its arthropod hosts in ways that favors its own spread through the host population. Because only females can pass on the *Wolbachia* infection, the effects *Wolbachia* cause are generally related to producing more daughters (parthenogenesis; making genetics males into functional females), fitter daughters (male killing), or cytoplasmic incompatibility (sperm from infected males kills eggs of uninfected females). A further effect may be that *Wolbachia* provides infected individuals with some benefits that enhances their fitness.

The *Euwallacea fornicatus* species complex consists of at least four species and is an invasive forest pest worldwide. They have a haplodiploid sex determination system where fertilized (diploid) eggs become females and unfertilized (haploid) eggs become males. Offspring sex ratios are highly female biased, combined with sib-mating (mating between sibling). Taiwan lies within the native region and harbors three co-occurring species (*E. fornicatus, E. kuroshio,* and *E. perbrevis*). A further "probable" species, currently referred to as Haplotype 22, is also common. The incidence of *Wolbachia* infection in these four species in Taiwan was surveyed using PCR. *Wolbachia* strains were characterized using multilocus sequence typing (MLST).

結果/結論/應用啟示

Wolbachia infection frequencies differed among the four species. MLST revealed that *E. fornicatus* (partial infection) and Haplotype 22 (complete infection) were both infected with the same strain of *Wolbachia* in supergroup A, and *E, perbrevis* was 100% infected with a *Wolbachia* in supergroup B. No infection in *E. kuroshio* was found. Based on our knowledge of the reproduction of these beetles on artificial media, we can largely exclude the following effects: cytoplasmic incompatibility, feminization, male killing, and parthenogenesis. The most likely effect of *Wolbachia* is either a purely mutualistic role or *Wolbachia* is required for the development of eggs without *Wolbachia* fail to hatch. Currently we are investigating these possibilities.

關鍵詞（Keywords）：shothole borer, endosymbiont, cryptic, Scolytinae

OB_03

農業長期生態園區指標昆蟲-瓢蟲之調查

Surveys of insect as the indicator in experiment fields of long-term ecological research for agriculture - coccinellids

許北辰[1]，楊婉秀[1]，余志儒[2]，董耀仁[1]，陳琦玲[3]，石憲宗[4]
Pei-Chen Hsu[1], Wan-Shiou Yang[1], Jih-Zu Yu[2], Yew-Jen Dong[1], Chi-Ling Chen[3] and Hsien-Tzung Shih[4]
[1] 農委會農業試驗所應用動物組助理研究員。台灣 台中市。Assistant Research Fellow, Agricultural Zoology Division, Taiwan Agricultural Research Institute, Taichung, Taiwan, ROC
[2] 農委會農業試驗所應用動物組副研究員。台灣 台中市。Associate Research Fellow, Agricultural Zoology Division, Taiwan Agricultural Research Institute, Taichung, Taiwan, ROC
[3] 農委會農業試驗所農業化學組研究員。台灣 台中市。Research Fellow, Agricultural Chemistry Division, Taiwan Agricultural Research Institute, Taichung, Taiwan, ROC
[4] 農委會農業試驗所應用動物組研究員兼組長。台灣 台中市。Research Fellow and Division Director, Applied Zoology Division, Taiwan Agricultural Research Institute, Taichung, Taiwan, ROC
Presenting author's email: bchen@tari.gov.tw

背景/研究問題/材料方法

本研究以瓢蟲 (coccinellids)為指標昆蟲 (indicator)，於農業試驗所溪口農場進行長期調查，並建立基線資料(baseline data)。希望能觀察農業生產體系中肥料與農藥的投入，及氣候因子變化等對害蟲天敵族群的影響，有助於未來建立符合農業永續經營的作物管理模式時可提供參考資訊。本研究在溪口農場試區，於 2014-2019 年水稻之友善及周邊慣行兩種耕作操作之水田連作區與水旱輪作田區的兩個期作之分蘗初期起進行瓢蟲種類發生之調查，旱田與稻作同時進行。在二農場試驗小區田中央長軸前、後兩邊距離田埂約 20 m 處各設立一支 T 型支架，長 120 cm，高 150 cm，支架上懸掛一塊對折之黃色黏板，長 33 cm，寬 28 cm（如圖一）。每二星期將黃色黏板收回並置換上新黏板，於實驗室內鑑定記錄黏板上所捕獲瓢蟲的種類與數量。

結果/結論/應用啟示

本研究於 2014-2020 年在友善及周邊慣行兩種耕作操作之水田連作區與水旱輪作田區均調查到六條瓢蟲(*Cheilomenes sexmaculata* (Fabricius, 1781))、六星瓢蟲(*Oenopia formosana* (Miyatake, 1965))、七星瓢蟲(*Coccinella septempunctata* Linnaeus, 1758)、龜紋瓢蟲(*Propylea japonica* (Thunberg, 1781))、橙瓢蟲(*Micraspis discolor* (Fabricius, 1798))、錨紋瓢蟲(*Lemnia biplagiata* (Swartz, 1808))、波紋瓢蟲(*Coccinella transversalis* Fabricius, 1781)、赤星瓢蟲(*Lemnia saucia* (Mulsant, 1850))、八條瓢蟲(*Harmonia octomaculata* (Fabricius, 1781))、大十三星瓢蟲(*Synonycha grandis* (Thunberg, 1781))，及素鞘瓢蟲

(*Illeis koebelei* (Timberlake, 1943))等 11 種瓢蟲，發生的瓢蟲種類並無差異。其中，六條瓢蟲為兩地區之水稻第一期作與第二期作最具數量優勢之瓢蟲，佔總比例分別為 78.0%及 79.4%，其次依序為橙瓢蟲 (8.2%及 5.4%)、素鞘瓢蟲 (4.7%及 5.2%)、錨紋瓢蟲 (4.2%及 3.4%) 及赤星瓢蟲 (4.7%及 5.2%)。比較溪口農場友善水稻田及周邊慣行水稻田的瓢蟲平均數量，六條瓢蟲平均數量分別為 27.9 隻及 9.6 隻；橙瓢蟲為 9 隻及 0 隻；素鞘瓢蟲為 3.3 隻及 0.6 隻，推測耕作方式可能影響瓢蟲的平均數量。綜上所述，六條瓢蟲於水稻一期及二期作中調查數量最多，且耕作方式可能影響其發生數量，因此六條瓢蟲具有作為友善水稻生產指標昆蟲的潛力。

關鍵詞（Keywords）：長期生態（long-term ecological）、耕作系統（farming system）、永續耕作（sustainable farming）、瓢蟲（coccinellids）

OB_04

訪花膜翅目昆蟲多樣性與蜜源植被營造關聯性之研究
The study of relationship between bee (Hymenoptera) diversity and nectar vegetation planting

徐培修[1]，吳姿嫻[1]
Pei-Shou Hsu[1] and Tzu-Hsien Wu[1]
[1]行政院農業委員會苗栗區農業改良場 Miaoli District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan
Presenting author's email: pshsu@mdais.gov.tw

背景/研究問題/材料方法

為實現「與自然和諧共生」的世界，必須採取有效的行動維護生態永續性並兼顧經濟發展。蜂類昆蟲在植物開花期間進行訪花授粉同時可生產蜂產品，提供「調節」及「供應」的生態系服務，對於人類與生態系之連結和互惠極為重要。農業開發及棲地破碎導致蜂類可利用的蜜源植物資源發生變化甚至減少，如何營造友善蜂類生態環境成為刻不容緩的議題。果園生態系是人類、植物、授粉昆蟲三者互動頻繁之環境，過往已知果園草生栽培具覆土效果可抑制雜草滋生並改善土壤理化特性，本研究於果園地面種植蜜源植被，預期能加值作為訪花蜂類食物來源，後續進行訪花蜂類多樣性及棲群數量調查評估其效益。本研究場域位於苗栗縣西湖鄉一處有機柑橘果園，約 8 千平方公尺，試驗前無草生栽培，地面滿佈原生雜草。本研究目標為比較種植蜜源植被與否之差異，因此一半的場域維持原樣做為非植草區，另一半的場域於 2019 年初以白花三葉草(*Trifolium repens*)及赤道櫻草(*Asystasia gangetica* ssp. *gangetica*)進行為期一年之地面植被營造，作為植草區。接續自 2020 年 3 月至 2021 年 6 月為止每 3 個月進行一次訪花蜂類調查，共進行 6 次。每次調查由 2 名人員針對開放花朵進行 20 分鐘掃網，採集所有膜翅目昆蟲帶回實驗室鑑定，比較植草區與非植草區之訪花蜂類多樣性及個體數量差異。

結果/結論/應用啟示

本研究進行為期一年半總共 6 次的長時間訪花蜂類調查，植草區的總多樣性為 9 科 32 種、平均多樣性為 8 種、平均個體數為 110 隻，非植草區的總多樣性為 6 科 11 種、平均多樣性為 2 種、平均個體數為 36 隻，且每次調查植草區之物種數及個體數皆高於非植草區，代表植草區確實具有吸引較多訪花蜂類之效益，後續研究應著重於果樹授粉效益調查。此外整個調查期間僅在植草區發現者為小蜂總科、土蜂科、葉蜂科、蜜蜂科的 5 個物種、姬蜂總科的 6 個物種、切葉蜂科的 4 個物種、細腰蜂科的 3 個物種、胡蜂科的 3 個物種，可以作為後續指標物種之研究參考。個體數出現最多的物種為西方蜜蜂(*Apis mellifera*)，每次調查植草區平均出現 96 隻，非植草區平均出現 35 隻，代表經濟飼養的物種在農業生態系中仍為主要活動族群。

關鍵詞（Keywords）：蜂（bee）、蜜源植物（nectar plant）、生物多樣性（biodiversity）

OB_05

入侵小蜜蜂之畸翅病毒分離株研究
Deformed wing virus isolates of invasive dwarf honeybee *Apis florea*

田謹萱[1]，蔡文錫[1]，宋一鑫[1]
Jin-Xuan Tian[1], Wen-Shi Tsai[1] and I-Hsin Sung[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: jinshiuann123@gmail.com

背景/研究問題/材料方法

畸翅病毒 (Deformed wing virus, DWV) 是造成西洋蜂 (*Apis mellifera*) 蜂群異常，影響蜜蜂生產的重要病毒，研究證實典型畸翅病毒 A 類種 (DWV-A quasispecies)，最常發生於蜜蜂體內，也是 DWV 最容易形成跨物種傳播的類種。於 2017 年發現東南亞的小蜜蜂 (*A. florea*) 為台灣的入侵外來種，對本土生態、農業及社會安全造成威脅。本研究調查共域 (sympatric) 的入侵小蜜蜂與西洋蜂，其所被感染的 DWV 分離株。自 10 個採集地點採集大花咸豐草 (*Bidens pilosa* L. var. *radiata* Sch.) 上訪花的小蜜蜂與西洋蜂共 67 隻；另移除 10 個小蜜蜂蜂巢，各採 4–8 隻檢測 DWV。單隻抽取中腸萃取病毒，經 RT-PCR，以 DWV 及 KV 的通用性引子進行病毒檢測，後續基因選殖以 Q5 high-fidelity DNA polymerase 進行 RT-PCR，獲得 VP1+VP3 和 RdRp 基因片段序列與 GenBank 現有之 DWV-A、DWV-B (= 蜂蟹蟎病毒, *Varroa destructor virus-1*, VDV-1)，含感染西洋蜂、頭角竹節蟲 (*Medauroidea extradentata*)、黃跗虎頭蜂 (*Vespa velutina nigrithorax*)、*V. crabro* 與東方蜂 (*A. cerana*) 的 DWV 相對應序列，以 DNAMAN 進行相似度分析，並建立同源性親緣關係樹 (homology tree)。

結果/結論/應用啟示

對野外個體的 DWV 總檢出率，入侵小蜜蜂為 88.1% (n = 42)，西洋蜂為 36.1% (n = 25)；單一地點的檢出率，小蜜蜂為 83.5% (n = 10)，西洋蜂為 22.5% (n = 10)。而小蜜蜂蜂巢中，感染率為 100% (n = 10)，單一蜂巢內個體的平均感染率為 90% (n = 50)，。在病毒基因體部分序列分析上，西洋蜂的 DWV 之 VP1+VP3 基因序列與感染已知西洋蜂、頭角竹節蟲、*V. crabro*、與東方蜂的 DWV-A 核酸序列有高相似度 (96% – 100% nucleotide sequence identity)，而在 RdRp 序列的分析，相似度亦高達 96% – 99%；但感染入侵小蜜蜂 DWV 的 VP1+VP3 及 RdRp 序列則自成一群，與感染上述已知物種的 DWV-A 相對應片段的相似度，最高僅達 87%，與 DWV-B 只達 85%。綜合上述，入侵小蜜蜂高度受 DWV 感染，西洋蜂亦有一定比例受 DWV 感染。推測西洋蜂樣本上的 DWV 為 A 類種，而入侵小蜜蜂樣本的 DWV 並無證據可證明為 A 類種或 B 類種。推論入侵小蜜蜂之畸翅病毒具有威脅西洋蜂的可能，未來應考慮此病毒類種之跨物種感染及對西洋蜂異常之影響。

關鍵詞（Keywords）：小蜜蜂（*Apis florea*）、畸翅病毒（Deformed wing virus）、類種（quasispecies）、同源性親緣關係樹（homolgy tree）

OB_06

一種於臺灣寄生六條瓢蟲(*Cheilomenes semaculata*)的寄生蜂之分類與生活史研究

The study of taxonomy and life history of a parasitic wasp on *Cheilomenes semaculata* in Taiwan

鄭中涵[1]，黃紹毅[1]
Chung-Han Chang[1] and Shaw-Yhi Hwang[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: 0909348926@gmail.com

背景/研究問題/材料方法

六條瓢蟲(*Cheilomenes semaculata*)是一種廣泛分布在中緯度到赤道區域的瓢蟲，擁有較其他捕食者高的內在優勢(intrinsic advantages)，具有發展成為天敵防治的潛力。然而，鮮少有針對寄生六條瓢蟲的寄生蜂的紀錄，以及其生活史等資訊。本研究自國立中興大學校區採集一種六條瓢蟲的幼蟲寄生蜂，並於實驗室進行初步的研究，探討其分類、公母的分辨、生活史、寄生率、子代性別比。

結果/結論/應用啟示

該種寄生蜂屬於 Eulophidae 科，雄蟲及雌蟲的觸角結構有明顯的不同，在 25℃的環境下，主要於寄主 L2~L4 的階段開始寄生，屬於內寄生的寄生蜂，於寄主蛹期時羽化並破蛹而出，最終造成寄主死亡，極少數個體會寄生在 L1 或於寄主前蛹狀態時羽化。以 Fisher's protected LSD test 對在不同齡期被寄生的瓢蟲幼蟲發育時間進行比較，發現(1)不論何時寄生對 L2、L3、前蛹皆無顯著影響；(2)在 L4 寄生時會造成寄主 L4 發育時間顯著延長；(3)不論何時寄生皆會造成寄主蛹期顯著延長。寄生蜂在 L1 至 L4 的寄生率依序為 6.67%、80.95%、50%、100%。整體寄生蜂的性別比為 90.68，雌性多於雄性，但有不少組別的子代雄性與雌性比例非常懸殊，因此推測此種寄生蜂可能有產雄孤雌生殖的現象。這是台灣第一個研究這種寄生蜂的研究，未來會以了解雌蜂的繁殖力、子代數、子代性別比、孤雌生殖現象等為主要目標，建立寄生蜂的基礎資料。

關鍵詞(Keywords)：六條瓢蟲(*Cheilomenes semaculata*)、Eulophidae、寄生蜂(parasitic wasp)、生活史(life cycle)

OB_07

漂海性白蟻之雙重巢群拓殖策略
Dual-dispersal strategy of oceanic termite

邱奕寧[1]，邱俊禕[1]，劉佳穎[2]，林明德[2]，李後鋒[1]
Yi-Ning Chiu[1], Chun-I Chiu[1], Chia-Ying Liu[2], Ming-Der Lin[2] and Hou-Feng Li[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
[2] 慈濟大學分子生物暨人類遺傳學系 Department of Molecular Biology and Human Genetics, Tzu Chi University
Presenting author's email: bes8667tw@gmail.com

背景/研究問題/材料方法

Dispersal strategy is an important mechanism to the animals to adapt the varies environments. In social animals, dispersal was relating to the colony spread and the new colony founding. Previous studies hypothesized that ants and termites could display two dispersal strategies, alate-dispersal strategy and neotenic-dispersal strategy, producing winged or wingless reproductives, respectively. The oceanic termite, *Prorhinotermes* sp., had been recorded to have 2-12% of wingless reproductives, neotenics. A group of termite individuals could leave out of the nest then migrate to the new food resources that expressed the potential to use the neotenic-dispersal strategies. We studied 30 wild colonies of *Prorhinotermes flavus*, to test whether do the *P. flavus* perform both dispersal strategies. We analyzed the cost and benefits of the two strategies based on colony caste composition, morphology, body weights, and dispersal speeds.

結果/結論/應用啟示

The results supported that the both dispersal strategies adopted by *P. flavus*, but not likely occur simultaneously in one specific colony. According to the reproductive components, the 30 *P. flavus* colonies could be grouped into the alate-producing colony or neotenic-producing colony. The alates were 1.2 times heavier and have higher pronotum/ head width ratio than the neotenics. Alates had one more molting stage comparing to the stage of neotenics. The speed of alate flight was approximately 30 times faster than that of neotenic's locomotion. The results support that the neotenics caste is not only a breeder but also a disperser. Neotenic-dispersal strategy is a less energy investing and faster way to produce the reproductive than the alate-dispersal strategy. The dual-dispersal strategy could be the adaptive mechanism of social species to survive in fragmented habitats.

關鍵詞(Keywords)：Secondary reproductive, Colony colonization, Oceanic dispersal, Social evolution

OB_08

都市湧泉型溪流水棲昆蟲之生態初探：以台中南勢溪為例

A preliminary study of the ecology of aquatic insects in a spring originated stream in urban areas: The case of Nan-Shih Stream in Salu District, Taichung City

鍾濬宇[1]，張依潔[1]，黃彩瑜[1]，徐崇斌[1]
Chun-Yu Chung[1], Yi-Chieh Chang[1], Tsai-Yu Huang[1] and Chorng-Bin Hsu[1]
[1]靜宜大學生態人文學系 Department of Ecological Humanities, Providence University
Presenting author's email: sas96110@gmail.com

背景/研究問題/材料方法

湧泉因水質潔淨且水量穩定，除可孕育出豐富的生態資源，亦與聚落發展有密切的關係。沙鹿的南勢溪是天然湧泉形成的溪流，長久以來提供居民生活上的需求，也造就在地獨特的文化；然而由於位在都市區內，南勢溪同時肩負都市排水的功能，城市開發與廢水排入，對河溪生態與居民的利用造成不良的影響。以往對本南勢溪生態研究資料極為缺乏，臺中市政府 2018 年在前瞻計畫中推動水環境改善工程，運用生態工法增加生物棲地，並進行景觀改善。本研究於 2021 年開始，於南勢溪共設置 4 個採樣站，每兩個月利用定積面水網進行水棲昆蟲之監測，以探討都市的湧泉型溪流中水棲昆蟲群聚組成，並對植生區棲地之採樣，以瞭解棲地營造對生物多樣性所產生之效益。

結果/結論/應用啟示

前半年研究結果顯示，污染排入與湧泉的稀釋，南勢溪水質自上游往下游呈現逐漸改善的趨勢。在調查河段共記錄水棲昆蟲 30 科 43 個分類群(taxa)，其中物種數及個體數皆以雙翅目為最高；各樣站間分類群豐度與多樣性自上游往下游呈現增加的趨勢。水質參數中以導電度與生物群聚參數具顯著相關($p < 0.001$)。比較不同棲地的調查結果，顯示植生區棲地較急流棲地有更高的分類群豐度，並額外貢獻達 30%水棲昆蟲生物多樣性。

關鍵詞（Keywords）：湧泉（spring）、南勢溪（Nan-Shih Stream）、水棲昆蟲（aquatic insects）、群聚動態（community dynamic）、生物多樣性（biodiversity）

OB_09

A study on Taiwanese Erotylinae (Coleoptera: Erotylidae) species richness reveals conflicts morphological and genetic data

Guan Jie Phang[1,2] and Jen-Pan Huang[2]
[1]National Taiwan University
[2]Academia Sinica
Presenting author's email: phangguanjie@gmail.com

背景/研究問題/材料方法

Estimating species richness is important for biodiversity research for providing baseline data for future ecological, evolutionary, and conservation studies. The cosmopolitan family Erotylidae (pleasing fungus beetles) is a family of beetles that have distinct color patterns among species, which exhibiting bright colors in combination with black to form various elytral patterns such as bands, spots, speckles, and stripes. According to Birkemoe et al. 2018 and our personal observation, the mycophagous subfamily, Erotylinae has host fungal preferences, most beetles feed on polypores while and some species feed on gill mushrooms. Different beetle species specialized in different fungal hosts. Different fungi may be correlated with different forest types and may be indicative to the health of the forests. An estimate of the diversity and the comparison of beetle species diversity between forests can help to make conservation plans. Erotylinae species diversity has been challenging to study. The variation of elytral patterns and few diagnostic characters made the delineation of species difficult for traditional taxonomic studies. Our limited understanding of the species richness of fungal beetle may conceal the cryptic diversity of species and may cause over-splitting. In addition to the conventional use of morphological traits, there are some new approaches such as DNA barcoding, molecular species delimitation, and integrative taxonomy. In this study, we applied molecular and morphological data to study the species diversity of Erotylinae in Taiwan.

結果/結論/應用啟示

We found that there is some cryptic species diversity in the Erotylinae of Taiwan. For example, there is a species group that has divergent mitochondrial lineages, where the nucleotide divergence exceeds the minimum interspecific genetic distance. We concluded that Erotylinae stands out as a candidate to clue that there are conflicts between morphology and molecular species studies.

關鍵詞（Keywords）：Erotylinae, Species diversity, Cryptic diversity, Over-splitting, Molecular species delimitation

OB_10

What makes a nasty pest? - Unveiling the intestinal microbial profile of coconut rhinoceros beetles (*Oryctes rhinoceros*) in Taiwan

韓喬融[1]，薛馬坦[1]
Chiao-Jung Han[1] and Matan Shelomi[1]
[1] 國立臺灣大學昆蟲學系 Dept. of Entomology, National Taiwan University, Taipei
Presenting author's email: f09632003@ntu.edu.tw

背景/研究問題/材料方法

Coconut rhinoceros beetle (CRB, *Oryctes rhinoceros*), a notorious pest on palm trees (Arecaceae), poses destructive threats to the countries highly rely on coconut and date palm as economic crops. Many Arecaceae farms worldwide still suffer from the threat of CRB. Therefore, effective and solid strategies for CRB control are needed urgently.

What makes CRB such a nasty pest? First, they are hard to kill due to their ecology. Second, they have a broad host range of over 30 genera of plants, suggesting they may have general detoxification mechanisms. Third, they can digest the hard plant tissues with cellulolytic and hemicellulolytic bacteria. Microbes may play critical role for CRB becoming a destructive pest, contributing abilities such as insecticide-detoxification and host plant resistance along with plant-cell-wall-degrading enzymes (PCWDEs). This study focuses on the nutritional-mutualistic relationship between CRB and its microbes. We aim to (1) isolate and identify the microbes from the intestines of CRB from 16 different locations in Taiwan; (2) test the PCWDE activity of the microbes, and (3) eliminate and replace the intestinal microbes and measure CRB fitness to test if these microbes are vital to CRB or not.

結果/結論/應用啟示

Our preliminary results found that the bacterial genera *Bacillus*, *Lysinibacillus,* and *Citrobacter*, and fungal genus *Candida* were frequently isolated from different individuals and locations. Some isolates among these genera show PCWDE activity. We also isolated bacteria from genera *Leminorella*, *Klebsiella*, and *Acinetobacter*, and found they express PCWDE activity as well. These results suggested that CRB harbors distinct microbes in the intestine likely helping it digest. However, whether CRB depends on these microbes for digestion, or whether they could survive without gut microbes, remains to be seen. That research is ongoing.

關鍵詞（Keywords）：椰子犀角金龜（*Oryctes rhinoceros*）、昆蟲與微生物共生（Insect-microbe symbiosis）、營養互利共生（Nutritional mutualism）、植物細胞壁分解酵素（Plant-cell-wall-degrading enzymes (PCWDEs)）、棕梠科（Arecaceae）

系統分類、族群遺傳、演化

論文宣讀

Oral Session: Systematics, Population Genetics and Evolution

OS_01

臺灣產蠟蟬科 (半翅目：蠟蟬總科) 分類學研究現況

Taxonomic study of the Family Fulgoridae (Hemiptera: Fulgoroidea) of Taiwan

林佑昇[1]，廖治榮[1]，柯俊成[1]，蕭旭峰[1]
You-Sheng Lin[1], Jhih-Rong Liao[1], Chun-Cheng Ko[1] and Shiuh-Feng Shiao[1]
[1]國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email:yslin063@gmail.com

背景/研究問題/材料方法

The taxonomic studies of the family Fulgoridae of Taiwan began at the Japanese colonial era. To date, 8 genera and 11 species have been recorded in Taiwan. However, due to the man-made development for decades, habitats were destructed, and many species become under threatened nowadays. Unfortunately, the species conservation has not been fully implemented owing to the lack of knowledge about the species diversity and their biology. Therefore, the basic research of the lanternfly of Taiwan is urgently needed. In the present study, some taxonomic issues about Taiwanese lanternfly species were discussed.

結果/結論/應用啟示

Detailed redescriptions of the endemic species *Saiva formosana* and the first description of its fifth-instar nymph were provided, including the body color polymorphism of the adults. Besides, the synonymy of two *Lycorma* species of Taiwan was proposed based on the evidence of their biology and the morphology of male genitalia. Furthermore, a new record species of the genus *Limois* from Taiwan was reported. The questionable records of some species in Taiwan were also discussed.

關鍵詞(Keywords)：蠟蟬科(Fulgoridae)、臺灣(Taiwan)、重新描述(Redescription)、同物異名（Synonym）、新紀錄種（New record species）

OS_02

一種出乎意料之外的荔枝細蛾新種在台灣的發現及其對荔枝與龍眼害蟲管理策略的意涵

Discovery of an unexpected new species of *Conopomorpha* (Gracillariidae) in Taiwan and its implications on pest management for lychee and longan orchards

顏聖紘[1]，王崇羽[1]，廖士睿[1]，賴柏羽[2]，劉耕樵[3]，許如君[3]
Shen-Horn Yen[1], Chung-Yu Wang[1], Shi-Rei Liao[1], Keng-Chiao Liu[2] and Ju-Chun Hsu[3]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
[2] 農業試驗所嘉義分所 Chiayi Agricultural Experiment Branch, Agricultural Research Institute, Council of Agriculture
[3] 國立台灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: shenhornyen@gmail.com

背景/研究問題/材料方法

The moths of the genus *Conopomorpha* are considered as the serious pests in lychee and longan orchards in Taiwan. Historically the species infesting lychee and longan in Taiwan were mis-identified as *C. cramerella* (Snellen, 1904) until Bradley's taxonomic revision, which confirmed that two species, namely *C. litchiella* and *C. sinensis*, occurred in Taiwan. Since then, scientists started to realize that the lychee and longan trees in Taiwan are infested by two *Conopomorpha* species although the phenology, host plant uses and identification in literature remain chaotic. In April of 2021, during a routine monitor of litchi fruit borer using pheromone lure of *C. cramerella*, a *Conopomorpha* species was found distinctive from all the known species based on male genitalia. We then obtained the COI sequence data and reconstructed the phylogeny by using all the available sequences of congeneric species plus a *Stomphastis* species as the outgroup from GenBank and BOLD Systems. The purpose is to determine if the morphologically distinctive sample represents an undescribed species.

結果/結論/應用啟示

According the phylogeny reconstructed in the present study, the Chiayi sample represents an unexpected new species which is closely related to *C. sinensis.* The larvae of the new species are supposed to be seed predator of longan, while its association and uses of lychee are yet to be confirmed. Since both lychee and longan are not native plants of Taiwan, and *Conopomorpha* has never been discovered in any indigenous Sapindaceae tree in Taiwan. We therefore suspect that the new species should have occurred in the surrounding regions and colonized Taiwan for a period of time. The addition of the new species has also increased the complexity of regional pest management in lychee and longan orchards.

關鍵詞（Keywords）：隱藏種（cryptic species）、性費洛蒙（sex pheromone）、入侵物種（invasive species）、物候（phenology）、種子取食者（seed predator）

OS_03

社會性蚜蟲短角綿蚜之生殖限制：胎生昆蟲兵蚜階級不孕之調控

Reproductive constraint in the social aphid *Ceratovacuna japonica*: sterility regulation in the soldier caste of a viviparous insect

鍾成侑[1]，重信秀治[1,2]
Chen-yo Chung[1] and Shuji Shigenobu[1,2]
[1] 日本基礎生物学研究所遺傳基因體學研究室 Laboratory of Evolutionary Genomics, National Institute for Basic Biology, Japan
[2] 総合研究大学院大学基礎生物學系 Department of Basic Biology, School of Life Science, SOKENDAI (The Graduate University for Advanced Studies), Japan
Presenting author's email: chungjaijay@yahoo.com.tw

背景/研究問題/材料方法

Sterile labor caste differentiation is a unique feature of eusocial insects. Apoptosis and mislocalized gene expression in oocytes play roles in constraining the reproductivity of bees, ants, and termites. However, the regulation of reproductive constraint in labor castes of primitively eusocial insects other than hymenopterans and blattodeans is almost unknown. Here, we employed a laboratory strain of the social aphid *Ceratovacuna japonica* for this investigation. We compared the gonads of soldiers and reproductives.

結果/結論/應用啟示

Interestingly, a pair of ovaries was found in the sterile soldier. The soldier ovary presents two types of ovariole: the ovariole with germarium only and the ovariole with germarium plus few embryos. Our cell observations indicate that the soldier ovary applies two strategies to restrict its reproductivity. In addition, germline genes are ubiquitously expressed in the embryo of the soldier ovary, which is in contrast to the germline specific pattern detected in the reproductive ovary. This indicates that the embryo of the soldier ovary does not develop normally. Moreover, the abnormal posterior axis in the embryo within the soldier ovary was observed. This is the first report concerning the reproductive constraint of viviparous social insects at the molecular level. Our findings suggest a different mode of sterility regulation in the social aphid than in other social insect models and shed light on the insect origin of reproductive constraint.

關鍵詞（Keywords）：蚜蟲（Aphids）、生殖細胞（Germ cells）、生殖限制（Reproductive constraint）、社會昆蟲（Social insects）

OS_04

台灣家白蟻與格斯特家白蟻的種間隔離

Species barrier between Formosan and Asian subterranean termites

陳冠豫[1]，黃詩穎[1]，靖永皓[2]，李後鋒[1]
Guan-Yu Chen[1], Shih-Ying Huang[1], Yung-Hao Ching[2] and Hou-Feng Li[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
[2] 慈濟大學人類暨遺傳學系 Department of Molecular Biology and Human Genetics, Tzu Chi University
Presenting author's email: marco92245@gmail.com

背景/研究問題/材料方法

The two most devastated invasive termite pests, *Coptotermes formosanus* Shiraki and *C. gestroi* (Wasmann), were found having conservative mating behavior, identical mating pheromones, overlapped mating seasons, and overlapped geographical distributions. Recently their natural hybrids were discovered in Taiwan. *C. gestroi* have invaded into Taiwan, expensing their colonization, and encountered with *C. formosanus* for more than one hundred years. However, low discover rate of hybrids of the two *Coptotermes* species were reported by Huang (2020) (7.3%) and even lower in the NCHU Termite Database (0.15%). We hypothesized an undocumented high level of prezygotic or postzygotic barrier presents between *C. formosanus* and *C. gestroi*. A three-year monitoring on the dispersal flight season of the two *Coptotermes* species and their hybrids were conducted to test the level of temporal barrier of the hybrids. In addition, different rearing combinations between hybrids and parental species were paired to examine the viability and fertility of the hybrids.

結果/結論/應用啟示

We documented that the alates of *C. formosanus* and *C. gestroi* encounter annually, and among 15 times of hybrid swarming events, 13 times were concurrent with either or both parental species. The temporal barrier was weak to prevent the genetic flow between the two species. Hetero-species colonies reared in the lab produced viable F1 workers and soldier, in the field, dispersing hybrid alates were observed. However, we found the hybrid females scarcely produce any eggs, and these eggs were inviable. Finally, we integrate all the evidences from previous and current studies to discuss the possible outcome of the hybridization between *C. formosanus* and *C. gestroi*.

關鍵詞（Keywords）：*Coptotermes gestroi*, *Coptotermes formosanus*, dispersal flight, hybridization, hybrid breakdown

OS_05

台灣產新白蟻屬的分類學研究
Taxonomy of *Neotermes* (Blattodea: Kalotermitidae) in Taiwan

吳佳倩[1]，蔡經甫[2]，李後鋒[1]
Chia-Chien Wu[1], Jing-Fu Tsai[2] and Hou-Feng Li[1]
[1] 國立中興大學昆蟲學系 National Chung Hsing University, Department of Entomology
[2] 國立自然科學博物館生物學組 Department of Biology, National Museum of Natural Science
Presenting author's email: daisy100406@gmail.com

背景/研究問題/材料方法

新白蟻屬 (*Neotermes*) 是蜚蠊目 (Blattodea) 木白蟻科 (Kalotermitidae) 中物種數量第二多的屬，一共包含 117 種，廣泛分布在熱帶、亞熱帶還有溫帶地區。台灣及日本琉球群島過往紀錄的新白蟻屬僅有一個物種，恆春新白蟻 *N. koshunensis* (Shiraki)。2019 年 Yashiro 等人在日本琉球群島發現一個新種新白蟻：杉尾新白蟻 *N. sugioi* Yashiro et al.，同時確認琉球群島的新白蟻皆為杉尾新白蟻，並非恆春新白蟻。為釐清台灣產新白蟻物種的身份問題，本研究一共檢視 299 筆來自台灣各地的新白蟻屬標本，結合形態及分子特徵 (mtDNA COI、16S rDNA、ITS2) 探討台灣的新白蟻屬物種多樣性。

結果/結論/應用啟示

結合形態與分子結果，台灣的新白蟻屬可分為三群，包含已記錄的恆春新白蟻以及兩個未記錄的新白蟻屬物種。在與新白蟻屬現存物種進行形態與基因序列比對後，確認台灣有三種新白蟻：恆春新白蟻、杉尾新白蟻、和一個新種。三種新白蟻體色及體型大小相似，可從有翅生殖型翅的顏色以及兵蟻的大顎和後頦 (postmentum) 進行區分。分布在台灣本島的有恆春新白蟻及杉尾新白蟻兩個物種，蘭嶼僅有杉尾新白蟻，綠島僅存在未紀錄的新種。本研究更新台灣的新白蟻屬物種紀錄，並提供三個新白蟻屬物種的檢索特徵、自然史以及分布資訊。

關鍵詞（Keywords）：新紀錄種（New record species）、新種（New species）、隱蔽種（Cryptic species）、檢索表（Identification key）、地理分布（Geographic distribution）

OS_06

探討長毛跗蠕屬 (*Sennertia*) 蜂蠕種群於木蜂體上之分布

Exploratory on *Sennertia* bee mites (Sarcoptiformes: Chaetodactylidae) phoretic on *Xylocopa* bees (Hymenoptera: Apidae)

趙家慧[1]，陸聲山[2]，宋一鑫[1]
Chia-Hui Chao[1], Sheng-Shan Lu[2] and I-Hsin Sung[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
[2] 行政院農業委員會林業試驗所福山研究中心 Fushan Research Center, Taiwan Forestry Research Institute
Presenting author's email: w9413331@gmail.com

背景/研究問題/材料方法

長毛跗蠕屬 (*Sennertia*) 是蜜蜂亞科木蜂屬 (Apinae: *Xylocopa*) 昆蟲中極為常見的攜播 (phoresy) 蜂蠕 (bee mite)，分類地位為疥蠕目 (Sarcoptiformes) 無氣門亞目 (Astigmata) 毛趾蠕科 (Chaetodactylidae)。該屬蜂蠕與木蜂有密切的寄生關係，兩者間有協同收斂演化 (codivergence)的現象；牠們對於寄主之危害雖並未被直接證實，但對於擴散能力強、具入侵風險的木蜂，其攜帶之蜂蠕有轉移寄主的可能性，因而具有重要的研究價值。本研究著重在東方區常見的長毛跗蠕屬 *Sennertia* 亞屬之 3 個種群 *cerambycina*-、*japonica*-、*horrida*-groups，以 *si* 剛毛及第 4 對足跗節剛毛做為區別。總計從黃胸木蜂 (*X. appendiculata*)、藍翅木蜂 (*X. auripennis*)、白領帶木蜂(*X. collaris sauteri*)、灰胸木蜂 (*X. phalothorax*)、紅胸木蜂 (*X. ruficeps*)、銅翼背木蜂 (*X. tranquebarorum*) 等 6 種木蜂身上採樣並鏡檢 51 隻蜂蠕，將其製成標本以利形態鑑定，並記錄蜂蠕攜播於蜂體之部位。DNA 之 COI 序列使用 *Sennertia* 專一性引子對增幅取得。

結果/結論/應用啟示

長毛跗蠕屬於 6 種木蜂總檢出率達 52.9%，並鑑定 6 種形態種，其中 *cerambycina*-、*japonica*-、*horrida*- 各有 2 種。*japonica*-group 可同時於單隻木蜂體表採集，具有複合攜播的情形。蜂蠕攜播部位比例以木蜂之翅基部佔 56%、後胸背板 32%、並胸腹節 (propodeum) 40% 及蠕室 (acarinaria) 佔 32%。已獲得之* DNA 序列經建構親緣樹支持種群間的分類，與形態鑑定之種群分類結果相符，但 *japonica*-group 種群內序列極度近似，*S. alfkeni* 與 *S. japonica* 種間序列無明顯分支，因此仍有賴分子鑑定、形態特徵與寄主等多方資訊參照，以協助種級分類。

關鍵詞（Keywords）：攜播（phoresy）、蜂蠕（bee mites）、木蜂（*Xylocopa*）、長毛跗蠕屬（*Sennertia*）

OS_07

臺灣產擬瘦姬蜂屬 (膜翅目：姬蜂科：柄卵姬蜂亞科)之分類學回顧

A taxonomic review of *Netelia* species (Hymenoptera: Ichneumonidae: Tryphoninae) of Taiwan

陳玄樸[1]，蕭旭峰[1]
Hsuan-Pu Chen[1] and Shiuh-Feng Shiao[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: pooh890510@gmail.com

背景/研究問題/材料方法

Netelia Gray, 1860 is a nocturnal koinobiont ectoparasitoid wasp genus of high species richness with over 320 described species. Larvae of *Netelia* using nocturnal lepidopterans (mostly the species of Geometridae, Noctuidae and Notodontidae) as hosts, attaching on their body surface and consuming the caterpillars until they died. Most species in this genus are closely similar in external morphology, causing several misidentifications and confusions in the past. Until 1938, it was found that *Netelia* species can be well distinguished by specialized structure on parameres of male genitalia and the taxonomic system of this genus was then better established. Including downgrade of some morphologically similar genera, *Netelia* is now subdivided into 12 subgenera based on characters of male genitalia and external morphologies. Currently, twenty *Netelia* species in 8 subgenera have been recorded in Taiwan. However, clear identification of Taiwanese species is still pending. In this study, we review the taxonomy of Taiwanese *Netelia*, specimens examined were mainly collected by light trap and borrowed from NMNS and TARI.

結果/結論/應用啟示

Two subgenera, *Paropheltes* Cameron, 1907 and *Monomacrodon* Cushman, 1934 are newly recorded from Taiwan, including *Netelia* (*M.*) *bicolor* (Cushman,1934) and 2 unidentified *Paropheltes* species. In other Taiwanese subgenera, at least 5 new records are found, including *N.* (*Amebachia*) *vicinalis* Konishi, 2010, *N.* (*Apatagium*) *longicauda* Konishi, 1986, *N.* (*Parabates*) *nigricarpus* (Thomson, 1888), *N.* (*Prosthodocis*) *hikosana* Konishi 1991, *N.* (*Netelia*) *rapida* Tolkanitz, 1981 and some unidentified species. Morphological comparison of these species as well as their diagnostic photography are provided for identification. Taxonomic status of some previously recorded species is also discussed.

關鍵詞（Keywords）：擬瘦姬蜂屬（*Netelia*）、新紀錄種（New record species）、臺灣（Taiwan）、分類學（Taxonomy）

OS_08

台灣產背寡毛實蠅屬形態與分類學研究

Morphological and taxonomic study of genus *Bactrocera* (Diptera: Tephritidae) in Taiwan

黃千育[1]，蕭旭峰[1]
Chien-Yu Huang[1] and Shiuh-Feng Shiao[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: R09632011@ntu.edu.tw

背景/研究問題/材料方法

The majority of true fruit flies, family Tephritidae, develop in plant tissue during their larval stage. Species that are borers or miners of commercial crops can cause severe damage to the agricultural industries. The genus *Bactrocera* is considered as one of the most economically significant fruit fly genus. *Bactrocera* species generally shared similar appearances, while color patterns being the major characters used for species identification. In light of the economic importance of *Bactrocera* species, a study on the morphology and taxonomy of *Bactrocera* species occurring in Taiwan is of great importance. The aim of this research is to provide a morphological and taxonomic reference for the species of *Bactrocera* occurring in Taiwan.

結果/結論/應用啟示

Redescription and diagnosis of the species of *Bactrocera* Macquart, 1835 (Diptera: Tephritidae: Dacinae: Dacini) occurring in Taiwan is presented, including 12 previously reported and one newly recorded species, the latter being *B. abbreviata* (Hardy, 1974). Basic information for each species, including diagnostic characters, taxonomic status, global distribution, attractants and host records is provided.

關鍵詞(Keywords)：果實蠅科(Tephritidae)、形態學(morphology)、分類學(taxonomy)、台灣（Taiwan）

OS_09

臺灣產白斑翅野螟(鱗翅目：草螟科，斑野螟亞科)的分類檢討

A taxonomic revision of the genus *Bocchoris* Moore, 1885 (Lepidoptera: Crambidae, Spilomeinae) of Taiwan

蔡岳承[1]，王崇羽[1]，顏聖紘[1]
Yue-Cheng Tsai[1], Chung-Yu Wang[1] and Shen-Horn Yen[1]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: voyagueyct@gmail.com

背景/研究問題/材料方法

The genus *Bocchoris* was originally erected by Frederic Moore in 1885 for *Botys inspersalis* Zeller, 1852, of which the type locality is South Africa. The genus was monotypic until George Hampson extended the generic concept by recruiting 38 more species in 1898. Up to date, more than 70 species have been included in *Bocchoris* and thus the genus has become cosmopolitan in distribution. Despite of its wide distribution, the monophyly of the genus, however, has never been questioned or examined using modern methods. In order to define the generic boundary of the genus, we attempt to investigate the morphological diversity and species delimitation of the *inspersalis* species-group based on the material obtained in Taiwan.

結果/結論/應用啟示

Having examined the genitalic and wing pattern characters of the specimens deposited in various insect collections, we have come to the conclusion that *Bocchoris inspersalis* has a very wide distribution from Africa to Japan, and the species is widely distributed in the lowland of Taiwan. *Bocchoris trimaculalis* (Snellen, 1880), previously only known from Indonesia, is newly reported from Lanyu and Hengchun peninsula. A third species, which is either *Bocchoris quaternalis* (Lederer, 1863) or a new species, is found sympatric with *inspersalis*. The present study reveals that, except for *Bocchoris albipunctalis* Shibuya, 1929, which is confined to Ogasawara, other species of the genus have much wider distribution than previously thought and the regional diversity of the genus was underestimated.

關鍵詞（Keywords）：雄性生殖器（male genitalia）、翅紋（wing pattern）、日行性（diurnality）、草螟科（Crambidae）、多系群（polyphyletic group）

行為、生理、個體生物學

論文宣讀

Oral Session: Ethology, Physiology and Organismic Biology

OE_01

尼泊爾埋葬蟲(*Nicrophorus nepalensis* Hope)(Coleoptera: Silphidae)之幼蟲回巢定位

Larva homing positioning of Burying beetle *Nicrophorus nepalensis* Hope(Coleoptera: Silphidae)

永政澤[1]，黃文伯[1]
Zheng-tsu Yung[1] and Wenbe Hwang[1]
[1] 國立台南大學生態暨環境資源學系 National University of Tainan, Department of Ecology and environmental resource
Presenting author's email: harry2000750309@gmail.com

背景/研究問題/材料方法

社會性昆蟲可藉由化學定位協助個體歸巢與覓食，大多數主要的研究對象為螞蟻和蜜蜂。尼泊爾埋葬蟲隸屬於社會性階層裡的亞社會性昆蟲，但定位研究甚少。埋葬蟲以屍體作為繁殖資源。當雌蟲在野外發現屍體時，會將其加工並從腹部分泌物質塗抹於屍體上，以防止腐敗，接著在窩的附近產卵。待卵孵化後，幼蟲可不失方向爬入窩內。故本研究目的為確認尼泊爾埋葬蟲幼蟲是否能透過雌蟲腹部分泌物，以辨識窩的位置。共三組實驗。實驗一、幼蟲分別在沾有親代與非親代分泌物的白紙上移動，使用 Wilcoxon Rank Sum Test 比較幼蟲在兩種味道下的最長移動距離。實驗二、於封閉 Y 型通道口一側分別放置雞肉、屍球或雌蟲腹部分泌物，而另一側不放東西，幼蟲由 Y 型通道單口側出發。利用 Kruskal-Wallis H test 比較幼蟲選擇目標氣味的比例。實驗三、使用 Friedman test 測試幼蟲在同時面對雞肉、屍球與雌蟲腹部分泌物三種味道下，其偏好是否有差異。

結果/結論/應用啟示

研究結果顯示，實驗一、幼蟲在親代分泌線上的移動距離為 6.69 ± 5.18 cm (n = 39); 非親代為 5.77 ± 5.45 (n = 39)，兩者無顯著差異(p = 0.21)。實驗二、幼蟲於 Y 型通道中的氣味選擇比例為屍球: 76 % (n =12); 新雞肉:27 % (n = 12); 雌蟲分泌物:65 % (n = 12)。實驗三、幼蟲的氣味偏好比例為屍球 43 % (n = 9); 新雞肉偏好: 10%(n = 9) ; 雌蟲分泌物: 45%(n = 9)。綜合上述結果，幼蟲雖然無法辨別親代與非親代的氣味，但可透過雌蟲分泌物來得知屍球位置。說明分泌物對幼蟲回巢而言，扮演重要的定位媒介。

關鍵詞（Keywords）：社會性昆蟲（social insects）、埋葬蟲（burying beetle）、化學定位（chemical locating）、幼蟲（larva）

OE_02

稻穀倉庫主要害蟲穀蠹對第滅寧抗藥性之探討
Deltamethrin resistance in major pest *Rhyzopertha dominica* in paddy rice warehouse

姚美吉[1]，李啟陽[1]，王泰權[1]，馮文斌[1]
Me-Chi Yao[1], Chi-Yang Lee[1], Tai-Chuan Wang[1] and Wen-Bin Feng[1]
[1] 行政院農業委員會農業試驗所應用動物組 Applied Zoology Division, Agricultural Research Institute, Council of Agriculture, Taichung City, Taiwan
Presenting author's email: yaomc@tari.gov.tw

背景/研究問題/材料方法

稻米是國人最主要糧食，在 2019 年稻作栽培面積計約 27 萬公頃，稻穀生產總量約 143 萬公噸，產值 399 億元，是所有農作物之首。政府為穩定國內稻米供需，會主動收購農民稻穀儲藏於農會或碾米廠之稻穀倉中，少則半年，長則兩年以上，每年累積貯藏稻穀量超過 50 萬公噸。由於台灣在地理環境及氣候等因素，極適合積穀害蟲的繁衍，貯藏期間因其危害，導致稻穀在貯藏期間損失約 2%，粗估每年損失為 2.8 億元以上。以往都偏重化學防治，主要使用 0.055% 第滅寧粉劑 (Deltamethrin) 與稻穀均勻混拌進行防治。但自從第滅寧粉劑推薦運用於稻穀至今已達 19 年，積穀害蟲對第滅寧極有可能已經產生抗藥性。本試驗從各地公糧稻穀倉庫採集其主要害蟲穀蠹 (*Rhyzopertha dominica*)，帶回飼養至 F2，隨後以稻穀與藥劑混拌處理進行抗藥性測試，此法較接近穀倉實際施藥狀況，得出各地品系之 LC50，並和感性品系比較得出抗藥性倍率 (Resistance ratio)，隨後測試高第滅寧抗藥性品系對其他藥劑的感受性測試，了解以其他藥劑替代第滅寧的可能性。

結果/結論/應用啟示

穀蠹共測試 44 個品系，發現確實有些品系已發展出極高第滅寧抗藥性，最高抗藥性倍率達 230 倍，隨後將第滅寧抗藥性 60~230 倍之品系進行其他藥劑感受性測試，發現高第滅寧抗性品系尚未發展對陶斯松 (Chlorpyrifos) 之交互抗藥性。未來將會測試其他不同機制殺蟲劑之抗藥性程度，篩選出能夠用於稻穀倉庫防治積穀害蟲之替代藥劑。為使化學防治能達到最佳防治成效，建議管倉人員使用本所研發之綜合防治技術，包含清除害蟲污染源、燈光誘殺、防蟲網隔絕等技術，將能降低農藥使用量，並延遲害蟲抗藥性發展速度，以減緩藥劑替代週期。

關鍵詞(Keywords)：稻穀倉庫(Paddy rice warehouse)、抗藥性(Insecticide resistance)、穀蠹（*Rhyzopertha dominica*）、第滅寧（Deltamethrin）、陶斯松（Chlorpyrifos）

OE_03

進口糙米倉庫主要積穀害蟲對磷化氫抗藥性之探討

Phosphine resistance in major pests of stored-product insect in imported brown rice warehouse

姚美吉[1]，李啟陽[1]，王泰權[1]，馮文斌[1]
Me-Chi Yao[1], Chi-Yang Lee[1], Tai-Chuan Wang[1] and Wen-Bin Feng[1]
[1]行政院農業委員會農業試驗所應用動物組 Applied Zoology Division, Agricultural Research Institute, Council of Agriculture, Taichung City, Taiwan
Presenting author's email: a82851725@gmail.com

背景/研究問題/材料方法

2002 年我國加入世界貿易組織 (World Trade Organization, WTO) 後，每年約從國外進口全年民生用量 8%之脫殼稻米，其中約 65%儲藏於政府所屬穀倉，儲藏時間短則半年，長則超過二年。由於台灣在地理環境及氣候等因素，極適合積穀害蟲的繁衍，儲藏期間經常受到積穀害蟲危害造成損失。目前儲藏期間之積穀害蟲當嚴重為害後，主要使用 57 % 磷化鋁 (Aluminum Phosphide) 產生磷化氫 (Phosphine) 進行燻蒸殺蟲，但是近年發現倉庫燻蒸次數及燻蒸失敗率有上升的趨勢，積穀害蟲可能已經產生磷化氫抗藥性。本試驗從各地進口米倉庫收集其主要害蟲米象 (*Sitophilus oryzae*) 及玉米象 (*Sitophilus zeamais*)，帶回飼養至 F2，隨後利用氣密注射器將磷化氫打入乾燥器中進行燻蒸，得出各地品系之 LC50，並和感性品系比較得出抗藥性倍率 (Resistance ratio)。

結果/結論/應用啟示

米象共測試 16 個品系，發現溪湖、花壇、二水及後壁之米象品系確實發展一定程度磷化氫，抗藥性倍率達 15~50 倍，另外自以磷化鋁燻蒸後之存活蟲體，經繁殖後測試發現並未產生磷化氫抗藥性，可能原因為倉型造成燻蒸效果不佳；玉米象共測試 11 個品系，發現只有台南地區之玉米象品系發展出對磷化氫抗藥性，抗藥性倍率僅 6 倍。目前以燻蒸方式殺蟲，尚未有其他藥劑之殺蟲成效足以替代磷化氫。為解決進口米倉庫因抗藥性發展造成之燻蒸殺蟲效果下降問題，未來除開發新類型燻蒸劑外，亦將嘗試在磷化氫額外添加氧氣、二氧化碳、氮氣等氣體進行燻蒸，提升磷化氫對具抗藥性米象品系之殺蟲效果。並建議各管倉人員提高倉庫通風性、善用非農藥防治資材，以延緩害蟲對磷化氫抗藥性之發展速度。

關鍵詞（Keywords）：磷化氫（Phosphine）、燻蒸（Fumigation）、抗藥性（Insecticide resistance）、米象（*Sitophilus oryzae*）、玉米象（*Sitophilus zeamais*）

OE_04

Biological control of *Forcipomyia taiwana* Shiraki by entomopathogenic fungi

Nian-tong Ni[1], Chuen-Fu Lin[2] and Yu-Shin Nai[1]
[1]Department of Entomology, National Chung Hsing University
[2]Department of Veterinary Medicine, College of Veterinary Medicine, National Pingtung University of Science &Technology
Presenting author's email: ap994039@gmail.com

背景/研究問題/材料方法

Forcipomyia taiwana (Diptera: Ceratopogonidae), also known as little black biting midge (LBBM), is a nuisance blood-sucking pest to human in Taiwan. The LBBM causes itch, swollen to people. During the larval rearing of LBBM, a symptom of mycosis was found in the larvae and pupae. Therefore, the fungi from diseased LBBM were isolated at first, and 6 fungal isolates were cultured and the activity for insect-killing, molecular identification, thermos-tolerance and conidia productivity assay were further determined. In this study, two fungal isolates which belong to *Purpureocillium lilacinum* (NCHU-NPUST 175) and *Fusarium verticillioides* (NCHU-NPUST 178) that has more stronger mortality on the mealworm and 4th instar larvae of LBBM were selected to virulence test against different life stages of LBBM larvae.

結果/結論/應用啟示

NCHU-NPUST 175 and NCHU-NPUST 178 showed 100% mortality to mealworm and supposed to have insect-killing activity, and the two fungal isolates showed the significant virulence to the last stage larvae of LBBM (5×10^7 to 5×10^5 conidia/mL inoculation, $P<0.05$). Bioassay on different life stages of LBBM with different concentrations of NCHU-NPUST 175 caused the highest mortality (38%) on 4th instar larvae at 5×10^7 conidia/mL and also revealed the ovicidal effects on the eggs (hatching rate= 26%) at 10^8 conidia/mL, and NCHU-NPUST 178 caused the highest mortality (46%) on last stage larvae at 5×10^7 conidia/mL and also showed the ovicidal effects (hatching rate= 23%) at 10^8 conidia/mL. In conclusion, NCHU-NPUST 175 and NCHU-NPUST 178 revealed a LBBM-larval-killing and ovicidal activities on LBBM. The two fungal isolates could be the potential candidates for the LBBM integrated controlling strategy.

關鍵詞（Keywords）：*Forcipomyia taiwana*, little black biting midge (LBBM), *Purpureocillium*, *Fusarium*

OE_05

大蠟蛾對 *Fusarium solani* 及 *F. rubicola* 病原菌之致病影響觀察
Pathogenic effect of *Fusarium solani* and *F. rubicola* on greater wax moth (*Galleria mellonella*)

余品臻[1]，傅于珊[1]，黃健瑞[1]，宋一鑫[1]
Pin-Chen Yu[1], Yu-Shan Fu[1], Chien-Jui Huang[1] and I-Hsin Sung[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: jennifer880506@gmail.com

背景/研究問題/材料方法

大蠟蛾 (*Galleria mellonella*) 因易於飼養及操作，有被應用於病原微生物的模式生物 (mode) 研究。本研究擬為大蠟蛾幼蟲注射鐮孢菌 *Fusarium* 植物病原真菌，分析對大蠟蛾之毒力。蟲源採自西洋蜜蜂 (*Apis mellifera*) 巢片，經定序鑑定為大蠟蛾，餵以人工飼料，於 32℃、30-50% RH 之全暗環控生長箱內行繼代飼養。純化 *Fusarium* 菌種 *Fusarium solani* species complex, FSSC 之 *F. solani* 及 *F. rubicola* 菌株各二隻，注射接種濃度為 1×10^3、1×10^5、1×10^7 spores/mL 的孢子懸浮液，注射於 1.5- 2.0 cm 幼蟲的 3th 足及 4rd 腹足，接種後 24 及 48 小時進行存活觀察，以存活分析 (Survival Analysis) 之 Kaplan-Meier 存活曲線 (Kaplan-Meier survival curves) 與 Cox 比例危險迴歸 (Cox proportional hazards model, cox regression) 四種菌株之幼蟲的存活率分析並檢定。

結果/結論/應用啟示

注射鐮孢菌 *F. solani* FS-A, FS-B 兩隻菌株及 *F. rubicola* FR-A, FR-B 兩隻菌株皆對大蠟蛾有致病力，注射位置及注射濃度皆有顯著影響 ($p < 0.05$)。其中各菌株配置 1×10^7 spores/mL 濃度注射於 3th 足，對存活產生具體影響，造成幼蟲蟲體僵直黑化。FS-A 與 FS-B 對幼蟲致死有顯著差異，而 FR-A 與 FR-B 則不顯著；其中 FS-A 對幼蟲於 24 小時即有 100% 死亡率，但 FS-B、FR-A 及 FR-B 對幼蟲於 24－48 小時呈 72%－96% 之死亡率。以大蠟蛾建立 *Fusarium* 致病力的應用，可在短時間內觀察結果，將致病力實驗從植物體轉移至模式昆蟲，對於芋頭等種植時期長之作物或欲節省栽種空間之目的，具可行性。

關鍵詞（Keywords）：大蠟蛾（*Galleria mellonella*）、芋軟腐真菌（*Fusarium*）、植物病原真菌（Phytopathogenic fungi）、致病力（pathogenesis）

OE_06

Analysis of germline development under heat stress in the asexual viviparous pea aphid

Mu-tzu Tsai[1] and Chun-che Chang[1]
[1]Department of Entomology, National Taiwan University
Presenting author's email: o860108pp@gmail.com

背景/研究問題/材料方法

Temperature is a key parameter for a physiological condition being composed of many biochemical reactions operating within an animal. In the fruit fly *Drosophila melanogaster*, for example, heat stress reduces the activity of sperms in males and decreases the proliferation of eggs in females. However, how heat stress regulates germline development within developing embryos is little known in *Drosophila* and other insects. In the ovaries of asexual pea aphid *Acyrthosiphon pisum*, consecutive embryogenesis occurs within a single ovariole. This allows us to observe how germline development, which is labeled by an antisense riboprobe of *Apvas1*, a known germline marker in the pea aphid, is regulated at various high temperatures.

結果/結論/應用啟示

According to Lu and Kuo (2008), *A. pisum* cannot produce offspring at 30°C and 35°C, indicating that reproduction is suppressed. However, our data show the pea aphid at 30°C can still produce offspring with a better supply of nutrients from the host plants. We found that ovariole numbers in adults remained 7 in an ovary of the pea aphid at 20°C and 30°C. However, the number of egg chambers reduced to 5 per ovariole at 30°C compared to 7 at 20°C. Moreover, whole-mount *in situ* hybridization showed that the intensity of the germline marker gene *Apvas1* reduced in the mid embryogenesis at 30°C. Taken together, it implies that heat stress leads to a reduction of both egg-chamber numbers and expression levels of *Apvas1*.

關鍵詞（Keywords）：*Acyrthosiphon pisum*, germ cell, heat stress, embryogenesis, oogenesis

OE_07

以 micro-CT 技術探討蜜蜂工蜂大腦的結構
Study of anatomical of honey bee worker's brain by micro-CT

扶尚睿[1]，楊恩誠[1]
Shang Jui Fu[1] and En Cheng Yang[1]
[1] 臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: ray810730@gmail.com

背景/研究問題/材料方法

蜜蜂是真社會性昆蟲，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的現象 (age polyethism)，意即工蜂成蟲在不同日齡階段會表現不一樣的行為。例如，年輕的工蜂會作為內勤峰在巢內工作，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需要解決的問題非常不同，表示工蜂大腦在不同日齡階段功能性亦不相同，因此推論蜜蜂工蜂的大腦在其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型態連續性變化則尚未探討。因此本研究首先將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照影。奈米斷層掃描透過 X 光照影，能在不破壞外骨骼的狀況下呈現蜜蜂腦的立體結構，免去解剖時影響腦部型態的風險，同時階析度最高可以達到 400 奈米，達到在不侵入的情況下精準呈現腦部各區域型態並計算體積的目標。

結果/結論/應用啟示

蜜蜂腦使用碘液以及磷鎢酸染色，經奈米斷層掃描後，影像顯示磷鎢酸染色對於各腦區間有更好的對比度，腦區如視葉(包含 lamina, medulla, lobula)、嗅葉、蕈狀體以及中心複合體階能區分。目前正嘗試以程式抓取各腦區範圍並計算體積，以便未來比較不同日齡的蜜蜂腦部結構變化。

關鍵詞（Keywords）：蜜蜂（honey bee）、大腦（brain）、日齡多型性（age polyethism）

OE_08

優化以氣相色譜質譜儀分析西洋蜂青春激素之方法

Optimizing the GC-MS protocol for juvenile hormone analysis of *Apis mellifera* L.

陳琬鎰[1]，楊恩誠[1]
Wan-Yi Chen[1] and En-Cheng Yang[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: julie951713@gmail.com

背景/研究問題/材料方法

西洋蜂為真社會性昆蟲，工蜂之日齡分工機制受諸多因子所調控。前人研究指出工蜂勤務由內勤轉換為外勤的過程中，必會伴隨青春激素含量急遽上升之現象，而以外力促使內勤蜂體內青春激素含量增加，則會誘使其提早成為外勤蜂。工蜂體內之青春激素含量為影響其內外勤務轉換之關鍵因子，然而至今尚未有研究監測工蜂完整生命週期之青春激素含量變化，及探討青春激素對工蜂巢內勤務轉換之影響。為檢測各日齡工蜂體內青春激素含量變化，本研究參照前人已發表文獻之純化程序進行測定，卻發現現有之程序難以有效地將目標化合物進行純化。因此，重新建立以氣相色譜質譜儀分析西洋蜂體內青春激素含量之最佳樣品純化流程為本研究之首要目標。

結果/結論/應用啟示

本研究現已建立優化之樣品純化程序，除了能更有效率地完成樣品純化外，以標準品或蜜蜂血淋巴樣品進行實測之結果，皆確認優化之純化程序能將九成以上之目標化合物完整保留於樣品中，同時還能分離樣品之背景雜訊，可避免雜訊影響數據判讀；並提供更簡易、快速且高回收率之樣品純化程序。此優化程序將應用於建立首個精確且完善之工蜂生命週期中生理數據變化資訊，並有助於釐清青春激素是否會影響工蜂的巢內勤務轉換。

關鍵詞（Keywords）：青春激素（juvenile hormone）、氣相色譜質譜儀（gas chromatography-mass spectrometry）、日齡多型性（age polyethism）、西洋蜂（*Apis mellifera*）

OE_09

氣候變遷對熊蜂震動授粉 (buzz pollination) 的影響
Effect of climate change on buzz pollination

郭耘[1]，吳岳隆[1]
Yun Kuo[1] and Yueh Lung Wu[1]
[1] 國立台灣大學昆蟲學系 National Taiwan University
Presenting author's email: b07612044@ntu.edu.tw

背景/研究問題/材料方法

因為現今人類活動頻繁，氣候變遷日益嚴重，全球平均溫度不斷上升，對自然環境以及生物造成影響。而大部分的作物都需要靠昆蟲授粉，才能孕育下一代。熊蜂為一種特殊的授粉昆蟲。其授粉方式為震動其翅膀，使花粉震出。因有些作物的花藥型態，必須依靠這種授粉方式，才能完成授粉。目前台灣的溫室番茄，已經有部分使用精選熊蜂作為授粉，提高番茄的品質。若溫度持續上升，高溫可能會影響熊蜂在溫室的授粉效率。為了了解高溫對熊蜂造成的生理或授粉行為的影響，我們從死亡率、取食量、振翅頻率及利用 qPCR 檢測糖類代謝及抵抗熱逆境的相關基因等，來了解熊蜂在高溫下生理及行為的變化。

結果/結論/應用啟示

結果顯示，受 35°C 處理的熊蜂死亡率高。雖然受 32°C 處理的熊蜂幾乎沒有死亡，不過其取食糖水的量明顯較少，並且糖代謝的路徑會走向無氧呼吸，以及形成許多抵抗熱逆境的蛋白質，如熱休克蛋白等。因能量轉移至抵抗熱逆境，所以飛翔肌的糖解作用與三羧酸循環的表現量有下降的趨勢，且受熱處理的熊蜂活動力較差。本研究從熊蜂生理及行為在高溫的變化，證明在高溫下，熊蜂的振翅頻率下降，最終使授粉效率降低。因此，如果未來溫度持續上升，勢必對熊蜂授粉產生不良影響，影響溫室授粉作物的產量。

關鍵詞（Keywords）：精選熊蜂（*Bombus eximius*）、熱休克（Heat shock）、氣候變遷（Climate change）、震動授粉（Buzz pollination）

OE_10

溫度影響紋白蝶翅黑化面積

Temperature affects the wing pattern on *Pieris rapae* (Lepidoptera: Pieridae)

陳柏凱[1]，朱清麟[1]，賴慶庭[1]，吳立心[1]
Po-Kai Chen[1], Ching-Lin Chu[1], Ching-Ting Lai[1] and Li-Hsin Wu[1]
[1] 國立屏東科技大學植物醫學系 National Pingtung University of Science and Technology Department of Plant Medicine
Presenting author's email: crowds1999@gmail.com

背景/研究問題/材料方法

棲息於不同季節的同種蝴蝶，翅的顏色會有些微差異。以紋白蝶 (*Pieris rapae*) 為例，於寒冷時生長的個體，前翅內緣的黑斑會相對佔有較大面積，而翅外緣的黑斑則會較不明顯；本試驗利用極端高/低溫度飼養 *P. rapae*，欲探討其翅黑斑相對面積、顏色改變及可能牽涉到的功能與適應。從高溫 30℃ 至低溫 10℃間，每隔 5℃一處理，共設置 5 處理；並在其餘條件相同狀況下，飼養 *P. rapae* 從卵期至成蟲並量化紀錄並分析每個體，1) 比較翅黑斑與整片翅面積得出黑化比率 (%)，同時 2) 固定翅黑斑閥值，利用 ImgaeJ 計算個體間不同的黑化程度。

結果/結論/應用啟示

結果顯示低溫 10℃時，使所有個體前翅內緣的黑化比率顯著擴大，而高溫 30℃僅雌蝶前翅外緣黑斑顯著地黑化。高溫環境下，雌蝶黑斑黑化的增加，能夠使其停棲時保持較低的陽光反射率，延遲體溫上升；相對地，雄蝶因較長時間的飛行，而外緣黑斑沒有特別黑化。低溫環境下，不論雌雄的翅均有增加黑色比率，能有效增加太陽反射有效保留熱能；本試驗成功利用不同飼養溫度得到不同翅黑化程度的紋白蝶，其背後決定機制與所衍生的行為適應對 *P. rapae* 體溫調節相當重要，亦可能使其能夠廣泛分布並適應世界各地的不同氣候。

關鍵詞（Keywords）：紋白蝶（Cabbage white butterfly）、黑化（Melanization）、氣候適應（Climate adaptation）、體溫調節（Thermoregulation）

OE_11

穀蠹 (鞘翅目：長蠹蟲科) Prip 水通道蛋白之表現調節及生理功能

The expression regulation and physiological function of aquaporin Prip in *Rhyzopertha dominica* (Coleoptera: Bostrychidae)

陳覽繽[1]，雷喬安[1]，陳美娥[1]
Lan-Pin Tan[1], Qiao-An Lei[1] and Mei-Er Chen[1]
[1] 國立中興大學昆蟲系 Department of Entomology, National Chung Hsing University
Presenting author's email: lanpintan@gmail.com

背景/研究問題/材料方法

穀蠹為分佈全世界之積穀害蟲。於穀倉乾燥環境下，減少體內水分喪失、維持體內水動態平衡為穀蠹生存的重要課題。水通道蛋白運輸水分的功能可維持組織細胞之水分動態平衡；再者，生物在面對逆境時會調節水通道蛋白的表現，以維持體內水動態平衡。因此本研究欲探討 Pyrocoelia rufa integral protein (Prip)水通道蛋白在穀蠹成蟲各組織所扮演的角色；并且分析穀蠹面臨殺蟲劑賜諾殺逆境時，Prip 水通道蛋白的表現情形。本研究第一步選殖穀蠹 Prip cDNA，進一步利用 qPCR 檢測成蟲各組織以及賜諾殺感、抗性品系之 Prip 基因轉錄表現量，並比較感、抗性親代所產之第一代子代成蟲數量。

結果/結論/應用啟示

穀蠹成蟲各組織中，後腸及卵巢之 Prip 轉錄表現量最多，推測 Prip 水通道蛋白參與後腸的水分再吸收作用，並在雌蟲生殖系統扮演重要角色。而 Prip 在賜諾殺抗性品系表現量顯著降低 (**P**=0.013)，推測其後腸的 Prip 表現量下降使再吸收效率降低，進而後腸水分增加，可提高排泄藥劑之效率。此外，抗性品系 Prip 表現量降低亦可能為卵巢之 Prip 表現量降低所致，影響雌蟲之生殖功能，使抗性品系所產之第一代子代成蟲數量顯著少於感性品系 (**P**=0.006)。為深入了解 Prip 水通道蛋白於穀蠹排泄及生殖之生理功能，未來將進行 RNAi 實驗探究之。

關鍵詞（Keywords）：穀蠹（*Rhyzopertha dominica*）、水通道蛋白（aquaporin）、排泄（excretion）、生殖（reproduction）、抗性（resistance）

OE_12

蟲生真菌防治偽菜蚜 (*Lipaphis erysimi* Kaltenbach) 及寄主免應反應探討

Controlling of mustard aphid (*Lipaphis erysimi* Kaltenbach) by entomopathogenic fungi and host immune responses to fungal infection

楊承儒[1]，乃育昕[1]
Cheng-Ju Yang[1] and Yu-Shin Nai[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: flintyang3969@gmail.com

背景/研究問題/材料方法

Mustard aphid (*Lipaphis erysimi* Kaltenbach) is one of the most destructive pests to Brassicaceae plants. With the accomplishment of the increasing pesticide resistance, more entomopathogenic fungi (EPF) has been developed as bio-pesticides for alterative pest controlling agents. However, little was known about the interaction between EPF and its hosts. In this study, we attempt to screen the pathogenicity of EPF to mustard aphids and to evaluate the immune responses of mustard aphids to fungal challenges. Mustard aphids were collected from kale and identified by random amplified polymorphic DNA (RAPD) method. The EPF, which were isolated by insect baiting method or provided by IPG Lab, were subjected to the pathogenicity screening against mustard aphids by detach leaf method with micro-sprayer. Immune-related genes of mustard aphid were identified by *de novo* assemblage of the mustard aphid transcriptomic data and homologues search by tBLASTn against immune genes of *Acyrthosiphon pisum*. Gene expression levels of seven genes from different immune pathway under the EPF infection will be evaluated by reverse-transcription quantitative PCR (RT-qPCR).

結果/結論/應用啟示

Twenty-two of EPF isolates were isolated, including twenty isolates of *Metarhizium* spp., *Cordyceps cicadae* (NCHU-213) and *Penicillium* sp. (NCHU-219). All the EPF were able to infect mustard aphids with mycosis and sporulation, except NCHU-219. After the pathogenic screening, NCHU-196 (*M. majus*), -197 (*M. majus*), -213, and -153 (*Beauveria bassiana*) were subjected to bioassay. Each isolate could cause 90% mortality within 4 days. NCHU-213 caused the fastest mortality (LT50= 2.08 days at 107 conidia /mL) to mustard aphids, thus NCHU-213 was subjected to fungal challenges. The result showed that five immune genes (GNBP1, GNBP2, PPO2, STAT1 and JNK) were induced after fungal infection at 48 hours post infection (h.p.i.). Among them, GNBP1 and JNK were highly upregulated (>2 fold change), suggested the involvement of host response to fungal infection.

關鍵詞(Keywords)：*Lipaphis erysimi*, entomopathogenic fungi, immune, *Cordyceps cicadae*, insect baiting

OE_13

馬尼拉小繭蜂共生病毒調控斜紋夜蛾營養代謝之研究

Snellenius manilae bracovirus-encoded microRNAs as regulators in *Spodoptera litura* nutrition and metabolism.

林鈺淳[1]，吳岳隆[1]
Yu Chun Lin[1] and Yueh Lung Wu[1]
[1] 國立台灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: Shelly52203@gmail.com

背景/研究問題/材料方法

馬尼拉小繭蜂(*Snellenius manilae*)為單元寄生的寄生蜂，主要寄主為斜紋夜蛾(*Spodoptera litura*)，雌蜂在產卵的同時會注入毒液與共生的病毒 *S. manilae* bracovirus (SmBV)，幫助小繭蜂幼蟲在斜紋夜蛾體內完成發育。目前已知 SmBV 會產生大量的 miRNA 來抑制斜紋夜蛾幼蟲的免疫反應，但是否造成其他生理代謝上的影響仍需更深入的研究，因此我們將進一步探討 miRNA 對斜紋夜蛾幼蟲醣類與脂肪代謝的影響。實驗使用二齡的斜紋夜蛾幼蟲，分為無處理組、寄生組與 SmBV 注射組，個別測定其脂肪合成相關基因表現量、脂肪含量、醣類代謝相關基因表現量與醣類含量。

結果/結論/應用啟示

預期脂肪與醣類相關基因表現量在寄生組與病毒注射組中皆有所下降，儲存於脂肪體中的醣類與脂肪減少，流動於血淋巴中的含量卻增加，提供小繭蜂幼蟲成長，相對延緩斜紋夜蛾幼蟲的發育。未來會進一步以次世代定序技術大規模分析不同處理後 miRNA 的組成，找出調控脂類與醣類代謝的部分，再利用 RNAi 的技術檢測確切調控昆蟲營養代謝的 miRNA。此研究將有助於釐清 miRNA 對寄主營養代謝的調控。

關鍵詞（Keywords）：*Snellenius manilae*, *Spodoptera litura*, *S. manilae* bracovirus, microRNA, metabolism

OE_14

雌性遭遇密度對尼泊爾埋葬蟲(*Nicrophorus nepalensis* Hope) (Coleoptera: Silphidae)繁殖策略的影響

The effects of female encountered density on reproductive strategy of *Nicrophorus nepalensis* Hope (Coleoptera: Silphidae)

鄭新翰[1]，黃文伯[1]
Hsin-Han Cheng[1] and Wenbe Hwang[1]
[1]國立臺南大學生態暨環境資源學系 Department of Ecology and Environmental Resources , National University of Tainan
Presenting author's email: raymond78461@gmail.com

背景/研究問題/材料方法

本研究探討尼泊爾埋葬蟲(*Nicrophorus nepalensis* Hope)在遭遇不同數量同種同性別個體的經驗下，對雌蟲繁殖策略的影響。於嘉義縣竹崎鄉以懸掛式誘餌陷阱誘集野蟲，回實驗室培育出 F1 世代，羽化後將雌蟲分別與 0、5、11 隻同種無親緣關係的雌蟲飼養在一起，此即定義為不同強度的「遭遇密度」經驗。不同遭遇密度下的雌蟲在性熟後分別配對，使用 One-way ANOVA 分析遭遇密度對繁殖成效的影響，測量的項目包含臨巢幼蟲數量、離巢幼蟲數量、離巢幼蟲重量與羽化成蟲前胸背板寬度。

結果/結論/應用啟示

雌蟲在面對 0、5、11 的遭遇密度下，所產下的幼蟲數量有顯著差異($p = 0.016$)，事後檢定雌蟲差異存於遭遇密度為 0 與遭遇密度為 11。離巢幼蟲數量無顯著差異($p = 0.102$)，但離巢幼蟲重量則有顯著差異($p = 0.018$)，事後檢定差異存於遭遇密度為 5 與遭遇密度為 11。後代羽化後成蟲的前胸背板寬度則無顯著差異($p = 0.134$) 。此結果顯示族群成長的密度依變效應，當遭遇密度愈高，將產下較少的卵，離巢幼蟲數量也較少，而三齡幼蟲較重，羽化後的成蟲體型較大，此皆顯示埋葬蟲雌蟲養育具競爭力後代的生殖策略。另外經歷高遭遇密度的雌蟲，其子代雄/雌性別比有較高的趨勢，遭遇密度為 0 的雌蟲子代性別比為 0.4，遭遇密度為 5 為 0.696，遭遇密度為 11 為 0.716，即雌蟲在遭遇經驗下，所遇雌蟲數量越多，可能具有生下更多雄蟲的策略能力。推論埋葬蟲雌蟲能感知環境中族群的密度大小，在繁殖時採取相對應的繁殖策略，以提升其適存值。

關鍵詞（Keywords）：埋葬蟲（burying beetle）、殺嬰現象（filial cannibalism）、遭遇密度（encountered density）、繁殖策略（reproductive strategy）、適存值（fitness）

OE_15

為何昆蟲無法叮咬斑馬？以蜜蜂著陸行為為例
Why can't insects bite zebra? Study landing behavior of honey bee as an example

謝祥文[1]，楊恩誠[1]
Hsiang-Wen Hsieh[1] and En-Cheng Yang[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: xiangwen6.tw@gmail.com

背景/研究問題/材料方法

斑馬條紋的功能在 150 年來一直是未解之謎。學者依據生物的特性，建立了許多假說，包括讓捕食者困惑、增加社會凝聚力、降低體溫等，至目前為止，最讓人信服的假說是避免外寄生蟲 (Tabanid) 的攻擊。前人研究已經證實，斑馬條紋可以減少 Tabanids 著陸的數量，且寬度越窄的條紋圖案其 Tabanids 著陸的數量就越少，但是直到目前為止，只知斑馬紋與條紋圖案會影響 Tabanids 的著陸行為，而其原理仍然是未知。為了探討其原理，本研究使用蜜蜂作為實驗對象，探討不同條紋圖案影響蜜蜂著陸之行為。蜜蜂具有固定往返同一採蜜點的習性，此對定點行為觀察十分有利。以蜜蜂找尋並停留在糖水邊所花費的時間與是否可直接著陸於糖水邊，為判斷蜜蜂著陸行為的標準。

結果/結論/應用啟示

初步研究結果證實，條紋圖案會影響蜜蜂的著陸行為；且 0.95 公分寬的黑白條紋間隔圖案，明顯地增加了蜜蜂尋找糖水的時間，並導致 60% 的蜜蜂無法直接降落在糖水邊上；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。推測條紋圖案很可能使蜜蜂產生視覺的空間混疊 (spatial aliasing)，進而影響著陸成敗，確切的原因仍需更多的實驗證明。未來將比較不同條紋圖案造成著陸成功與失敗的行為差異，以釐清條紋圖案影響著陸行為的原理。

關鍵詞（Keywords）：斑馬紋（zebra stripes）、著陸行為（landing behavior）、蜜蜂（honey bee）、空間混疊（spatial aliasing）

OE_16

台灣秋行軍蟲(*Spodoptera frugiperda* J.E. Smith)腸道菌相宏基因體調查(metagenomics)

Metagenomics investigation on the gut microbiota of fall armyworm, *Spodoptera frugiperda* (J.E. Smith) (Lepidoptera: Noctuoidea) in Taiwan

劉曜嘉[1]，乃育昕[1]
Yao-Chia Liu[1] and Yu-Shin Nai[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: b10527042@gmail.com

背景/研究問題/材料方法

Gut microflora influence the development and physiology of insects. Besides, gut microflora could also help insect hosts survive in varied environments. Several studies have shown that gut microflora protected hosts from pathogens and supported detoxification of pesticides or harmful toxins in insects. Therefore, unravel and compare the gut microbiota of insects, especially pests, under different circumstances can assist to comprehend the relationship between microbiota and their hosts' response to the environments. This study performed the bacterial metagenomics investigation on *Spodoptera frugiperda* (FAW) from six cornfields and compared it with that of the laboratory population.

結果/結論/應用啟示

Based on the results, the dominant microbial community of laboratory population in both hind and middle gut was phylum Firmicutes (93 and 95%), class Bacilli (93 and 95%), order Lactobacillus (92%), and genus *Enterococcus* (93 and 92%), while in cornfield population, the dominance microbial community were phyla Proteobacteria (61%) and Firmicutes (60%), class Gammaproteobacteria (57%) and Bacilli (70%), order Enterobacteriales (51%) and Lactobacillus (71%), genera *Klebsiella* (45%) and *Enterococcus* (72%). In alpha diversity analysis, cornfield population showed uniformity higher diversity than laboratory. Besides, in beta diversity analysis, laboratory and wild populations can separate two groups in principal co-ordinates analysis, indicated that different compositions of gut microbiota were found between cornfield and laboratory populations. It was noted that the *Klebsiella* sp. (proteobacteria) (26% of total sequence reads), which was reported its insecticide-degradation activity, was dominant in FAW in cornfields, suggested that *Klebsiella* sp. in the gut may contribute the insecticidal resistance in FAW. In the future, the association between entomopathogenic fungi (EPF) infection and gut microbiota in FAW will be investigated. The EPF infection is supposed to induce the pathobiome status (alter the microflora to related low diversity) to reduce the fitness of FAW and provide a new pest control strategy.

關鍵詞（Keywords）：腸道菌相（Gut microbiota）、宏基因體（Metagenomics）、秋行軍蟲（*Spodoptera frugiperda*）、蟲生真菌（Entomopathogenic fungi）、致病菌群（Pathobiome）

OE_17

亞致死劑量益達胺對蜂后幼蟲發育之影響

The effect of sublethal dosage of imidacloprid on honey bee queen gene expression

陳韻如[1]，林詩舜[2]，楊恩誠[1]
Yun-Ru Chen[1], Shih-Shun Lin[2] and En-Cheng Yang[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
[2] 國立臺灣大學生物科技研究所 Institute of Biotechnology, National Taiwan University
Presenting author's email: milkingroom@gmail.com

背景/研究問題/材料方法

亞致死劑量益達胺對蜜蜂與其他授粉昆蟲造成嚴重的生存危機。本團隊先前研究證實，工蜂幼蟲暴露在亞致死劑量益達胺環境下，年幼內勤蜂之轉錄組會與外勤蜂之基因表現類似，亦即內勤蜂極可能有早熟現象。蜂后是蜂巢中唯一的生殖性個體，然而，亞致死劑量益達胺對蜂后發育之影響仍然未知。為了完整釐清亞致死劑量益達胺對蜜蜂族群的影響，本研究從基因層次探討亞致死劑量益達胺對蜂后幼蟲發育之影響。蜂后幼蟲連續三日暴露於 1 ppb 與 10 ppb 的益達胺溶液，取剛羽化之蜂后進行轉錄組之定序，並檢視差異性表現基因。

結果/結論/應用啟示

不論是以 1 ppb 或是 10 ppb 益達胺處理之蜂后幼蟲，死亡率均會高於控制組，且 10 ppb 益達胺處理之幼蟲有極高之死亡率。我們進一步檢測餵食含有 1 ppb 益達胺蜂王乳所發育的蜂后基因表現狀態，與控制組比較，總共 215 個基因有差異性表現，基因本體分析顯示，差異性表現基因之功能與 chitin binding、phototransduction、fatty acid biosynthetic、和 visual perception 相關。幼蟲期暴露在亞致死劑量益達胺環境下提高蜂后幼蟲死亡率，並減弱其對環境的耐受性，更影響羽化後 0 日齡蜂后之基因表現。亞致死劑量益達胺降低蜂后幼蟲存活率，極可能對蜂群經營產生難以頻估的負面影響。

關鍵詞（Keywords）：蜜蜂（honey bee）、蜂后幼蟲（larvae of queen bee）、亞致死劑量效應（sublethal effect）、益達胺（imidacloprid）、差異性表現基因（differentially expressed genes, DEGs）

農業昆蟲學

論文宣讀

Oral Session: Agricultural Entomology

OA_01

彰化與雲林地區之黃條葉蚤對藥劑感受性之探討
Research on the insecticides susceptibility of *Phyllotreta striolata* (Fabricius) from Changhua and Yunlin districts

洪欽麟[1]，魏紹華[1]，林明瑩[1]
Chin-Lin Hung[1], Shao-Hua Wei[1] and Ming-Ying Lin[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: s1014111@gmail.com

背景/研究問題/材料方法

黃條葉蚤屬鞘翅目 (Coleoptera)、金花蟲科 (Chrysomelidae) 的小型害蟲，現今在臺灣種植的十字花科作物普遍受到此蟲嚴重的危害。此蟲的成蟲以葉片為食，導致葉片佈滿孔洞，幼蟲危害根部影響植株生長，此蟲的發生常常影響作物產量與品質，嚴重失去商品價值。蔬菜產區之農友普遍反應黃條葉蚤不易防治，為了解此蟲對現今殺蟲劑之抗藥性，本試驗自雲林西螺與彰化芳苑地區採集田間之黃條葉蚤，以浸葉法進行 8 種市售藥劑防治黃條葉蚤之探討。供試藥劑係國內登記使用防治黃條葉蚤之商品農藥，分別為阿巴汀、亞滅培、加保利、培丹、達特南、馬拉松、毆殺滅、佈飛松等。主要進行上述藥劑之藥效快速檢測及感受性分析。

結果/結論/應用啟示

藥效快速檢測所使用的藥劑濃度，為根據各種藥劑登記於防治黃條葉蚤之田間推薦濃度。以浸葉法進行供試藥劑之試驗，48 小時後，不論是彰化芳苑或雲林西螺地區之黃條葉蚤，以 8 種登記藥劑處理之死亡率均低於 70%。推測 2 個不同地區之黃條葉蚤對不同藥劑均已產生抗藥性。另外，在進行感受性分析的部份，以不同濃度之稀釋農藥浸葉，供黃條葉蚤成蟲取食，並於 48 小時後紀錄其死亡蟲數進行對機數分析 (Probit analysis)。試驗結果顯示，彰化芳苑與雲林西螺地區的黃條葉蚤對相同藥劑均呈現出不同的感受性。其中以毆殺滅之差異最大，2 個地區半致死濃度 (LC50) 之抗性比達 9.8 倍；馬拉松次之，其半致死濃度之抗性比為 3.1 倍。2 個地區的黃條葉蚤感受性分析結果，以對培丹之半致死濃度之差異最小，抗性比僅 0.1 倍。由於不同地區之栽培作業及農事管理之相異，顯著存在著不同程度之抗藥性，實應持續地進行相關之藥劑試驗，以長期監測及掌握不同地區黃條葉蚤對不同藥劑之抗藥性資訊。

關鍵詞（Keywords）：黃條葉蚤（*Phyllotreta striolata*）、殺蟲劑（insecticides）、抗藥性（resistance）

OA_02

光敏劑對菸草粉蝨 (*Bemesia tabaci*) 之光活化致死效果及殺蟲機制
Light-activated lethal effect and killing mechanism of photosensitizer on *Bemesia tabaci*

黃玉媛[1]，李威樺[1]，宋一鑫[2]，蔡志偉[1]
Yu-Yuan Huang[1], Wei-Hua Li[1], I-Hsin Sung[2] and Chi-Wei Tsai[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
[2] 國立嘉義大學植物醫學系 Department of plant medicine, National Chiayi University
Presenting author's email: vivian1997729@gmail.com

背景/研究問題/材料方法

光敏劑 (Photosensitizer) 作為殺蟲劑防治害蟲已經數十年。當光敏劑被昆蟲攝入並受光照激發後，透過能量轉移產生具細胞毒性的活性氧 (reactive oxygen species)，導致昆蟲腸道細胞死亡，最終達到殺死害蟲的目的。光敏劑不同於傳統殺蟲劑，產生的活性氧可以作用在多位點使昆蟲無法產生抗藥性。本研究測試六種光敏劑 (Rose Bengal、Cyanosine、TMAP、TPPS2、PC1 與 PC3.4) 對菸草粉蝨 (*Bemesia tabaci*) 的光活化致死效果並確認其殺蟲機制。粉蝨於黑暗環境中取食光敏劑 16 小時後，暗處理組保持黑暗、光處理組移出照光 48 小時。比較光、暗處理組受試粉蝨的死亡率，判斷光敏劑的光活化致死效果。並試驗亞致死濃度 (0.1 μM) 是否會影響粉蝨的生育力 (fecundity)。然後，利用螢光激發、H2DCFDA 偵測活性氧含量與 TUNEL assay 確認光敏劑會被粉蝨中腸細胞吸收、粉蝨體內光敏劑受光照後會激發產生活性氧以及會導致粉蝨的中腸細胞死亡。

結果/結論/應用啟示

光敏劑對菸草粉蝨具有光活化致死效果，且與光敏劑濃度及光照時間呈正比。當光敏劑濃度為 5 mM 時，除 PC1 和 PC3.4 以外其它四種藥劑在光照 24 小時後致死率達 100%。亞致死濃度 (0.1 μM) 的光敏劑既不會造成粉蝨的死亡，也不會影響粉蝨的生育力。當光敏劑被粉蝨取食後，會被腸道細胞吸收、受光照後激發產生活性氧。TUNEL assay 證明光敏劑光活化作用會導致粉蝨腸道內細胞死亡，最終導致粉蝨死亡。上述結果證實 Rose Bengal、Cyanosine、TMAP 及 TPPS2 具有作為替代性殺蟲劑的潛力。光敏殺蟲劑或許可以協助我們發展新穎的害蟲防治策略，保護農作物免於粉蝨的危害。

關鍵詞(Keywords)：殺蟲劑(insecticide)、致死率(mortality)、光敏劑(photosensitizer)、活性氧（reactive oxygen species）、粉蝨（whitefly）

OA_03

不同定溫下伊凡氏葉蟎在龍葵上之生活史

The life history of *Tetranychus evansi* (Acari: Tetranychidae) on *Solanum nigrum* at varied temperatures

葉千榕[1]，林明瑩[1]
Chien-Yong Yeh[1] and Ming-Ying Lin[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: qaz59820qaz@gmail.com

背景/研究問題/材料方法

伊凡氏葉蟎 (*Tetranychus evansi*) 源於南美洲，具極高的入侵能力，現今隨著運輸而逐漸擴散至世界各地，是嚴重危害茄科作物的害蟎。臺灣亦已於 1992 年確認此蟎的發生，伊凡氏葉蟎可在番茄上繁殖並導致植株侏儒化，在臺灣此蟎主要發生於龍葵，龍葵為臺灣常見之野菜，目前全臺均能發現龍葵被危害蹤跡。而現今以設施進行番茄之種植，雖然能有效的降低部份病蟲害發生卻有助於蟎類的滋長，若不慎讓伊凡氏葉蟎進入設施中，恐對番茄造成嚴重危害。本試驗旨在探討伊凡氏葉蟎在 21、24 及 27℃ 三個不同定溫下的族群表現，以龍葵為供試寄主在 12: 12 (L: D) 、 RH 70 ± 10% 的供試條件下，探討其發育時間、產卵量等基礎生態資訊，並進行統計分析以掌握其生活史特徵及族群介量等資訊。

結果/結論/應用啟示

於 21–27℃ 下，伊凡氏葉蟎之卵期分別為 5.90、4.62 及 3.90 日，幼蟎期分別為 2.42、2.53 及 1.15 日，前若蟎期分別為 2.02、1.73 及 1.18 日，後若蟎期則分別為 2.63、2.25 及 1.56 日。整體而言，幼期所需發育日數隨溫度上升而遞減，在 21℃ 下需時 12.96 日，而較高溫之 27℃ 則縮短至 7.80 日。於繁殖表現上，雌成蟎在 21、24 及 27℃ 之繁殖量分別為 169.84、160.10 及 162.73 eggs/female，產卵天數分別為 21.00、16.90 及 13.28 日，不同定溫間產卵天數具顯著差異。於族群表現上，淨繁殖率 (*R*0) 在 27℃ 下最高，為 125.67 eggs/individual，在 24℃ 下最低，為 116.87 eggs/individual。內在增殖率 (*r*) 在 27℃ 下最高，為 0.3811 /day，而 21℃ 則最低，為 0.2279 /day。終極增殖率 (*λ*) 在 27℃ 下最高，為 1.4638 /day，而 21℃ 則最低，為 1.2560 /day。而平均世代時間 (*T*) 在 21℃ 下最長，為 20.97 日，而 27℃ 下最短，為 12.69 日。本試驗結果提供伊凡氏葉蟎之基礎生態資訊，可供日後相關研究之參考。

關鍵詞（Keywords）：伊凡氏葉蟎（*Tetranychus evansi*）、龍葵（*Solanum nigrum*）、生活史（life history）、族群介量（population parameters）

OA_04

甜菜夜蛾 (鱗翅目: 夜蛾科) 在青蔥上之生命表與取食量

Life table and consumption of *Spodoptera exigua* (Lepidoptera: Noctuidae) on green onion

阮韞澔 [1]，林明瑩 [1]
Yun-Hao Juan[1] and Ming-Ying Lin[1]
[1] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: yunhaojuan@gmail.com

背景/研究問題/材料方法

甜菜夜蛾為夜蛾科的主要害蟲之一，為咀嚼式口器之雜食性害蟲，在多種作物上啃食莖、葉、花等，造成作物大量的經濟損失，包括茄科、十字花科、石蒜科等多種作物皆受其危害，且在青蔥上的危害尤其顯著。然目前在青蔥上仍然缺乏完整的基礎生態資訊，因此本試驗目的便是了解此蟲於青蔥上之生命表與取食量。試驗在 27 ± 1℃、12:12 (L：D)、RH 70 ± 10% 的供試條件下，觀察甜菜夜蛾幼蟲之發育與取食；成蟲壽命及繁殖表現，並進一步進行兩性生命表與取食量之分析以掌握其生命表及族群介量等資訊。

結果/結論/應用啟示

在 27℃ 下，甜菜夜蛾於青蔥上，卵期 2.00 日，幼蟲各齡期發育時間一至五齡分為 2.92、1.98、1.86、3.10 及 3.04 日，而一至五齡各齡期之取食量則分別為 4.52、21.37、75.71、700.98 與 3129.11 mm2，以五齡之取食量為最大。蛹期為 6.29 日，成蟲壽命雄蟲平均為 18.27 日，明顯較雌蟲的 13.45 日長，平均產卵量為 1026.14 粒卵/雌蟲。在族群介量的表現上，淨取食率 (*C*0)、淨繁殖率 (*R*0)、內在增殖率 (*r*)、終極增殖率 (*λ*) 與平均世代時間 (*T*) 分別為 2148.67 mm2/individual、245.38 offspring/individual、0.2232/day、1.2501/day 與 24.65 日。此試驗結果提供對甜菜夜蛾在青蔥上之生活史與取食量之基礎資訊，日後仍需更多的相關研究，以利於防治上建構完整的參考基礎。

關鍵詞（Keywords）：青蔥（*Allium fistulosum*）、生活史（life history）、取食量（consumption）、族群介量（population parameters）

OA_05

乙基或甲基取代的呋喃和噻吩作為控制昆蟲的新型燻蒸劑的潛力

Potential of ethyl- or methyl-substituted furan and thiophene as novel fumigants for insect control

黃勝[1]，姚美吉[2]，李成正[3]，呂維茗[3]，戴淑美[4]，孟孟孝[3]

Joey Huang[1], Me-Chi Yao[2], Cheng-Cheng Lee[3], Wei-Ming Leu[3], Shu-Mei Dai[4] and Menghsiao Meng[3]

[1] 國立中興大學和中央研究院微生物與基因體博士學位學程 Ph.D. Program in Microbial Genomics, National Chung Hsing University and Academia Sinica, Taiwan, ROC

[2] 行政院農委會農業試驗所台中本所應用動物組 Applied Zoology Division, Agricultural Research Institute, Council of Agriculture, Taichung, 41362 Taiwan, ROC

[3] 國立中興大學生物科技學研究所 Graduate Institute of Biotechnology, National Chung Hsing University, 250 Kuo-Kuang Road, Taichung, 40227 Taiwan, ROC

[4] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University, 250 Kuo-Kuang Road, Taichung, 40227 Taiwan, ROC

Presenting author's email: asd85531@gmail.com

背景/研究問題/材料方法

Fumigation in a closed space using volatile insecticides, such as methyl bromide and phosphine, has been an effective practice to control insect pests in the food production and supply chain. Nonetheless, alternative fumigants are urgently needed mainly because of legislative prohibition against methyl bromide and emergence of phosphine-resistant insects. In this study, we demonstrated that 2,5-dimethylfuran, identified as a vapor component emitted by *Burkholderia gladioli* previously, exhibits fumigant toxicity toward a variety of insects, including *Sitophilus oryzae, Rhyzopertha dominica*, *Cylas formicarius*, *Blatta lateralis* and *Tapinoma melanocephalum*. The correlations between mortality of *S. oryzae* and fumigation dosage of 2,5-dimethylfuran, 2-methylfuran, 2-ethylfuran, 2,5-dimethiophene, 2-methylthiophene, and 2-ethylthiophene were established, showing that the efficacy is in the order of 2-ethylthiophene > 2-methylthiophene > 2,5-dimethylfuran > 2,5-dimethylthiophene > 2-ethylfuran > 2-methylfuran. In view of the broad-spectrum insect toxicity, the low toxicity to mammals, and no known hazard to the atmosphere, 2,5-dimethylfuran and its thiophene analogs may have potential as novel fumigants to complement or even replace the conventional ones for insect control.

結果/結論/應用啟示

In this study, we discovered that a couple of simple furans and thiophenes exhibit fumigant toxicity to *S. oryzae*. In speaking of the killing efficacy, thiophenes with an ethyl or methyl substituent at the 2' position are better than their furan counterparts. However, according to the toxicity data to mammals, described in the manufactures' safety data sheet, 2-ethylthiophene and 2-methylthiophene are relatively safer than 2-ethylfuran and 2-methylfuran. The inconsistency between toxicity levels to insects and to mammals suggests that the mechanisms

underlying killing insects and mammals are different. How the insects are killed by these simple furans and thiophenes is an interesting query deserving further investigation in the future.

關鍵詞（Keywords）：燻蒸劑（Fumigant）、呋喃和噻吩（Furans and thiophenes）、昆蟲的廣譜毒性（broad-spectrum insect toxicity）

OA_06

桿狀病毒表現醣類結合蛋白提升殺蟲活性之研究

Enhancing the insecticidal potential of baculovirus by overexpressing the mammalian β-galactosyl binding protein galectin-1

林家揚[1]，吳岳隆[1]，黃榮南[1]
Chia-Yang Lin[1], Yueh-Lung Wu[1] and Rong-Nan Huang[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: steven09194@gmail.com

背景/研究問題/材料方法

桿狀病毒(baculoviruses)屬於桿狀病毒科(Baculoviridae)，是一種桿狀、雙股 DNA 病毒，具有感染多種的鱗翅目、雙翅目及膜翅目昆蟲的能力，所以桿狀病毒也是防治上非常重要的生物性農藥，但是由於桿狀病毒在寄主的感染力、致病力之效率不佳，導致其無法被大規模或廣泛性的作為生物殺蟲劑來使用，如何提升桿狀病毒的作用效率成為防治研究上的首要目標。而 Galectin-1 (GAL1) 蛋白是一種哺乳動物的醣類結合蛋白，參與諸多的細胞與細胞之互相作用，舉凡細胞的成長、增殖、黏附、分化、凋亡等等，本實驗室已證實 GAL1 可結合至昆蟲幾丁質之構造單元(N-acetyl-D-glucosamine)，影響昆蟲之正常發育，但是因為蛋白質無法在田間穩定的存續，導致以蛋白質作為農藥來施用相當困難，而蛋白質的大量製造及純化成本高亦是難以大規模生產的問題。所以我們利用桿狀病毒作為表現 GAL1 基因的載體，建構一種結合 GAL1 與桿狀病毒的雙效生物殺蟲劑。

結果/結論/應用啟示

藉由桿狀病毒多角核蛋白基因之啟動子的強效高表現效率，在斜紋夜蛾取食病毒後會侵入中腸上皮細胞，開始大量表現 GAL1 蛋白於其腸道中，導致中腸圍食膜的穿孔，導致斜紋夜蛾取食作物能力下降，同時該蛋白也具有抑制免疫系的能力，能夠使其他病原菌更容易入侵甚至是直接導致死亡。表現 GAL1 蛋白之桿狀病毒具有更迅速的致死率，顯示 GAL1 蛋白提升其應用潛力。

關鍵詞（Keywords）：baculovirus, galectin-1, bio-control, β-galactosyl binding protein

OA_07

The interaction of two tomato-infecting begomoviruses in *Bemisia tabaci* and its effect on virus transmission

Wei-Hua Li[1] and Chi-Wei Tsai[1]
[1] Department of Entomology, National Taiwan University, Taipei, Taiwan
Presenting author's email: f06632007@ntu.edu.tw

背景/研究問題/材料方法

According to a field survey, tomato yellow leaf curl Thailand virus (TYLCTHV) quickly replaced tomato leaf curl Taiwan virus (ToLCTV) after the former invaded Taiwan. Both viruses are exclusively transmitted by *Bemisia tabaci*, so the virus replacement in tomato fields is possibly related to the virus-vector interaction. In this study, *B. tabaci* was given two virus acquisition periods on single infected or co-infected plants, and the amount of virus in the organs and hemolymph of *B. tabaci* were determined by quantitative PCR to study the interaction of these two viruses in whitefly. Further, transmission assays were conducted to examine the effect of virus-virus interaction on whitefly transmission of the viruses.

結果/結論/應用啟示

When the whiteflies acquired TYLCTHV first and ToLCTV later, the titers of ToLCTV in the midgut and salivary glands of whiteflies were significantly lower than those of whiteflies that acquired ToLCTV only. However, the titer of ToLCTV in the organs and hemolymph of whiteflies were not different between the whiteflies acquired ToLCTV first and TYLCTHV later and the whiteflies acquired ToLCTV only. In contrast, the titers of TYLCTHV in the organs and hemolymph of whiteflies were not changed no matter ToLCTV was acquired earlier or later than TYLCTHV. Whitefly transmission assays found that the infection rate of TYLCTHV were higher than that of ToLCTV no matter that the whiteflies acquired these viruses first or later. Taken together, TYLCTHV had an antagonistic effect on the infection of ToLCTV in *B. tabaci*, and TYLCTHV was more competitive than ToLCTV in host plant. This study provides a new insight to understand the effect of virus-vector interaction on the epidemiology of plant viruses.

關鍵詞（Keywords）：antagonism, *Begomovirus*, Geminiviridae, virus-vector interaction, whitefly

OA_08

The emerging pest of tea plants, *Euwallacea fornicatus* (Coleoptera: Curculionidae), in Taiwan

Liao, Yi-Chang[1], Paul Rugman-Jones[1], Fan-Ling Liu[2], Hui-Hung Liang[2], Chun-Yen Lee[3], Lan-Yu Liu[4], Shu-Jen Tuan[2] and Richard Stouthamer[1]
[1]Department of Entomology, University of California, Riverside, CA, U.S.A.
[2]Department of Entomology, National Chung Hsing University, Taichung, Taiwan
[3]Taiwan Agriculture Chemicals and Toxic Substances Research Institute, Council of Agriculture, Executive Yuan, Taichung, Taiwan
[4]Department of Science Communication, Pingtung University, Pingtung, Taiwan
Presenting author's email: ycliaopsyllids@gmail.com

背景/研究問題/材料方法

The major pests of tea (*Camellia sinensis*,Theaceae) in Taiwan include lepidopterans, hemipterans, thrips and spider mites. However, in January 2020, ambrosia beetles were found attacking tea bushes in central Taiwan. The specimens were identified as belonging to the *Euwallacea fornicatus* Eichoff (Coleoptera: Curculionidae: Scolytinae: Xyleborini) species complex, commonly called shot hole borers (SHBs). The last record of SHBs infesting tea in Taiwan was from 1939. The level of infestation of tea in Taiwan is unclear. Here, we report on a survey of tea throughout island.

結果/結論/應用啟示

Beetles belonging to the *E. fornicatus* species complex attacking tea were found mostly in central and eastern Taiwan. Adults usually construct the galleries in the main trunk and in underground parts of the trunk. The creation of galleries in stems can result in the breaking of branches, recognizable in the field by branches with shriveled leaves. The gallery structure was observed using micro-computerized tomography. A survey of the flight activity of beetles in one specific tea garden showed the lowest flight activity in summer and the highest in winter. Several of the cryptic species making up the species complex were found, but not the Tea Shot Hole Borer (*E. perbrevis*). In Sri Lanka, the Tea Shot Hole Borer is a major pest in tea. In our survey we did not find it attacking tea, even though the species is present in Taiwan. Locally, the infestation of SHBs varied, an infested tea garden could be found adjacent to a tea garden without SHBs. Several factors including tea cultivar, agricultural practice and environmental factors would need to be further examined to determine what influences the level of infestation by SHBs in tea.

關鍵詞（Keywords）：polyphagous shot-hole borer, Kuroshio shot-hole borer, quercivorol, cryptic

OA_09

旋轉式避蛾燈開發及防治水蜜桃吸果夜蛾之效果評估

Development of rotary moth-repellent lamps and evaluation of the effectiveness of controlling the fruit-piercing moths on peach

陳巧燕[1]，莊國鴻[1]，李汪盛[1]，施錫彬[1]
Chiao-Yen Chen[1], Kuo-Hung Chuang[1], Wang-Sheng Li[1] and His-Pin Shih[1]
[1] 行政院農業委員會桃園區農業改良場 Taoyuan District Agricultural Research and Extension Station, Council of Agriculture, Executive Yuan
Presenting author's email: yen@tydais.gov.tw

背景/研究問題/材料方法

經 2019-20 年 7 月夜間調查桃園市復興區上巴陵水蜜桃吸果夜蛾種類，計有 2 科 13 屬 19 種，以口器具硬棘能穿刺套袋者為甚，占調查總蛾數 80%以上，成為水蜜桃果實成熟期重要害蟲。以黃色避蛾燈管可趨避吸果夜蛾，但光源照射處以外之暗部仍見吸果夜蛾出沒危害果實。本研究開發「旋轉式避蛾燈」用於忌避吸果夜蛾，其包含特殊避蛾波長燈源，結合減速馬達與導電滑環造成旋轉，利用驅動晶片控制閃爍，裝置於集束燈罩內，使之產生明滅及旋轉光束，改進傳統避蛾燈管忌避範圍不足問題。於水蜜桃果園進行旋轉式避蛾燈架設(點燈處理)，並以未架設燈之未點燈區作為對照，調查水蜜桃果實成熟期夜間吸果夜蛾侵入果園數量；標定點燈區及未點燈區之果實套袋，於採收時調查吸果夜蛾危害率，完成旋轉式避蛾燈田間防治效果驗證。

結果/結論/應用啟示

2021 年旋轉式避蛾燈完成開發，並取得我國新型專利。水蜜桃園採收期田間效果測試結果，架設旋轉式避蛾燈之點燈區吸果夜蛾單夜侵入數量為 2 隻，全期果實危害率 5.2%；未點燈區吸果夜蛾單夜侵入數量為 54 隻，全期果實危害率 25.1%，結果顯示果園架設旋轉式避蛾燈可忌避吸果夜蛾入侵果園，有效減少其危害果實。未點燈區吸果夜蛾危害以緊鄰森林之果園區塊最多，占受害果實比例 55.0%，顯示吸果夜蛾夜間自森林方向進入果園。本研究提供水蜜桃等高經濟價值果樹成熟期吸果夜蛾物理防治方法，未來將進一步測試燈源有效範圍，確立田間燈具布建數量，於吸果夜蛾易侵入果園區段，以避蛾燈設立光柵（Light barriers），配合食物誘引誘捕吸果夜蛾，建立吸果夜蛾綜合管理技術。

關鍵詞（Keywords）：吸果夜蛾（Fruit-piercing moths, FPMs）、水蜜桃害蟲（Peach fruit pest）、燈光驅避（Light repellent）、物理防治（Physical control）

OA_10

荔枝椿象蟲生真菌淡紫菌(*Purpureocillium takamizusanense*)之寄主範圍與固態發酵條件初步研究

Preliminary study on host range and solid-state fermentation of *Purpureocillium takamizusanense*, an entomogenous fungi on litchi stink bug (*Tessaratoma papillosa* (Drury))

陳盈丞[1]，陳奐宇[1]，林慧婷[1]，黃慈閔[1]，蔡孟旅[1]
Ying-Cheng Chen[1], Huan-Yu Chen[1], Hui-Ting Lin[1], Tzu-Min Huang[1] and Meng-Lu Tsai[1]
[1]行政院農業委員會臺南區農業改良場 Tainan District Agricultural Research and Extension Station
Presenting author's email: kindericchen830204@gmail.com

背景/研究問題/材料方法

荔枝椿象(*Tessaratoma papillosa* (Drury))的害物綜合管理(Integrated pest management, IPM)，主要是以化學防治搭配移除卵塊，以及釋放平腹小蜂等策略進行。蟲生真菌淡紫菌(*Purpureocillium takamizusanense*)分離自臺南市南化區受感染之荔枝椿象成蟲蟲體，若能將其作為開花期的防治策略之一，除可解決農藥影響平腹小蜂與授粉昆蟲問題，亦有助於農藥減量。本研究主要測試淡紫菌 TNZZS6 菌株的寄主範圍與固態發酵最適培養方式，以評估未來發展成有效防治作物害蟲的微生物製劑之潛力。寄主範圍測試選用膜翅目的平腹小蜂(*Anastatusschichengensis*)；纓翅目的小黃薊馬(*Scirtothrips dorsalis* (Hood))；半翅目的睡蓮蚜(*Rhopalosiphum nymphaeae*)、二點小綠葉蟬(*Amrasca biguttula*)與亞洲柑橘木蝨(*Diaphorina citri*)；鱗翅目的斜紋夜蛾(*Spodoptera litura*)、甜菜夜蛾(*Spodoptera exigua*)與秋行軍蟲(*Spodoptera frugiperda*)。另外在最適培養方式試驗中，選用玉米粉、黃豆粉、麩皮、米糠與稻米作為固態培養介質，藉此篩選產孢效果最佳的介質與條件。

結果/結論/應用啟示

寄主範圍測試結果發現 TNZZS6 菌株除可感染荔枝椿象之外，亦可感染小黃薊馬、二點小綠葉蟬與亞洲柑橘木蝨，但對平腹小蜂、睡蓮蚜、斜紋夜蛾、甜菜夜蛾與秋行軍蟲不具感染能力。在最適培養介質試驗中，選用玉米粉、黃豆粉、麩皮、米糠與稻米，依據不同介質與比例製成 8 組處理，於培養之第 7 天與第 14 天調查，均以麩皮處理產孢效果最佳。而最佳培養天數試驗結果顯示，於發酵第 12 天達到高峰，產孢量可達 7.24×10^9cfu/g。綜合以上結果，推測淡紫菌(*Purpureocillium takamizusanense*)TNZZS6 菌株寄主範圍主要為半翅目昆蟲，但仍需對更多重要害蟲進行感染測試，以釐清其寄主範圍。同時由於不具備感染平腹小蜂能力，未來應可靈活運用於荔枝龍眼花期之荔枝椿象防治。固態發酵初步試驗結果，最適培養介質為麩皮，將作為該菌大規模量產之參考依據。

關鍵詞（Keywords）：蟲生真菌（Entomogenous fungi）、淡紫菌（*Purpureocillium takamizusanense*）、固態發酵（Solid-State Fermentation）、荔枝椿象（*Tessaratoma papillosa* (Drury)）

OA_11

淡紫菌液態發酵初探及化學藥劑之抑制效果
Preliminary study on liquid fermentation of *Purpureocillium takamizusanense* and the inhibition effect of pesticides

林慧婷[1]，陳盈丞[1]，陳奐宇[1]，蔡孟旅[1]
Hui-Ting Lin[1], Ying-Cheng Chen[1], Huan-Yu Chen[1] and Meng-Lu Tsai[1]
[1]行政院農業委員會臺南區農業改良場 Tainan District Agricultural Research and Extension Station
Presenting author's email: miko5660@gmail.com

背景/研究問題/材料方法

本場自臺南市南化區受感染的荔枝椿象 *Tessaratoma papillosa* (Drury)分離出淡紫菌 *Purpureocillium takamizusanense* TNZZS6 菌株，該菌株展現其對荔枝椿象成蟲及若蟲之致病性，具有發展為微生物農藥之潛力。為求能與化學藥劑配合防治，應考量化學藥劑對 TNZZS6 菌株之抑制效果，同時克服量產之問題，以達到商品化之價值。試驗使用登記於荔枝龍眼之防治藥劑依使用範圍之稀釋倍數與 TNZZS6 菌株進行測試，探討化學藥劑對孢子發芽率及菌絲生長之影響。液態發酵具有縮短培養時間及提高產量之優點，為篩選最適合淡紫菌生長之液態培養基，將不同液態培養基配方以 30%裝液量、5%接菌量、26 ℃培養溫度以及轉速 150 rpm 之發酵條件進行搖瓶培養，取定量發酵液進行系列稀釋，塗盤測定活菌數，藉此篩選淡紫菌之最適液態培養基以及最佳發酵時間。

結果/結論/應用啟示

藥劑抑制試驗結果顯示，供試殺蟲劑第滅寧及丁基加保扶皆會降低孢子發芽率，孢子發芽抑制率分別為 36.68%及 26.72%，而賽洛寧及亞滅培則不會影響該菌株之孢子發芽，孢子發芽抑制率皆為 0%。殺菌劑甲基多保淨及亞托敏皆會降低孢子發芽率，孢子發芽抑制率分別為 7.95%及 22.19%。化學藥劑對菌絲生長之影響的部分，殺蟲劑第滅寧對該菌株之影響最明顯，菌絲生長抑制率為 67.26%。而賽洛寧、丁基加保扶及亞滅培皆會輕微影響菌絲生長，菌絲生長抑制率分別為 15.66%、17.44%及 7.47%。殺菌劑甲基多保淨及亞托敏皆會抑制菌絲生長，甲基多保淨對該菌株的菌絲生長抑制率高達 100%，而亞托敏的菌絲生長抑制率為 32.38%。液態發酵曲線顯示，液態培養基 PDB、medium b 及 medium E16 皆在發酵 5 天達到高峰，活菌數分別為 1.5610^{8}、7.810^{8} 及 2.0510^{9} cfu/ml。綜合上述結果，甲基多保淨、亞托敏及第滅寧對淡紫菌 *Purpureocillium takamizusanense* TNZZS6 菌株抑制效果明顯，綜合防治策略最好與上述三種化學藥劑分別單獨使用。淡紫菌液態發酵初步試驗之最適液態培養基及發酵條件，將作為該菌大規模量產之參考依據。

關鍵詞（Keywords）：淡紫菌（*Purpureocillium takamizusanense*）、藥劑抑制效果（inhibition effect of pesticides）、液態發酵（liquid fermentation）、荔枝椿象（*Tessaratoma papillosa* (Drury)）

OA_12

無人植保機防治蓮花小黃薊馬之研究

The study of using Unmanned Plant Protection Machine to control *Scirtothrips dorsalis* Hood on lotus

陳盈丞[1]，黃美靜[1]，張淳淳[1]
Ying-Cheng Chen[1], Mei-Jing Huang[1] and Chun-Chun Chang[1]
[1]行政院農業委員會臺南區農業改良場 Tainan District Agricultural Research and Extension Station
Presenting author's email: meijing0425@gmail.com

背景/研究問題/材料方法

近年來無人植保機應用於病蟲害防治日益廣泛，其省工且可減少藥液使用量之優點逐漸受到農業重視。蓮花遭受小黃薊馬危害嚴重，加上蓮田泥濘難以行走，傳統人工進行病蟲害防治多為站立於田埂上噴施藥劑，藥液不易噴及田區中心及蓮葉葉背，然而小黃薊馬多躲藏於葉背，導致農民防治困難。本試驗透過無人植保機(佐翼 DX-5)測試三種噴頭類型：空心圓錐噴頭 TR80-01、塑鋼扇形 ST110-01 和扇形噴頭 XR110-01，將水試紙架設於飛行路徑之兩側 30 m、45 m、60 m 共 6 處，每處設置 6 張水試紙，分別為葉片兩側之正、反面及葉柄各 2 張水試紙，測試不同供試噴頭之藥劑霧滴分布情形，以篩選適用於蓮花田之無人植保機噴頭。最後以 20%覆滅�螨水溶性粉劑進行田間防治小黃薊馬試驗，評估無人植保機防治效果。

結果/結論/應用啟示

噴頭試驗結果顯示距離無人植保機航線 30 m 處，其水試紙覆蓋率於葉背及葉柄以 TR80-01 最高，葉面最高為 ST110-01；而距離 60 m 處，水試紙覆蓋率於葉面及葉柄以 XR110-01 最高，葉背最高為 ST110-01。小黃薊馬大多躲藏於蓮葉葉背，三種噴頭之噴灑效果以 TR80-01 較適用於防治蓮花小黃薊馬。因此田間防治試驗以無人植保機裝載 TR80-01 噴頭噴施 20%覆滅�螨水溶性粉劑，結果顯示防治前處理組小黃薊馬平均數量為 6.02 隻，於第一次防治後降至平均 1.04 隻，防治率 87.5%；第二次防治後平均數量為 1.44 隻，防治率 86.2%，且後續調查中觀察到防治效果可長達 6 週，期間內處理組平均數量皆在 6 隻以下。綜合上述結果，蓮花田進行無人植保機防治小黃薊馬，使用 TR80-01 噴頭，配合系統性藥劑於小黃薊馬發生初期進行防治，能有效將藥液帶至葉背，且減少用藥頻率及藥水量。

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

OA_13

蓮花小黃薊馬之空間分布與最適取樣數估算
Spatial distribution and estimates of optimal sample size for *Scirtothrips dorsalis* Hood on lotus

陳盈丞[1]，黃美靜[1]，林金樹[2]
Ying-Cheng Chen[1], Mei-Jing Huang[1] and Chin-Su Lin[2]
[1]行政院農業委員會臺南區農業改良場 Tainan District Agricultural Research and Extension Station
[2]國立嘉義大學森林暨自然資源學系 Forestry and Natural Resources NCYU
Presenting author's email: larvaephage@gmail.com

背景/研究問題/材料方法

害物整合管理(Integrated Pest Management, IPM)是作物保護過程中的一個決策支援系統，其策略架構包括「預防」、「監測與評估」及「干預」等 3 項。而族群數量的監測為掌握蟲害管理決策程序中核心的工作。為提供後續防治基準的判定，本試驗取樣自 110 年 5 月 21 日至 8 月 25 日於雲林縣林內鄉之蓮花田，每週調查一次，共 15 次，每次於田間隨機選取已完全展開之 20 片新葉，其中開花時期隨機選取已完全展開之 60 片新葉，計算蓮葉葉背上小黃薊馬成、若蟲數量，利用樣本變方與平均之比值(S^2/m)、平均擁擠度(mean crowding, *m*)與樣本平均的比值(m/*m*)、Iwao's m-m regression 及 Taylor's power law 等方法分析成、若蟲空間分布類型並估算最適取樣數。

結果/結論/應用啟示

結果顯示 15 次調查所得之空間分布判別指標，包括樣本變方與平均之比值(S^2/m)及平均擁擠度與樣本平均的比值(*m*/m)，自調查第 6 至 15 次不論成、若蟲均大於 1，空間分布為聚集型。但成蟲於第一次調查時兩項比值均小於 1，顯示為均勻型分布，至第 5 次調查時兩項比值均等於 1，此時成蟲為逢機型分布。經由 Iwao's m-m regression 可得知成蟲之方程式截距 α=-6.22，斜率 β=5.14；若蟲之方程式截距 α=174.24，斜率 β=1.79，顯示成、若蟲皆為聚集型分布。其中若蟲個體間對擁擠之忍受性較高，而成蟲個體間初期具有排斥作用。依 Taylor's power law 顯示成蟲及若蟲均為聚集型分布(成蟲:b=1.77, 若蟲:b=1.75)。田間調查數據顯示若蟲樣本平均於第 8 次調查大幅上升，因此以第 7 次調查之若蟲樣本平均 21.6 值估算防治最適時期之取樣數，利用 Iwao's m-m regression 及 Taylor's power law 所得之數值估算最適取樣數，當精密度設在 0.2 時，小黃薊馬平均密度為 20 隻時，最適取樣數分別為 47.8 及 56.0 片葉。因此欲於蓮花田調查小黃薊馬數量，最適取樣數為隨機選取 50-60 片葉。

關鍵詞（Keywords）：小黃薊馬（*Scirtothrips dorsalis* Hood）、空間分布（spatial distribution）、最適取樣數（optimal sample size）、平均擁擠度（mean crowding）

OA_14

以不同介質飼育外米綴蛾生長表現比較
Evaluation of different food substrates for *Corcyra cephalonica*

潘光琦[1]，林立[1]
Kuang-Chi Pan[1] and Li Lin[1]
[1]行政院農業委員會花蓮區農業改良場 Hualien District Agricultural Research and Extension Station COA
Presenting author's email: ahhpan@hdares.gov.tw

背景/研究問題/材料方法

外米綴蛾 (*Corcyra cephalonica* (Stainton)) 為世界廣布之倉儲害蟲，由於其便於飼養、產卵量高等特性，近年來廣泛被作為生物防治天敵昆蟲之食餌或替代寄主使用，國內主要應用於生產赤眼卵寄生蜂。由於昆蟲之大量飼育成本較高，導致售價與推廣難度提升，若能以縮短世代時間或提高出蛾率、產卵率之方式提升外米綴蛾之飼育效率，將有助於降低生產天敵所需成本，利於生物防治之推廣與應用。本試驗使用秈稻與粳稻之糙米與白米，搭配米糠、酵母等添加物作為外米綴蛾之飼育介質，紀錄其成蛾之羽化時間、出蛾率以及成蟲之蟲體重，以比較不同飼育介質之飼育效果。

結果/結論/應用啟示

以 800 克介質飼育結果顯示，使用糙米或白米對外米綴蛾發育時間造成顯著影響，以糙米飼育之米蛾較白米飼育組可提早 8 至 15 日進入羽化期，而使用秈稻白米飼育之雌成蟲平均體重最輕為 0.0181g，其餘為秈稻糙米 0.0235g、粳稻糙米 0.0244g、粳稻白米 0.0256g ，且秈稻白米飼養外米綴蛾所需發育時間亦最長。從介質添加物之試驗中發現，若將碎白米以 9:1 比例混拌米糠，可大幅縮短外米綴蛾之發育時間，且其雌蟲體重（0.0281g）與糙米飼育組（0.0274g）無顯著差異，顯示米糠具有增添外米綴蛾所需養分之效果。此外，以蘇氏人工飼料飼育之米蛾蟲體重顯著大於他組（0.0358g），亦是一值得發展之介質。但由於人工飼料之原料成本較高，未來可著重於探討其最佳之飼育密度、以及重複使用介質的可能性，方可進一步評估其應用於外米綴蛾生產技術之潛力。

關鍵詞（Keywords）：外米綴蛾（*Corcyra cephalonica*）、生物防治（biological control）、大量飼育（mass production）、人工飼料（artificial diet）

OA_15

Interaction of two host-specific begomoviruses in *Bemisia tabaci* and its effect on virus transmission

蘇珊媞[1]，李威樺[1]，黃玉媛[1]，蔡文錫[2]，蔡志偉[1]
Sushanthi Poovendhan[1], Wei-Hua Li[1], Yu-Yuan Huang[1], Wen-Shi Tsai[2] and Chi-Wei Tsai[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
[2] 國立嘉義大學植物醫學系 Department of Plant Medicine, National Chiayi University
Presenting author's email: sushanthip96@gmail.com

背景/研究問題/材料方法

Polyphagous insects may acquire multiple viruses from various infected plants. The interaction between multiple viruses in an insect vector may be classified to be synergistic, antagonistic or neutral and may contribute to a huge shift in the disease epidemics. This study examined the interaction of two host-specific begomoviruses, squash leaf curl Philippines virus (SqLCPV) and tomato yellow leaf curl Thailand virus (TYLCTHV), in their common vector, *Bemisia tabaci*. A series of experiments were conducted to study whether pre-acquisition of one virus affects the acquisition, infection, and transmission of the other. Quantitative real-time polymerase chain reaction was performed to examine the interaction of SqLCPV and TYLCTHV in whitefly body.

結果/結論/應用啟示

Pre-acquisition of SqLCPV and TYLCTHV had no effect on the acquisition of the other virus. However, the titer of TYLCTHV in the midgut and primary salivary gland increased with SqLCPV pre-acquisition, whereas the titer of SqLCPV was suppressed by TYLCTHV pre-acquisition. Transmission of the two viruses to their respective host plants depicted that pre-acquisition of SqLCPV increased the transmission rate of TYLCTHV, whereas the transmission of SqLCPV was suppressed by TYLCTHV pre-acquisition. Altogether, these results provide a basis for future exploration of the molecular mechanism of synergistic interaction of SqLCPV to TYLCTHV and antagonistic response of TYLCTHV to SqLCPV, which would add insights to our existing knowledge of interplay between plant viruses in insect vector.

關鍵詞（Keywords）：acquisition, infection, vector transmission, virus-virus interaction, whitefly

OA_16

臺灣荔枝害蟲(蟎)名錄之修訂
The revised checklist of litchi insects and mites in Taiwan

王泰權[1]，李啟陽[1]，賴柏羽[2]
Tai-Chuan Wang[1], Chi-Yang Lee[1] and Po-Yu Lai[2]
[1]行政院農業委員會農業試驗所應用動物組 Applied Zoology Division, Taiwan Agricultural Research Institute, Council of Agriculture, Executive Yuan. Wufeng, Taichung 413, Taiwan
[2]行政院農業委員會農業試驗所嘉義農業試驗分所植物保護系 Department of Plant Protection, Chaiyi Agricultural Experiment Station, Taiwan Agricultural Research Institute, Council of Agriculture, Executive Yuan. Chaiyi 600, Taiwan
Presenting author's email: insect6925@tari.gov.tw

背景/研究問題/材料方法

本研究進行台灣荔枝害蟲名錄整理，針對於 1943-2008 年間，使用「台灣害蟲名彙」、「台灣植物害蟲名彙」、「台灣和中國大陸果樹害蟲名錄」「植物保護圖鑑系列 16-荔枝保護」共 4 本書籍及有關台灣荔枝害蟲之學術發表所列害蟲(蟎)的種類，並加入實際田間收集的物種資料。害蟲(蟎)的學名比對與校正以全球生物多樣性資訊機構(Global Biodiversity Information Facility)網站資料中查詢，同時進行物種同物異名(synonym)的整理，並針對每種害蟲進行判斷是否為台灣的荔枝害蟲。

結果/結論/應用啟示

本研究共整理出臺灣荔枝害蟲名錄 88 種昆蟲(蟎)，分別為直翅目 1 種、纓翅目 13 種、半翅目 32 種、蜚蠊目 2 種、鱗翅目 29 種、鞘翅目 5 種、雙翅目 2 種及 4 種蛛形綱的害蟎。新入侵有害生物包括荔枝椿象(*Tessaratoma papillosa*)及荔枝癭蚋(*Litchiomyia chinensis*)。文獻所記錄的黑紅捲葉蛾(*Theorica lamyra*)、荔枝擬木蠹蛾(*Squamura dea*)因學名無法找到；相思樹擬木蠹蛾(*Indarbela discipuncta*)、烏龍默袋蛾(*Mahasena colona*)、茶木蛾(*Linoclostis gonatias*)、膠蟲(*Kerria greeni*)、荔枝刺粉介殼蟲(*Planococcus dorsospinosus*)、棉並盾介殼蟲(*Pinnaspis strachani*)、山篩鰓金龜(*Apogonia cribricollis*)無法於台灣物種資料庫中找到而列為存疑種，黑腹果蠅(*Drosophila melanogaster*)於田間觀察無法直接為害荔枝而列為非荔枝害蟲。本研究提供研究荔枝管理之研究人員與農民了解本地荔枝害物資訊，並可作為荔枝外來有害生物檢疫之參考依據。

關鍵詞（Keywords）：荔枝（Litchi）、害蟲（Pests）、蟎（Mite）、名錄（Checklist）、台灣（Taiwan）

醫學昆蟲學/都市昆蟲學

論文宣讀

Oral Session: Medical Entomology / Urban Entomology

OM_01

遠紫外光 (222 nm) 對白線斑蚊生長的影響
Effects of far-UVC light (222 nm) on the development of *Aedes albopictus*

陳盈瑄[1]，蕭旭峰[1,2,3]，蔡坤憲[1,4,5]
Ying-Hsuan Chen[1], Shiuh-Feng Shiao[1,2,3] and Kun-Hsien Tsai[1,4,5]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, College of Bioresources and Agriculture, National Taiwan
[2] 國立臺灣大學植物醫學碩士學位學程 Master Program for Plant Medicine, College of Bioresources and Agriculture, National Taiwan University, Taipei, TaiwanUniversity, Taipei, Taiwan
[3] 國立臺灣大學醫學院法醫學科暨研究所 Department and Graduate Institute of Forensic Medicine, College of Medicine, National Taiwan University, Taipei, Taiwan
[4] 國立臺灣大學公共衛生學院環境與職業健康科學研究所 Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan
[5] 國立臺灣大學公共衛生學系 Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: liney93424@gmail.com

背景/研究問題/材料方法

Mosquito is considered as one of the deadliest animals in the world because of mosquito-borne diseases like malaria, Dengue fever, Zika, Chikungunya, and Japanese encephalitis. Therefore, integrated vector control strategies are in urgent. Ultraviolet C light (254 nm) is used as an effective germicidal lamp, but it is harmful to human skin and eyes. Nowadays, there is a new device with 222 nm far-UVC light, which was also used as microbicidal tool but harmless to mammalian cells. Nevertheless, there are no related researches about using 222 nm UVC light on insects, and we wonder if they can be applied on mosquito control. Investigation on the effects of life stages of mosquitoes was conducted in this study, and 222 nm UVC light was applied to irradiate *Aedes albopictus*. Daily mortality rates and the criteria for nonlethal effects were evaluated.

結果/結論/應用啟示

Larvicidal effect of far-UVC light were convinced. Mortality rates of 100% were observed in the 1st to 4th instars larvae after 15, 60, 90, and 180 seconds of exposure, respectively. Irradiation experiments of eggs did not result in significant differences. Besides, some nonlethal effects were observed after irradiation, such as melanization, anal gill bites, and staggering. Larvae with staggering motion would die later because of the failure in ecdysis or pupation. According to these phenomena, we could further use qPCR with primers related to melanization, juvenile hormone, or ecdysone to quantify the gene expression, and investigate the mechanism of larval death. The results suggested the optimal timing to apply this physical control was at the larval stage. Far-UVC light can be further installed on the bucket and set to activate automatically which could periodically serve as a pesticide-free larvicidal ovitrap.

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

OM_02

利用體腔真菌防治白線斑蚊
Using *Coelomomyces* spp. to control *Aedes albopictus*

林芳伶[1]，蕭旭峰[1,2,3]，蔡坤憲[1,4,5]
Fang-Ling Lin[1], Shiuh-Feng Shiao[1,2,3] and Kun-Hsien Tsai[1,4,5]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, College of Bioresources and Agriculture, National Taiwan
[2] 國立臺灣大學植物醫學碩士學位學程 Master Program for Plant Medicine, College of Bioresources and Agriculture, National Taiwan University, Taipei, TaiwanUniversity, Taipei, Taiwan
[3] 國立臺灣大學醫學院法醫學科暨研究所 Department and Graduate Institute of Forensic Medicine, College of Medicine, National Taiwan University, Taipei, Taiwan
[4] 國立臺灣大學公共衛生學院環境與職業健康科學研究所 Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan
[5] 國立臺灣大學公共衛生學系 Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: yqp20275@gmail.com

背景/研究問題/材料方法

Mosquitoes are great threat to human health because of vector-borne diseases. Conventional insecticides have raised insecticide resistance and adverse environmental impacts. Eco-friendly approaches using entomopathogenic fungi to control mosquitoes have gained an increasing interest. Species in the genus *Coelomomyces* (Blastocladiomycetes: Blastocladiales) are obligatory parasitic fungi, with a life cycle involving alternating hosts of microcrustacean and mosquitoes. *Coelomomyces* species have potential for mosquito control because of their high prevalence and lethal effects to the hosts. Four genomic data of *Coelomomyces* have been published, however, data in Taiwan are limited. Infected *Aedes albopictus* were collected from northern Taiwan, including Guizikeng, Beitou and Taipei Botanical Garden. Afterwards, the resting sporangia of *Coelomomyces* sp. were identified by molecular and morphological characters. Susceptibility of mosquitoes to zygotes was evaluated for their potential on mosquito control.

結果/結論/應用啟示

Coelomomyces sp. was cultured in *Ae. albopictus* and Phyllognathopodidae in the laboratory *in vivo*. Based on the sequences of small subunit rDNA, the collected *Coelomomyces* was 89.29% identical to *C. stegomyiae*. The shape, size and host of resting sporangia of *Coelomomyces* sp. matched those of *C. stegomyiae* var. *stegomyiae*, but the punctae have no depressed margins which characterizing in *C. stegomyiae*. We speculated that it may be a novel species. The susceptibility of the 1st instar larvae was higher than that in the 2nd instar larvae, and the larval mortality exposed in 10^2.43 resting sporangia/ml solution for 3 days was 60±24%. Preliminary results showed that *Coelomomyces* did affect the larval survivorship. The

infected larvae were filled with resting sporangia inside the bodies, melanization was triggered on the cuticle and larval leg in some of them. QPCR will be used to quantify the sporangia which can inhibit the growth of larvae in the on-going study.

關鍵詞（Keywords）：白線斑蚊（*Aedes albopictus*）、體腔真菌（*Coelomomyces*）、生物防治（biological control）、蟲生病原真菌（entomopathogenic fungi）

OM_03

Detection of *Rickettsia* spp. and *Bartonella* spp. in fleas and small mammals in Chiayi and Tainan area in Taiwan

Pei Yun Deng[1], Chuen Fu Lin[2] and Kun Hsien Tsai[1,3]
[1]Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan
[2]Department of Veterinary Medicine, National Pingtung University of Science and Technology, Pingtung, Taiwan
[3]Department of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: r8852030@ntu.edu.tw

背景/研究問題/材料方法

Small mammals in farmland include rodents and shrews, which play major ecological roles of contributing to the ecosystem diversity and consuming plant material and invertebrates. However, small mammals may carry pathogens and are considered important reservoirs of zoonotic diseases. Moreover, they harbor hematophagous ectoparasites serving as vectors of pathogens, such as fleas. Due to their high reproduction rate and rodent-borne diseases that impacted the agricultural economy and public health, the Taiwan Bureau of Animal and Plant Health Inspection and Quarantine (BAPHIQ) used to promote chemical controls to poison small mammals in fields, called the nationwide campaign of the anti-rodent week. To reduce the environmental impact of rodenticides, this campaign had been stopped since 2015. Nevertheless, there is a concern about their proliferation due to a perceived reduction in rodent control efforts. A long-term surveillance program to monitor the population of small mammals, fleas, and the associated pathogens is essential after the cessation of the relevant rodent control measures. In this study, small mammals were captured by using live traps with baits in agricultural fields including Yijhu Township and Lucao Township of Chiayi County and Xuejia District and Yanshui District of Tainan City from 2019 to 2020 bimonthly. A total of 274 spleen samples and 160 fleas from 302 small mammals (seven species) were investigated for potential pathogens including the genera of *Rickettsia* and *Bartonella* and Anaplasmataceae by Polymerase Chain Reaction (PCR). *Rickettsia* spp. were not detected in fleas and spleen samples, using the *gltA* gene and the *ompB* gene.

結果/結論/應用啟示

Bartonella spp. were detected in 78.75% (126/160) of fleas and 19.3% (53/274) of spleen samples, using the *gltA* gene, the *ftsZ* gene, and the *rpoB* gene. *Bartonella rochalimae*-like, *B. tribocorum*-like, *B. elizabethae*-like, *B. queenslandensis*-like, and *Bartonella* spp. were detected, using PCR-RFLP analysis. Besides, 59.5% (75/126) of fleas and 7.5% (4/53) of small mammals carried *B. rochalimae*-like. Anaplasmataceae was detected in 41.25 % (66/160) of fleas and 26.6% (73/274) of spleen samples, using 16S and ITS-23S-5S genes. Periodic investigations of wild small mammals and pathogenic detections are important for the

prevention of rodent-borne disease, providing data to formulating effective strategies of prevention and control in the future.

關鍵詞（Keywords）：small mammals, *Rickettsia*, *Bartonella*, RFLP

OM_04

Neglected phthiriasis in Taiwan: a case of *Pthirus pubis* hyperinfestation, comparative morphological and molecular identification, and retrospective clinical case series

Yu-Feng Tsai[1], Chia-Wen Lee[2], Wen-Jer Wu[3] and Kun-Hsien Tsai[1, 3, 4]
[1] Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan
[2] Fengshan Lee Chia Wen Urologic Clinic, Kaohsiung, Taiwan
[3] Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan
[4] Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: f07632001@ntu.edu.tw

背景/研究問題/材料方法

Pubic or crab lice, *Pthirus pubis* (Linnaeus, 1758), feed on human blood and are known solely as a human ectoparasite that often infests pubic hair (phthiriasis pubis) and eyelashes (phthiriasis palpebrarum). The primary route of transmission of pubic lice is through sexual or intimate contact. The clinical manifestations of phthiriasis include pruritus, allergic reaction, and post-inflammatory hyperpigmentation. Here, we present a case of *Pt. pubis* hyperinfestation, review the clinical case reports and demonstrate molecular identification using *Pt. pubis* specimens collected from pubic regions of 9 patients. In addition, a retrospective investigation was performed by reviewing 126 cases in Kaohsiung from 2016 to 2021 to reveal the epidemiological characteristics of phthiriasis in Taiwan.

結果/結論/應用啟示

A 70-year-old man came to the clinic with a complaint of severe itching in the pubic region. He reported receiving a full-body massage. More than a thousand *Pt. pubis* were found on the hairs in his pubic and anal regions. In Taiwan, the clinical case report of phthiriasis was documented sporadically. A total of 11 cases were reported in 8 articles in Taipei, Taichung, and Chiayi from 1942 to 2012. One was parasitized in the pubic region, 3 were with phthiriasis palpebrarum, 1 was with phthiriasis capitis, 1 was with both phthiriasis palpebrarum and phthiriasis capitis, and 5 were parasitized in both the eyelashes and pubic regions. On the other hand, 27 pubic lice from 9 cases were analyzed using molecular methods to target the cytochrome c oxidase subunit I (*COI*) gene and the pathogenic *Rickettsia* or *Acinetobacter* that pubic lice carry. Sequencing results suggested a lack of diversity. Compared with references in the NCBI database, the sequences were discovered identical to those in the suburbs of Paris, France and Florida, United States. PCR analysis of pathogenic *Rickettsia* or *Acinetobacter* yielded negative results. From 2016 to 2021, 126 patients, including 118 males (93.65%) and 8 females (6.35%), were diagnosed with phthiriasis in a single clinic in Kaohsiung, with an average of 2 cases per month. Among them, 16 patients (12.70%) were 15-24 years old, 84 patients (66.67%) were 25-44 years old, 22 patients (17.46%) were 45-64 years old, and 4

patients (3.17%) were over 65 years old. This study showed that phthiriasis has not been eliminated in Taiwan, but was neglected. Future clinical studies are needed in other parts of Taiwan to establish basic medical entomological knowledge and facilitate public health education.

關鍵詞（Keywords）：*Pthirus pubis*, phthiriasis, *COI* barcode, sexually transmitted diseases, *Rickettsia*

OM_05

六伏隆白蟻餌劑在養菌白蟻防治上的應用

Application of hexaflumuron termite bait in controlling fungus-growing termites

邱俊禕[1]，莊雅惠[2]，梁維仁[1]，葉信廷[3]，楊小瑩[4]，蔡明哲[3,5]，Neil A. Spomer[6]，李後鋒[1]

Chun-I Chiu[1], Ya-Hui Chuang[2], Wei-Ren Liang[1], Hsin-Ting Yeh[3], Hsiao-Ying Yang[4], Ming-Jer Tsai[3,5], Neil A. Spomer[6] and Hou-Feng Li[1,7]

[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University

[2] 國立中興大學土壤環境科學系 Department of Soil and Environmental Sciences, National Chung-Hsing University

[3] 國立臺灣大學生物資源暨農學院實驗林管理處 The Experimental Forest, College of Bio-Resources and Agriculture, National Taiwan University

[4] 行政院農業委員會茶業改良場凍頂工作站 Dongding Station, Tea Research and Extension Station, Council of Agriculture, Executive Yuan

[5] 國立臺灣大學森林環境暨資源學系 School of Forestry and Resource Conservation, College of Bio-Resources and Agriculture, National Taiwan University

[6] 美國科迪華農業科技 Corteva™ Agriscience, Indianapolis, USA

Presenting author's email: tim77918@msn.com

背景/研究問題/材料方法

養菌白蟻 (fungus-growing termite) 為熱帶及亞熱帶地區常見的農業害蟲，土壤殺蟲劑灌注為其主要的防治方法，較少應用白蟻餌劑進行防治。本研究為評估以餌劑防治養菌白蟻之效力，於一公頃林地樣區內以 5 公尺等距之方式安裝 484 根木樁每月持續監測台灣土白蟻 (*Odontotermes formosanus*) 之取食頻率並於樣區內以 15 公尺等距之方式投入共 36 根長效型六伏隆 (hexaflumuron) 餌劑進行防治。為確認六伏隆傳遞至蟻巢且造成蟻巢死亡，於監測期間內採集死亡蟻巢樣本，以 LC-QTOF/MS 分析內含之殺蟲劑成分。

結果/結論/應用啟示

結果顯示，台灣土白蟻於 10 個月內取食約 50%的白蟻餌劑、於 2 年內取食 90%的白蟻餌劑。於投藥後的第二年，木樁上的每月白蟻發生率從 34.7±1.8 根降至 17.6±2.5 根，降低約 49.1%，而木樁的每月白蟻取食量則從 17.7±0.8 根降至 13.3±1.2，降低約 25.7%。於兩個死亡蟻巢共 5 個菌圃及菌圃上生長的炭角菌 (*Xyleria* sp.) 中偵測到六伏隆，濃度為 0.31–20.11 mg kg-1 乾重。根據以上結果，六伏隆可傳遞至養菌白蟻蟻巢造成蟻巢死亡，而長效型六伏隆餌劑可有效防治廣域的養菌白蟻族群。相較於傳統的土壤殺蟲劑灌注防治方法，利用白蟻餌劑防治有專一性，可降低對環境其他節肢動物之影響。.

關鍵詞（Keywords）：六伏隆（hexaflumuron）、諾伏隆（noviflumuron）、廣域白蟻餌劑防治（area-wide termite baiting）、養菌白蟻（fungus-growing termite）、綜合害蟲管理（integrated pest management）

OM_06

熏香對埃及伊蚊影響的初步研究

Preliminary studies on the effects of Taiwanese ritual smoke on *Aedes aegypti*

Ching-Yu Shu[1], Hsueh-Lien Lai[1], Pei-Yin Lin[2], Kevin Chi-Chung Chou[2] and Matan Shelomi[1]

[1] 國立臺灣大學昆蟲系 Department of Entomology, National Taiwan University

[2] 國立臺灣大學生物資源暨農學院共同儀器中心 Joint Center for Instruments and Researches, National Taiwan University

Presenting author's email: mshelomi@ntu.edu.tw

背景/研究問題/材料方法

Smoke from burning plants is a traditional spatial repellent against insects worldwide. Smoke is also commonly used in religious rituals. In Chinese folk religion and Taoism as practiced in Taiwan, Asiatic wormwood leaves, agarwood incense sticks, and joss paper ("ghost money") are often burned or carried to pray for health or at festivals that overlap with peak mosquito seasons. The possibility exists that some of these rituals became popular due to repellent effects of the smoke reducing the impact of insect-vectored pathogens. The effects of these smokes on the Dengue-vectoring mosquito *Aedes aegypti* (Linnaeus, 1762) (Diptera: Culicidae) was measured following the World Health Organization guidelines for spatial repellency testing. The chemical constituents of the smoke were identified using a solid-phase microextraction fiber for extraction followed by gas chromatography/mass spectrometry.

結果/結論/應用啟示

Smoke from wormwood weakly repelled mosquitoes and had some knock-down effects. Smoke from incense showed consistent but weak repellency effects, with no knock-down. Smoke from joss paper had no effect overall, with some mosquitoes seemingly attracted to the flames. While air pollution remains a concern regarding smoky incense, the possibility that mosquito-repelling volatiles can be isolated from the incense and utilized without smoke justifies deeper investigation into the source of these repellent effects.

關鍵詞（Keywords）：埃及伊蚊（*Aedes aegypti*）、煙（smoke）、香（incense）、空間排斥（spatial repellency）、揮發性有機化合物（volatile organic compounds）

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

Gut anatomy and micro-anatomy of several beetle species over their life cycle

江旻柔[1]，薛馬坦[1]
Min-Rou Chiang[1] and Matan Shelomi[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: r08632012@ntu.edu.tw

背景/研究問題/材料方法

Holometabolous insects such as beetles radically change their form as they metamorphosize from larvae to pupae to adults. The most significant change is during the pupal stage as they adapt for their adult habitats and feeding habits. In addition to their external appearance, their internal structures, such as the digestion tract, will change in pupal stage. There is surprisingly little literature about the morphology of the digestive system during the pupal stage, and how it changes. Thus, the aim of my research is observing the gut transformation across a holometabolous insects life cycle. Using light and electron microscopy, I examined changes in the digestive tract macro- and micro-structure in several life stages in these easily-reared Scarabaeidae beetles as the focus of my experiments: *Thaumastopeus shangaicus* (Cetoniinae), three species of *Protaetia* (Cetoniinae), and *Oryctes rhinoceros* (Dynastinae).

結果/結論/應用啟示

Our preliminary results show that these beetles' digestion tracts changes across the life cycle, in each instar becoming longer and thinner until the adult stage. The transformation of the digestion tract is complete by the later period of pupal stage, when it resembles the digestion tract in the adult. The larval beetles' hindguts have a thin ileum, a large fermentation chamber lined internally with a microbial biofilm, and a thin rectum. The biofilm grows larger with each molt. The hindgut forms an S-shape, with fermentation chamber directed backwards compared to the rest of the gut. The rectum and ileum are physically touching in the Cetoniinae. Research is ongoing at this time.

關鍵詞（Keywords）：holometabolism, gut morphology, gut transformation, flower chafers

PB_02

逆襲的象鼻蟲——生態棲位模擬揭示澳洲蘇鐵蛀莖象鼻蟲入侵臺灣的潛在風險

Weevil attack: niche modelling highlights risks of potential invasion of Australian trunk-boring cycad weevils in Taiwan

蕭昀[1,2]，廖治榮[3]
Yun Hsiao[1,2] and Jhih-Rong Liao[3]
[1] 澳大利亞聯邦科學與工業研究組織—澳洲國立昆蟲標本館 Australian National Insect Collection, CSIRO, Australia
[2] 澳洲國立大學生物學研究院生態暨演化學部 Division of Ecology and Evolution, Research School of Biology, The Australian National University, Australia
[3] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: yunhsiao@outlook.com

背景/研究問題/材料方法

Biological invasion can cause serious economic issues for humans and ecological influences on native biota. Cycads (Cycadales) are palm-like gymnosperms, with some species commonly used in horticulture but many of them included on the IUCN Red List. In Taiwan, the endemic *Cycas taitungensis* is protected by government regulations, and Hongye Village in Taitung has been designated as the natural reserve for this plant. Australian trunk-boring cycad weevils of *Demyrsus* and *Siraton* sometimes can be transported beyond their natural geographical barriers to other countries and are considered as significant cycad pests due to their recorded infestation of non-Australian cycad genera in foreign countries. Ecological niche modelling (ENM), also known as species distribution modelling, is a practical tool for estimating species niche based on environmental factors. In this study, we assess the suitability of natural habitats on Taiwan for invasion by Australian cycad-boring weevils using the maximum entropy modelling (MaxEnt), aimed at determining the risks of potential establishment of these weevils on the island.

結果/結論/應用啟示

The results show that the potential distribution area of *D. meleoides* includes most mountainous regions except in northern and southwestern Taiwan, and that of *S. internatus* includes lowland to mid-altitude mountainous regions in both northwestern and eastern Taiwan. The niche modelling reveals that *D. meleoides* has the potential to establish populations in Taiwan due to the existence of large areas of suitable habitats. The prediction also suggests that the Taitung Hongye Village Taitung Cycas Nature Reserve contains suitable habitats for *S. internatus*, which had infested *C. revoluta* in the U.S.A., identifying another possible threat to Taiwan's endemic cycads.

關鍵詞（Keywords）：澳洲（Australia）、生物入侵（Biological invasion）、蘇鐵害蟲（Cycad pest）、生態棲位模擬（Ecological niche modeling）、象鼻蟲（Weevils）

PB_03

造癭強度與其寄主植物誘導植化物質之關係:以長葉楠姬布癭蚋(*Bruggmanniella litseae*)蟲癭為例

The effect of galling intensity of *Bruggmanniella litseae* on phytochemicals of *Litsea acuminate*

王克軒[1]，楊曼妙[1]，黃盟元[2]
Charles Ko-Hsuan Wang[1], Man-Miao Yang[1] and Meng-Yuan Huang[2]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
[2] 國立中興大學生命科學系 Department of Life Science, National Chung Hsing University
Presenting author's email: wangcharles89@gmail.com

背景/研究問題/材料方法

蟲癭是由造癭昆蟲刺激植物體，形成不正常增生的植物組織，其生理機制受到造癭昆蟲調控，而植物受到造癭昆蟲的造癭行為刺激，會被動產生化學物質，以調節植物體內的生理平衡，以及對抗食葉昆蟲的取食。由過去生態調查發現，被造癭葉片蟲癭的數量並不固定，具有造癭強度上的差異，因此，透過分析植物葉片光合作用與防禦反應相關的化學物質，及測量葉片受食葉昆蟲取食面積，研究葉片對於不同造癭程度之光合能力和逆境表現差異，以及蟲癭周圍葉片受非造癭昆蟲取食之情形。

本研究以長葉木薑子及其造癭者 *Bruggmanniella litseae* 作為研究材料，對照組為無蟲癭葉片，實驗組為帶有蟲癭之葉片，將蟲癭從葉片切除，以葉片上蟲癭數量作為造癭強度指標，依原帶有蟲癭葉片上具有 1、2、3、4、5-6、7 個以上的蟲癭分成六組，掃描葉片並利用 imageJ 軟體計算植食性危害面積及還原危害前之總面積，及測定葉綠素 a+b、類胡蘿蔔素、多酚和類黃酮四種植化物質，利用 RStudio 進行數據分析，比較不同造癭強度之葉片大小和植物化學物質的關係，並嘗試釐清寄主植物光合作用與防禦反應是否受造癭強度不同而有區別。

結果/結論/應用啟示

結果顯示總葉面積因造癭強度越高而增加，光合色素不會因造癭強度有變化，顯示蟲癭數量不影響植物光合作用，防禦物質中抗植食性昆蟲的多酚含量會因造癭強度提升而增加，造癭昆蟲能提高對食葉昆蟲的防禦能力，但食葉昆蟲危害葉面積未有減少的趨勢，未來將探討被造癭葉片受食葉昆蟲取食與否所誘導的防禦代謝物之含量差異。

關鍵詞（Keywords）：長葉木薑子（*Litsea acuminate*）、造癭強度（Galling intensity）、植化物質（Phytochemicals）、昆蟲與植物交互作用（Insect-plant interaction）、防禦代謝物（Defense metabolites）

PB_04

追溯台灣的大燕蛾(鱗翅目：燕蛾科)，一種最大的迷蛾的地理起源

Tracking the geographical origin of *Lyssa zampa* (Lepidoptera: Uraniidae), the largest stray moth in Taiwan

顏聖紘[1]，王崇羽[1]，徐碩謙[1]
Shen-Horn Yen[1], Chung-Yu Wang[1] and Shuo-Chian Shiu[1]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

Various species of butterflies and moths are known to undergo long-distance dispersal or passive transport by prevailing winds. Previously most studies regarding the origin of such species focus on migratory butterflies and several medium- to small-sized moths which are regarded as migratory pests, such as fall armyworm. Among the studied species, many moths are polyphagous and the resources for survival and sustainable reproduction are available so that the migration becomes rationale. However, there is a case that the moth, which is a specialist, is often dispersed from tropical to subtropical or temperature region by wind, but the hostplant resource does not exist in the destination. The moths of the genus *Lyssa* are giant nocturnal species that occur from India, Indochina, southern China, and the Indo-Australian tropics. A species of the genus, namely *Lyssa zampa*, has 3-4 subspecies ranging throughout the southeast Asia. Since 1985, near 300 individuals have been recorded in Taiwan and the timing was strongly associated with the typhoons in each year. In order to clarify the source of the *Lyssa zampa* found in Taiwan, we reconstructed the phylogeny of 5 species of *Lyssa* (including 34 samples from Taiwan) and 1 species of Microninae by using the COI sequence data. We wish to elucidate whether all the *Lyssa* samples found in Taiwan belong to the same subspecies or species, and blown to Taiwan from the same region.

結果/結論/應用啟示

Our analysis shows that the Taiwanese samples belong to the nominotyipcal subspecies of *Lyssa zampa*, and most of the sources are not the Philippines. This finding reveals that Indochina can be a possible source of migratory moths of Taiwan, and the role of southwesterly flow in shaping the biogeographical pattern of Taiwan might have been underestimated.

關鍵詞（Keywords）：西南氣流（southwesterly flow）、長距離播遷（long distance dispersal）、颱風（typhoon）、燕蛾科（Uraniidae）、氣候變遷（climate change）

PB_05

校園封閉對病媒蚊族群之影響—以國立中興大學為例
The influence of campus closed on vector mosquitoes population, a case in National Chung Hsing University

鄭中涵[1]，黃紹毅[1]
Chung-Han Chang[1] and Shaw-Yhi Hwang[1]
[1] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: a0909348926@gmail.com

背景/研究問題/材料方法

2021 年 5 月 28 日(第二十週)因全國三級警戒，使學校等公共場所開始進行人流管制，間接減少了蚊子的食物來源。為了瞭解校園封閉對病媒蚊族群有無顯著影響，本研究於國立中興大學以病媒蚊誘卵桶對白線斑蚊(*Aedes albopictus*)族群進行長期的監測，探討病媒蚊族群的大小與可能的影響原因；並於 9 月 1 日(第三十五週) 進行病媒蚊孳生源的清除，評估其對病媒蚊族群的影響。

結果/結論/應用啟示

截至第三十四週結束，每週平均卵數為 1,320.0 ± 843.2 顆，與 2020 年同時期相比，2020 年每週平均卵數 1,380.3 ± 903.9 顆，兩年相差不大。病媒蚊卵數於第十四週開始顯著提高，校園管制期間(第二十週~第三十四週)仍較管制前(第十四週~第十九週)顯著上升。而梅雨季節(第二十二週~第二十六週)與颱風季節(第二十三週~第三十四週)間並無顯著差異，但是雨季(梅雨季+颱風季)相較雨季前(第十四週~第二十一週)則顯著下降。第三十五週共發現 97 個孳生源及 41 個陽性孳生源，容器指數為 29.7%(第七級)，清除後單週病媒蚊的總卵數由 1,668 顆降至 1,143 顆，但實際的影響仍需累積數據後才能得知。綜上所述，校園封閉對病媒蚊族群並無顯著影響，氣溫及雨量才是影響族群的主因。

關鍵詞（Keywords）：白線斑蚊（*Aedes albopictus*）、病媒蚊監測（vector mosquitoes surveillance）、疫情（epidemic）、誘卵桶（ovitrap）、族群變動（population dynamic）

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

PS_01

擬硬象天牛（*Doliops* spp.）與球背象鼻蟲（*Pachyrhynchus* spp.）的擬態相似度與共演化關係

Mimetic similarities and coevolution between *Pachyrhynchus* weevils and *Doliops* longhorn beetles

孫誼[1]，陳彭珉[1]，吳立偉[2]，顏聖紘[3]，曾惠芸[1]
Yi Sun[1], Shan-Min Chen[1], Li-Wei Wu[2], Shen-Horn Yen[3] and Hui-Yun Tseng[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
[2] 東海大學生命科學系 Department of Life Science, Tunghai University
[3] 國立中山大學生命科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: b06612042@ntu.edu.tw

背景/研究問題/材料方法

防禦型擬態是種複雜的生物間交互作用，並由擬態者（Mimic）、模式物種（Model）以及掠食者（Predator）共同參與塑造。擬態者會展示出與模式物種相似的特性，如形態外觀、顏色、行為、聲音、化學氣味，並藉此誤導掠食者，使其無法分辨擬態者與模式物種，並使擬態者分享模式物種的利益而獲得保護並提高其適存度（Fitness）。擬硬象天牛（*Doliops* spp.）經常被視為球背象鼻蟲（*Pachyrhynchus* spp.）的貝氏擬態者之一，研究亦證實了球背象鼻蟲身上的花紋顏色以及保護機制能有效使掠食者學習並降低捕食率，然而過去除了由研究者根據人類視覺狀態主觀描述兩造之間的斑紋相似度外，並無使用現代方法支持其擬態關係假說，且未墨於兩類群間的演化關係。本研究在假設擬硬象天牛與球背象鼻蟲的關係為精確擬態的前提下，利用視覺模型檢測多組先前文獻推測的天牛-象鼻蟲擬態群在斑紋的顏色之相似度，透過電腦模擬在多種掠食者的視覺系統下，掠食者能否區分兩者斑紋的顏色差異。並利用分子證據（全粒線體基因組）重建這兩類群的演化樹，比較兩者間演化關係來探討模式物種與擬態者間可能的共演化相關性與演化歷程。

結果/結論/應用啟示

由於在電腦模擬多種掠食者視覺系統之下，多組擬硬象天牛與球背象鼻蟲的 JND 值皆小於 1，這個結果顯示鳥類與蜥蜴等掠食者無法分辨擬硬象天牛與球背象鼻蟲間斑紋的顏色差異。這也就是說擬硬象天牛所具備的斑紋的顏色應可有效欺騙掠食者，而這種研究策略也有別於傳統主觀的描述，以可被量化的視覺模擬證據來支持擬硬象天牛與球背象鼻蟲間的擬態關係假說。初步親緣關係樹比較發現，親緣關係相近的天牛並未擁有相似的形態特徵，反而與為其模式物種的球背象鼻蟲有較相似的形態特徵，因此推論擬硬象天牛可能受到強烈選汰壓力，使其演化出與球背象鼻蟲相似的形態特徵。

關鍵詞（Keywords）：球背象鼻蟲（*Pachyrhynchus*）、擬硬象天牛（*Doliops*）、擬態（Mimicry）、掠食者視覺模型（Predator visual model）、全粒線體基因組（mitochondrial genome）

PS_02

利用親緣基因體學探討球背象鼻蟲屬親緣關係與擬態
Phylogenomics and mimetic relationship of *Pachyrhynchus* weevils

陳彭珉[1]，孫誼[1]，Ace Kevin S. Amarga[2]，Reagan Joseph T. Villanueva[3]，曾惠芸[1]
Shan-Min Chen[1], Yi Sun[1], Ace Kevin S. Amarga[2], Reagan Joseph T. Villanueva[3] and Hui-Yun Tseng[1]
[1] 國立臺灣大學 National Taiwan University
[2] 國立臺灣師範大學 National Taiwan Normal University
[3] 民答那峨大學 University of Mindanao
Presenting author's email: sammychen3786@gmail.com

背景/研究問題/材料方法

生物身上的斑紋與色彩是物種種內、種間或與環境間交互作用的複雜訊號，了解這些特徵的演化有助於理解選汰壓力對斑紋與色彩的影響。球背象鼻蟲屬（*Pachyrhynchus*）具有多樣的色彩斑紋，而這些特徵與警戒色或隱蔽有關。在球背象鼻蟲屬的不同物種常具備類似的色彩斑紋，然而，對於這些特徵的演化仍不清楚，加上球背象鼻蟲屬的親緣關係仍然缺乏完整的研究，因此本研究欲藉由親緣基因體學的方式重建球背象鼻蟲的親緣關係，釐清色彩的演化以及擬態的關係。本研究使用鞘翅目專用的超保守元素（UCE）大量定序目標基因座，共取樣 115 隻球背象鼻蟲重建親緣關係。此外，本研究亦分析球背象鼻蟲的色彩距離與光譜以研究色彩斑紋的演化。

結果/結論/應用啟示

在所有樣本中，平均回收 608（125-782）個 UCE 基因座。球背象鼻蟲的親緣關係在不同的數據矩陣（50%和 70%）以及分析方法（ML 和 BI）所得到的結果大多是一致的。然而過去由形態所定義的物種群與本研究分析結果並不一致。另外，顏色的分析中發現大部分的顏色及斑紋是獨立演化而來，顯示穆氏擬態確實多次發生於球背象鼻蟲屬內。斑紋光譜分析顯示擬態對之間的色彩並沒有顯著的差異。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，並初步了解多樣化色彩斑紋的演化。

關鍵詞（Keywords）：球背象鼻蟲（*Pachyrhynchus* weevils）、超保守元素（ultraconserved elements）、親緣分析（Phylogenetic analysis）、色彩斑紋（color pattern）、擬態（mimicry）

PS_03

利用次世代定序從博物館典藏樣本中獲取粒線體基因體進行譜系關係研究

Two complete mitochondrial genomes of Papilio butterflies obtained from historical specimens (Lepidoptera: Papilionidae)

鄭明倫[1]，陳明玉[2]，吳立偉[2]
Ming-Luen Jeng[1], Ming-Yu Chen[2] and Li-Wei Wu[2]
[1] 國立自然科學博物館生物學組 Department of Biology, National Museum of Natural Science, Taichung, Taiwan
[2] 東海大學生命科學系 Department of Life Science, Tunghai University. Taichung, Taiwan
Presenting author's email: liweiwu@go.thu.edu.tw

背景/研究問題/材料方法

Museum specimens are collected for education, exhibition, and various multiple scientific purposes. However, millions of specimens remain in their collection boxes for years without being analyzed. Historical specimens have been known to contain low-quality DNA; hence, it is difficult to utilize their sequence information in phylogenetic studies. However, recent advances in high throughput sequencing (HTS) make these collections amenable to phylogenomic studies. In this study, two historical specimens (*Papilio xuthus* Linnaeus, 1767, and *Papilio thoas* Linnaeus, 1771) were sampled and DNA extracted for high throughput sequencing via the Miseq platform.

結果/結論/應用啟示

Two complete mitogenomes were assembled, even though the DNA quality of those specimens was highly fragmented, below 250 bp in length. The 37 genes of 60 mitogenomes were aligned and used for inferring the phylogenetic relationships of Papilioninae. These two newly sequenced mitogenomes are correctly grouped in the genus *Papilio*, and this result indicates that historical specimens shows great potential for phylogenetic studies with HTS technology. Our results demonstrated that with the HTS technology, extracting DNA data from historical specimens warrants more investigation and further studies of mitogenomic sequences in museum collection are recommended.

關鍵詞(Keywords)：meta-genomics, mitogenomic phylogeny, low-quality DNA, Papilionini, ancient DNA

PS_04

DNA 條碼與形態學證據揭露台灣的禾本科作物田間有三種黏夜蛾族昆蟲
DNA barcode and morphology reveal that three species of Leucaniini occur in Poaceae croplands in Taiwan

顏聖紘[1]，王崇羽[1]，謝佳宏[2]
Shen-Horn Yen[1], Chung-Yu Wang[1] and Chia-Hung Hsieh[2]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
[2] 中國文化大學森林暨自然保育學系 Department of Forestry and Nature Conservation, Chinese Culture University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

The tribe Leucaniini comprises 563 medium-sized noctuid species placed in 3 genera and has a cosmopolitan distribution. The larvae of the entire tribe are exclusively Poaceae-feeders so that the rise and diversification of the tribe are considered relevant to the evolutionary success of Poaceae after the late Cretaceous. In Taiwan, at least 48 species of the genus *Mythimna* are recognized. Despite of their incredible high diversity, many of the species, however, are also considered significant pests in field. The chaos in their taxonomic identity and identification has also increased challenges in pest management and monitoring. Since June, 2019, when *Spodoptera frugiperda* (FAW) started to invade Taiwan, a long term monitoring action has been initiated by using pheromone lure for attracting FAW. We incidentally found that in some areas, the moths of Leucaniini were abundant in corn and rice fields, but local farmers and researchers were unfamiliar with them and the information regarding identification and control were either confusing or lacking. For the purpose of pest management, it has become necessary to identify the species being detected in croplands. We reconstructed the phylogeny of Taiwanese Leucaniini by including most of the COI sequences of the tribe from GenBank and BOLD systems and employed Maximum Likelihood and Bayesian estimation as the tree-building criteria.

結果/結論/應用啟示

The resulting phylogeny suggests that *Mythimna* and *Leucania* are separate genera and both are distinguishable from each other based on male genitalia, but not on female genitalia, wing pattern and larval morphology. Three species, namely *Mythimna separata* (corn), *Mythimna loreyi* (rice) and *Leucania roseilinea* (rice) are confirmed to infest Poaceae croplands in Taiwan. The phylogenetic analysis also suggests the necessity to revised the classification of the Leucaniini in Taiwan in order to stabilize the uses of scientific names in agricultural literature and to enhance information circulation.

關鍵詞（Keywords）：夜蛾科（Noctuidae）、系統分類（systematics）、蛀莖性昆蟲（stem borer）、親緣關係學（phylogenetics）、禾本科（Poaceae）

PS_05

寬肩蝽亞科(半翅目:寬肩蝽科)臺灣首次紀錄
First record of the subfamily Veliinae (Hemiptera: Veliidae) in Taiwan

劉興哲[1]，胡芳碩[1,2]
Hsing-Che Liu[1] and Fang-Shuo Hu[1,2]
[1] 臺灣昆蟲同好會 Taiwanese Society of Insect Natural History
[2] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: td965771@gmail.com

背景/研究問題/材料方法

寬肩蝽科 (Veliidae) 是棲息於水面的小型半水棲昆蟲 (semi-aquatic insect)，該科中的寬肩蝽亞科 (Veliinae) 包含了寬肩蝽科中最大型的種類，體長大多為 4 至 7 毫米，其中的齒臀寬肩蝽屬 (*Angilovelia*) 由 Andersen 根據東南亞的標本於 1981 年所建立，目前該屬僅 1 種，且分布非常侷限，僅分布於香港、中南半島、印度(阿薩姆邦)。本次研究首次發現齒臀寬肩蝽屬分布於臺灣，亦為臺灣首次寬肩蝽亞科的報導，將臺灣的寬肩蝽種類增加至 4 亞科，分別為寬肩蝽亞科、小寬肩蝽亞科 (Microveliinae)、礁寬肩蝽亞科 (Haloveliinae)、裂寬肩蝽亞科 (Rhagoveliinae)，共計 4 亞科 7 屬 14 種。

結果/結論/應用啟示

本次研究針對臺灣本島與金門群島的靜水濕地做調查，共發現 1 屬 1 種的寬肩蝽亞科成員，此種為齒臀寬肩蝽屬的丫紋齒臀寬肩蝽 (*Angilovelia yalba* (Paiva, 1918))，體長約 5 毫米，前胸背板具大點刻且邊緣鈍角，上翅基部兩側與末端具白斑，足部深色與淺色相間，後足近基部處佈滿深色微刺，在臺灣分布於金門本島與宜蘭縣，本文另提供物種的特徵照片、線圖及文字描述，在臺灣的棲息環境皆為水生植物密集的靜止水域，數量稀少且不群聚。根據文獻與標本資訊顯示出臺灣的齒臀寬肩蝽屬皆為該屬緯度最北的分布範圍。

關鍵詞（Keywords）：水棲昆蟲（aquatic insect）、新紀錄（new record）、金門群島（Kinmen islands）、齒臀寬肩蝽屬（*Angilovelia*）、半翅目（Hemiptera）

PS_06

大紫蛺蝶(鱗翅目：蛺蝶科)亞種間之親緣關係及其在協助鑑識流通於國際貿易中蝶類標本的意涵

Phylogenetic relationship of the subspecies of *Sasakia charonda* (Lepidoptera: Nymphalidae) and its application on identification of the butterfly taxidermy in trade

顏聖紘[1]，王崇羽[1]
Shen-Horn Yen[1] and Chung-Yu Wang[1]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

Among all the butterfly species protected by the Wildlife Conservation Law (WCL) in Taiwan, *Sasakia charonda* is the only one that has multiple subspecies, wide distribution in E. Asia, and distinct trade patterns in different areas. *S. c. charonda*, the nominotypical subspecies in Honshu (Japan) is common and local trading and collecting are not prohibited. *S. c. coreana* from Korean peninsula and NE China and *S. c. yunnanensis* from Vietnam and SW China are currently heavily harvested for butterfly taxidermy. The Taiwanese *S. c. formosana*, of which the hunting is now strictly banned by WCL since 1989 was heavily harvested for specimen trade. Identification of the butterfly taxidermy using this species circulated in trade has recently become important in the aspect of verification of the legal status of the specimens in trade. However, most of the Sasakia specimens in trade are not labelled with locality and the wing patterns are not useful for subspecies discrimination. It is therefore necessary to investigate the validity and relationship among the subspecies and verify the utility of morphological characters in defining the subspecies.

結果/結論/應用啟示

We attempted to extract mitochondrial DNA from various individuals of the subspecies from Hokkaido, Honshu, Taiwan, NE China, SW China (Guangxi, Yunnan) and Vietnam to clarify the phylogenetic relationship among them. We then included some specimens from butterfly taxidermy and without locality in the analysis. The results suggest that all the specimens being traded in recent years were collected from NE China, SW China and N. Vietnam. The Taiwanese subspecies was once used for butterfly artwork, but it has not been used in butterfly specimen artwork since 1990s. However, we also found that the differentiation among subspecies varies a lot and the subspecies classification of this species is in need of major revision.

關鍵詞（Keywords）：瀕危物種（endangered species）、標本貿易（specimen trade）、蛺蝶科（Nymphalidae）、野生動物保育法（Wildlife Conservation Law）、博物館典藏（museum collection）

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

PE_01

評估如何利用鳥類掠食者進行昆蟲警戒性與擬態之行為學測試
Evaluation of the uses of avian predators in behavioral tests of insect aposematism and mimicry

陳俊博[1]，顏聖紘[1]
Jun-Bo Chen[1] and Shen-Horn Yen[1]
[1] 國立中山大學 National Sun Yat-Sen University
Presenting author's email: m082010002@g-mail.nsysu.edu.tw

背景/研究問題/材料方法

動物體色花紋的功能通常具有多種面相，除了熱能調節、性擇、種內競爭之外，禦敵是最重要的功能之一。而對於昆蟲而言，使用體色進行防禦的方式大致上能分為警戒性、隱蔽性和擬態三種。警戒性是使用顯眼的色彩或高度對比的紋路，搭配自身所擁有毒素來降低掠食者攻擊的機率。隱蔽性是藉由模仿與環境相似的顏色，來混淆掠食者的視覺判斷。擬態則將自己模仿成特定的物種，以此來欺騙掠食者來達到生存的目的。然而體色花紋的禦敵機制並不能由人類認知來判斷，因此掠食者的反應是評估動物體色花紋功能的重要依據。其中鳥類是最常做為測試昆蟲禦敵機制的掠食者，因為鳥類具有發達的視力能辨別昆蟲體色的差異，也具有強大的學習能力來去回想過去的經驗以迴避有害的獵物。但在過往的研究當中，大部分的討論多著重在獵物體色所代表的意涵，少有針對掠食者本身現有的問題來進行整理與討論。因而導致隨著研究者與研究對象的不同，掠食者的種類、數量、性別、行為差異、年齡與實驗方法也隨之不同，進而導致之後的研究難與先前的試驗結果進行衡量與比較的基準。為了瞭解在不同試驗中鳥類掠食者的使用情況，此次研究將收集有關昆蟲警戒性與擬態機制的文獻，並藉由實驗方法歸納出多種不同以鳥類做為掠食者的研究，試圖釐清不同試驗目的與試驗設計對鳥類掠食者用途的要求條件與差異。

結果/結論/應用啟示

在鳥類的研究中，許多證據表明有許多不同的因數會影響鳥類的判斷。例如：年齡、性別、經驗與環境等等。但是許多使用鳥類作為警戒性的掠食者大多鮮少為上述因子進行統整與比較。因此，我們的研究結果將可對使用鳥類作為試驗中的掠食者的使用條件，為後續研究相關研究提供更佳實驗設計的方案與分析方法的匯整。

關鍵詞（Keywords）：行為生態學（Ethology）、警戒性（Aposematism）、擬態（Mimicry）、掠食者認知（Cognition of predator）

PE_02

畸翅病毒改變能量代謝影響蜜蜂工蜂分工之研究
Study of the division of labor in honey bee change due to energy metabolic altered under deformed wing virus infection

張維展 [1]，吳岳隆 [1]
Wei-Chan Chang[1] and Yueh-Lung Wu[1]
[1] 國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: alexzergling@gmail.com

背景/研究問題/材料方法

蜜蜂是一種真社會性昆蟲，具備生殖分工、共同育幼的特殊體系。除了生殖階級的分工外，工蜂也可依任務不同而分為維護巢內的內勤蜂及出外採集食物的外勤蜂。剛羽化的工蜂會在巢內執行內勤蜂的工作，隨著日齡的增加，則會漸漸轉變為外勤蜂。蜜蜂的分工狀況會依據壓力及刺激而改變，使蜂群得以適應變動的環境。最近的研究顯示，遭受病毒感染的蜂群，會出現分工重組的現象；另近期果蠅的研究發現，受到病原體感染時，蟲體內的腺苷含量會因此增加，引起發育組織和免疫細胞之間的能量轉換，當能量轉移到免疫系統對抗外來病原體時，正常生理代謝所需之能量受到抑制。我們的早期研究指出，受畸翅病毒感染的蜜蜂其腺苷在有明顯的變化，能量從腦部轉移至免疫系統，這些能量轉移會造成蜜蜂的生理機制受影響，但對是否會影響工蜂分工的狀況尚不得而知。此研究將分析病毒感染後蜜蜂體內的能量轉移與內分泌變化，並進一步與分工狀態做連結。

結果/結論/應用啟示

在畸翅病毒感染之下的工蜂出現提早轉變為外勤蜂的現象，我們將進一步測量分工相關激素及基因，並以 ATP、腺苷、血糖來了解工蜂在逆境之下能量代謝的改變，並在飼養的糖水中額外添加人工腺苷是否增加腦部生理代謝效力，並觀察工蜂分工是否回復正常。

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

PE_03

球背象鼻蟲的物種形成機制：以 *P. moniliferus* 和 *P. orbifer* 兩姐妹種為例

Speciation mechanism in *Pachyrhynchus* weevil: the case of two sister species *P. moniliferus* and *P. orbifer*

何芸[1]，曾惠芸[1]
Yun Ho[1] and Hui-Yun Tseng[1]
[1] 國立臺灣大學 National Taiwan University
Presenting author's email: amyho1997@gmail.com

背景/研究問題/材料方法

物種形成的機制是演化生物學最核心的問題之一，而生殖隔離是物種形成的重要關鍵。生殖隔離包括合子前隔離和合子後隔離：合子前隔離包括行為隔離（交配偏好）、物理隔離（生殖器結構差異）等，而合子後隔離包含子代發育遲緩或雜交不孕等。球背象鼻蟲是一群不會飛的昆蟲，主要分佈於菲律賓，並快速地在這些海洋島嶼上形成高度多樣化的分類群，然而是甚麼樣的因子造成球背象鼻蟲的快速種化仍然未知。本研究假設生殖隔離為近緣物種分化的機制，個體會偏好與同種交配，且同種交配後產生的子代有較高的適存度。研究中比較了兩個姊妹種（*P. moniliferus* 和 *P. orbifer*）之間的交配偏好與交配行為（合子前隔離），與雜交子代和非雜交子代的存活率與發育等（合子後隔離）。

結果/結論/應用啟示

在合子前隔離實驗中，雄性 *P. moniliferus* 與雌性 *P. orbifer* 均可與同種或異種交配，並未表現出交配偏好。而合子後隔離的結果顯示，雜交子代與同種子代間不論是孵化率、存活率、體型大小與發育期等都沒有差異。本研究初步結果顯示兩種近緣種的球背象鼻蟲間並無明顯生殖隔離的現象。

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）、生殖（reproduction）

PE_04

台灣咖啡果小蠹沃爾巴克氏體之檢測分析
Detection of *Wolbachia* infection in the coffee berry borer from Taiwan

吳翊彥[1]，呂曉鈴[1]
Yea-Yan Wu[1] and Hsiao-ling Lu[1]
[1] 國立虎尾科技大學生物科技系 Department of Biotechnology, National Formosa University
Presenting author's email: ilate199512@gmail.com

背景/研究問題/材料方法

沃爾巴克氏體 (*Wolbachia*) 為節肢動物之共生菌，估計多達 66% 的昆蟲物種體內都能偵測到此共生菌。*Wolbachia* 為透過母系生殖細胞垂直遺傳的絕對性胞內共生菌，演化出可誘導胞質不相容 、孤雌生殖、雌性化與殺雄作用等現象，調控寄主昆蟲的生殖方式以增加其適應性。與 *Wolbachia* 共生之昆蟲物種族群多有高偏雌性的趨勢，而咖啡果小蠹在台灣田間亦展現高雌雄性比之特徵。本研究探討台灣咖啡果小蠹是否因有 *Wolbachia* 共生而造成族群高雌雄比之差異。在台灣中、南部地區共計 42 個樣品點進行咖啡果小蠹採樣，而後以聚合酶連鎖反應 (PCR) 增幅 *Wolbachia* 之表面蛋白 (*wsp*) 與 *16s rDNA* 基因片段，以確認台灣咖啡果小蠹的 *Wolbachia* 感染率。

結果/結論/應用啟示

首先以咖啡果小蠹 *Wolbachia* 之 *wsp* 專一性引子進行 PCR。每一個樣品點取 10 隻昆蟲個體進行檢測。初步結果顯示僅單一樣點可增幅出正確片段大小。選殖定序後與前人發表之序列比對相似度僅 83.4%，然而卻高度相近於 *Nephila clavata* 中 *Wolbachia* 的 *wsp* 序列 (相似度 97%)。我們推測可能是昆蟲個體上有寄生蟎類污染而導致非專一性增幅。*Wolbachia* 的低檢出率可能原因有 *Wolbachia* 在田間的寄生率不高，抑或在寄主體內含量不高。爾後改採使用單一個體進行檢測，並以廣效性引子增幅 *16s rDNA* 片段。我們的結果顯示台灣咖啡果小蠹的 *Wolbachia* 感染率甚低，其所展現之高雌雄性比特徵，可能是由其他機制所調控。

關鍵詞（Keywords）：咖啡果小蠹（*Hypothenemus hampei*）、內共生菌（Endosymbiont）、沃爾巴克氏體表面蛋白（*Wolbachia* Surface Protein）、16S 核糖體 DNA （16S ribosomal DNA）

PE_05

龍眼雞(半翅目：蠟蟬科)若蟲形態之個體發生學與渡邊氏東方蠟蟬之比較

Ontogenetic changes in the morphology of *Pyrops candelaria* (Hemiptera: Fulgoridae) and comparison with *Pyrops watanabei*

林亞琍[1]，林佑昇[1]，廖治榮[1]，蕭旭峰[1]，柯俊成[1]
Ya-Li Lin[1], You-Sheng Lin[1], Jhih-Rong Liao[1], Shiuh-Feng Shiao[1] and Chiun-Cheng Ko[1]
[1]國立臺灣大學昆蟲學系 Department of Entomology, National Taiwan University
Presenting author's email: r09632001@ntu.edu.tw

背景/研究問題/材料方法

龍眼雞為於 2018 年首次現蹤於臺灣的外來種，主要寄主植物為龍眼、柚子與芒果。目前對農作物危害程度尚未知，然外來種有對本土生態仍可能造成負面影響，故需進行移除。若能針對脆弱的若蟲期進行防治，將有助於移除成效。渡邊氏東方蠟蟬為臺灣原生的近似種蠟蟬，曾因數量稀少被列為保育類，其卵、若蟲的形態與龍眼雞相近，且龍眼雞亦能棲息於渡邊氏東方蠟蟬的寄主植物烏桕上，有棲地重疊的情形。若能找出兩者卵與若蟲的差異，便可避免錯誤鑑定，誤殺非目標物種。本研究針對兩物種之卵、若蟲的形態進行比較，找出可用於分辨兩者之形態特徵 （卵取卵蓋，若蟲取頭部突起長與體長），進行測量與平均值檢定，比較是否有顯著差異。

結果/結論/應用啟示

結果指出兩種蠟蟬，卵的部分，僅兩卵蓋間距、卵蓋長與卵蓋寬有顯著差異，龍眼雞的兩卵蓋間距較大，卵蓋長寬則是渡邊氏東方蠟蟬較大。若蟲部分，一齡若蟲形態難以區分，但前者五齡若蟲頭部較筆直、近末端處向外擴張的幅度小，後者向外擴張的幅度則明顯較大，故兩者頭部延伸部分的形態差異大。研究結果顯示，若遇卵塊與高齡若蟲，可藉由測量兩卵蓋間距、卵蓋長寬及頭部形態鑑定，針對目標蠟蟬進行防治，加強移除效率。

關鍵詞（Keywords）：龍眼雞（*Pyrops candelaria*）、渡邊氏東方蠟蟬（*Pyrops watanabei*）、蠟蟬科（Fulgoridae）、外來種（alien species）

農業昆蟲學

壁報展示

Posters: Agricultural Entomology

PA_01

蕃茄潛旋蛾在多種茄科植物上的產卵偏好與幼蟲發育表現

Oviposition preference and subsequent larval performance of tomato pinworm *Phthorimaea absoluta* (=*Tuta absoluta*) when offered a wide range of Solanaceous host plants

邱柏諺[1]，魏嬗如[1]，廖士睿[1]，顏聖紘[1]
Po-Yen Chiu[1], Shann-Ru Wei[1], Shih-Rei Liao[1] and Shen-Horn Yen[1]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

The tomato pinworm *Phthorimaea absoluta* (=*Tuta absoluta*) (Lepidoptera: Gelechuidae) is originated in South America and has now become the main tomato pest in Europe, Africa and Asia. The wide range of host plants utilized by this pest has been reported as one of the main reasons for the success of this important insect species. However, the information currently available on the biological performance on Solanaceae has been obtained from a limited number of host species in limited countries. The family Solanaceae is composed of thousands of species, many of which are potential hosts for *P. absoluta*. In order to assess the potential of new hosts serving as the alternative hostplants other than tomato, we carried out a series of bioassay to evaluate the oviposition preference of females and the performance of growth of larvae by using a wide range of Solanaceae plants that are common in cropland and horticulture nursery. The Solanaceae used here included tomato *Solanum lycopersicum*, green pepper *Capsicum annuum*, pepper *Capsicum chinense*, eggplant *Solanum melongena*, black nightshade *Solanum nigrum*, Jerusalem cherry *Solanum pseudocapsicum*, *Solanum nitidum*, twoleaf nightshade *Solanum diphyllum*, tree tomarillo *Solanum betaceum*, pepino dulce *Solanum muricatum*, Brazilian nightshade *Solanum seaforthianum*, tobacco *Nicotiana tabacum*, thron apple *Datura stramonium*, goldenberry *Physalis peruviana*, *Brunfelsia uniflora*, Chinese boxthorn *Lycium chinense* and *Petunia*.

結果/結論/應用啟示

Our results showed that the highest oviposition rates occurred on cultivated tomato, eggplant, thorn apple, Petunia, goldenberry, tree tomarillo, and Jerusalem cherry. However, the highest survival rates of the immature stages occurred on tomato, Jerusalem cherry, egg plant and black nightshade. These results clearly demonstrate that the choice of solanaceous host plant species by female has a direct impact on the fitness of larvae, but there is low correlation between host suitability and the phylogeny, growing form, phenology and physical characters of the platnts. These results are important for the planning of integrated pest management strategies.

關鍵詞（Keywords）：適應（adaptation）、食性寬度（diet breadth）、潛葉性昆蟲（leaf miner）、寄主範圍擴張（expansion of host plant）、入侵物種（invasive species）

PA_02

馬尼拉小繭蜂對於不同齡期秋行軍蟲之寄生及發育表現

Parasitism and developmental performance of *Snellenius manilae* on different instars of *Spodoptera frugiperda*

劉蕙如[1]，黃紹毅[2]
Hui-Ru Liu[1] and Shaw-Yhi Hwang[2]
[1] 國立中興大學植物醫學暨安全農業碩士學位學程 Master Program for Plant Medicine and Good Agricultural Practice, National Chung Hsing University
[2] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: liuru1016@gmail.com

背景/研究問題/材料方法

秋行軍蟲 (*Spodoptera frugiperda*) 屬鱗翅目 (Lepidoptera)、夜蛾科 (Noctuidae) 的多食性 (polyphagous) 害蟲，其繁殖能力與遷徙能力強，於 2019 年 6 月入侵台灣後已擴散至全台各縣市。其寄主範圍廣泛，已記錄之寄主植物多達 76 科 353 種，對多種作物具有經濟危害性，國內已知受秋行軍蟲危害之作物包括玉米、高粱、落花生、水稻等 9 種。馬尼拉小繭蜂 (*Snellenius manilae*) 為單元性 (solitary) 幼蟲內寄生蜂，以夜蛾科幼蟲為寄主，是秋行軍蟲潛在的天敵之一。目前已知馬尼拉小繭蜂能寄生秋行軍蟲並完成生活史，但國內尚無馬尼拉小繭蜂寄生於不同齡期秋行軍蟲之研究。本研究使用 2-3 日齡已交尾尚未產卵的馬尼拉小繭蜂雌成蜂寄生不同齡期之秋行軍蟲，寄生 6 小時後於 26 ± 1˚C、相對溼度 65 ± 10%、光週期 14L：10D 下以人工飼料單隻飼育秋行軍蟲，並紀錄馬尼拉小繭蜂之卵至幼蟲期、蛹期、繭重、寄生率、化繭率及羽化率，比較不同寄主齡期間之寄生及發育表現差異。

結果/結論/應用啟示

目前結果顯示，一齡至三齡末的秋行軍蟲皆可被馬尼拉小繭蜂寄生，其中二齡秋行軍蟲有最高的寄生率 (82.47%)，顯著高於一齡 (40.85%)、三齡初 (47.85%) 及三齡末 (53.02%)；而馬尼拉小繭蜂之卵至幼蟲期於一齡秋行軍蟲顯著長於二齡及三齡初，不同寄主齡期間之蛹期則無顯著差異。馬尼拉小繭蜂對秋行軍蟲具有一定防治潛力，未來將依據本研究結果，以秋行軍蟲二齡幼蟲進行後續防治試驗。

關鍵詞（Keywords）：馬尼拉小繭蜂（*Snellenius manilae*）、秋行軍蟲（*Spodoptera frugiperda*）、寄生率（parasitic rate）、發育表現（developmental performance）

PA_03

蕃茄潛旋蛾，一個新近入侵物種在台灣的快速擴張與遺傳同質性

Rapid expansion and genetic homogeneity of *Tuta absoluta*, a new invasive species in Taiwan

顏聖紘[1]，王崇羽[1]，魏嬗如[1]，徐碩謙[1]，廖士睿[1]
Shen-Horn Yen[1], Chung-Yu Wang[1], Shann-Ru Wei[1], Shuo-Chian Shiu[1] and Shi-Rei Liao[1]
[1]國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: shenhornyen@gmail.com

背景/研究問題/材料方法

The tomato borer, *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae), is a serious pest species native to South America that recently became a major threat to tomato production in various parts of the world and may become a problem in most countries of Africa and Eurasia. *Tuta absoluta* was first observed outside its native range in Eastern Spain in 2006 and can now be found throughout Southern Europe, North Africa, the Middle East, India, China and Taiwan. Precise knowledge of the source population of *T. absoluta* invading Taiwan is required to help develop strategies to monitor the invading pathway(s). Such knowledge is currently lacking. The tomato borer was first observed in Puli, Nantou in May, 2020. More than one year later this species has spread to most of the counties of Taiwan. This suggests a single introduction point in Taiwan followed by a geographical expansion. Indirect methods based on phylogenetics are needed to infer the invasion routes of *T. absoluta*. Here, we analyzed the genetic variability of samples collected in 4 cities of Taiwan and 10 countries to infer the source of the *T. absoluta* populations invading Taiwan. In total 442 COI sequences (658 bp) from 26 countries were available from GenBank, and *Phthorimaea operculella* was adopted as the outgroup.

結果/結論/應用啟示

In total 7 haplotypes were identified from the 442 COI sequences from 26 countries, and the majority of the haplotypes is KU565531 (97.5%), and all the 28 sequences from Taiwan belong to this haplotype. Either the Bayesian or Maximum Liklikhood tree of included sequences show that the sequences from Peru, Kenya and India were nested within the Taiwan sequences, and there is no obvious difference between the dissimilarity between Kenya/Taiwan and Peru/Taiwan samples. The results suggest that the highly homogeneous genetic characteristics of the invading population within Taiwan and among the invaded countries can not immediately help to track the source of the invading population, and thus the prevention of such new pest at ports cannot solely rely on on-site inspection and quarantine, but also adequate cleaning of containers.

關鍵詞（Keywords）：番茄（Tomato）、潛葉性昆蟲（leaf miner）、遺傳多樣性（genetic diversity）、入侵物種（invasive species）、旋蛾科（Gelechiidae）

PA_04

新近在台灣被確認的細蛾科害蟲之分類身份
Taxonomic identity of the newly confirmed gracillariid pests in Taiwan

顏聖紘[1]，王崇羽[1]，廖士睿[1]
Shen-Horn Yen[1], Chung-Yu Wang[1] and Shih Rei Liao[1]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

Gracillariidae is the most species-rich leaf-mining moth family with over 2,000 described species worldwide. In Taiwan, there are only 36 valid named species recognized, many of which are difficult to identify using morphology only, but many of them are emerging new pests on various crops, such as jambu, mango, peach, and various shrubs and trees. Here we explore the use of DNA barcodes as a tool for identification and species discovery in Taiwanese gracillariids, and here we report two study cases of newly discovered gracillariid pests in Taichung and Pingtung, respectively. The first species, which was found to cause defoliation of *Pterocarpus* tree in Taiwan, is believed to belong to the genus *Neolithocolletis*. The second species was found to cause bud damage of jambu during the outbreak, and the species is believed to belong to the genus *Macarostola*. We then present a barcode library including all the COI sequences of all the congeneric species and the potential outgroups. Both Maximum Likelihood and Bayesian inference were employed to reconstruct the phylogenetic trees, and the threshold of species delimitation followed the consensus generated by various studies using COI sequences to determine species of the Lepidoptera.

結果/結論/應用啟示

Our analysis show that two new gracillariid pest species are newly identified. The first species is identified as *Neolithocolletis pentadesma* (Meyrick, 1919). The species was known from Indonesia (Java), Malaysia (Sarawak, Malay peninsula), the Philippines (Luzon) and the Seychelles. The larvae feed on *Pterocarpus* and mine the leaves of their host plant. The second species is proven to be *Macarostola zehentneri* (Snellen, 1902), which was originated in Java. The species is not only reported from jambu, but also from other Myrtaceae trees. The larvae mine the abaxial side of the leave of jambu, forming a linear serpentine mine. The mature larvae become leaf roller and making cocoon by curling the leaves. In the future, it would be necessary to prove if the outbreak of *Niolithoceolltis* was due to incidental introduction from SE Asia, and if the outbreak of *Macarostola* was due to hostplant shift from native Myrtaceae species to jambu, or also an incidental introduction from SE Asia.

關鍵詞（Keywords）：印度紫檀（*Pterocarpus indicus*）、蓮霧（*Syzygium samarangense*）、潛葉性昆蟲（leaf miner）、捲葉性昆蟲（leaf roller）、外來入侵種（invasive species）

PA_05

抗啃食性害蟲大豆品系篩選與相關化學防禦之揮發性代謝物研究
Screening insect-resistant soybean and determine the volatile organic compounds involved in the chemical defensive mechanism against insect herbivores

張淵云[1]，林禎祥[2]，陳賢明[1]
Yuan-Yun Zhang[1], Chen-Hsiang Lin[2] and Hieng-Ming Ting[1]
[1] 國立臺灣大學植物科學研究所 Institute of Plant Biology, National Taiwan University
[2] 行政院農業委員會桃園區農業改良場 Taoyuan District Agricultural Research and Extension Station, COA
Presenting author's email: imperatoris0512@gmail.com

背景/研究問題/材料方法

大豆作為世界主要糧食作物，在目前政策下為提高國產雜糧自給率而推廣種植。然而全球氣候變遷導致害蟲大發生，對台灣大豆栽培造成嚴重危害。進而使農藥用量大量增加；為降低農藥用量，抗蟲害大豆育種成為至關重要課題。現階段台灣本土大豆種類缺乏抗蟲害品種(系)，需於現有之大豆中篩選出具有蟲害抗性之品種(系)。而前人研究中植物的不同的代謝物影響其生長發育與抵禦外在逆境如高溫與蟲害等。為加快育種進程，需優先了解具抗蟲害特性品種(系)與其化學防禦機制。本研究以斜紋夜盜蛾為標的害蟲，對台灣本土不同種類大豆進行抗蟲性的篩選，並將利用代謝體學方法研究大豆被害蟲啃食後產生的化學防禦機制。

結果/結論/應用啟示

目前本研究利用斜紋夜盜蛾取食不同品種(系)大豆之增重篩選出抗蟲與感蟲大豆各一種。未來將利用熱脫附式氣相層析法對其被蟲啃咬後產生之揮發性代謝物進行分析。而本試驗從植物代謝體學觀點切入篩選出抗蟲品種(系)與關鍵代謝物。其試驗結果可作為未來育種挑選抗蟲性親本選擇之依據，以降低栽培大豆之農藥使用量並提高大豆栽培面積。

關鍵詞（Keywords）：大豆（Soybean）、斜紋夜盜蛾（*Spodoptera litura*）、揮發性代謝物（Volatile Organic Compounds）、代謝體學（Metabolomics）

PA_07

Evaluation of disease resistance of melon plants by insect vector transmission

Yi-Hui Chen[1,2] and Chi-Wei Tsai[1]
[1] Department of Entomology, National Taiwan University, Taipei, Taiwan
[2] Agricultural Biotechnology Research Center, Academia Sinica, Taipei, Taiwan
Presenting author's email: chiwei@ntu.edu.tw

背景/研究問題/材料方法

Whitefly-transmitted viral disease is one of the destructive emerging diseases that threaten many crops worldwide. Squash leaf curl disease may cause yield losses of melons as much as 100%; therefore, the disease impairs the agriculture economic greatly. The disease is associated with a group of closely related viruses named squash leaf curl viruses. The most important vector of this group of viruses is the sweetpotato whitefly, *Bemisia tabaci*. Because these viruses are exclusively transmitted by *B. tabaci*, so we developed an efficient protocol to evaluate disease resistance of melon plants by insect vector transmission.

結果/結論/應用啟示

Three thousand whiteflies were allowed to feed on the squash leaf curl Philippines virus (SqLCPV)-infected melon plants for 72 h to acquire the virus, and then 20 viruliferous whiteflies per plant were transferred to a net bag and enclosed with a leaf of healthy melon seedlings (1-true-leaf stage). Three weeks later, a polymerase chain reaction assay was conducted to confirm the infection of SqLCPV. Because there are virtually no antiviral compounds available to cure plants with viral diseases, prevention of virus infection and insect vector infestation are important. Breeding for disease resistance is a safe and effective control strategy. We developed an efficient protocol to evaluate disease resistance of melon plants by insect vector transmission, which is essential for breeding for disease resistance.

關鍵詞（Keywords）：*Begomovirus*, *Geminiviridae*, melon, vector transmission, whitefly

PA_08

四種藥劑對越冬荔枝椿象之藥劑致死劑量測定

Lethal dose analysis of 4 insecticides on *Tessaratoma papillosa* (Drury)

陳盈丞[1]，黃慈閔[1]，林慧婷[1]，張淳淳[1]
Ying-Cheng Chen[1], Tzu-Min Huang[1], Hui-Ting Lin[1] and Chun-Chun Chang[1]
[1] 行政院農業委員會臺南區農業改良場 Tainan District Agricultural Research and Extension Station

背景/研究問題/材料方法

荔枝椿象(*Tessaratoma papillosa* (Drury))為一年一世代昆蟲，有越冬之習性，本試驗為探討荔枝椿象成蟲越冬前後對藥劑之感受性差異，將供試蟲源區分為越冬前成蟲以及越冬後成蟲。供試藥劑為 48.34%丁基加保扶水基乳劑、20%亞滅培水溶性粉劑、2.8%賽洛寧乳劑及 2.8%第滅寧乳劑，測試不同濃度下之藥劑致死反應。試驗結果以軟體 Probit-MSChart program(Chi,2021)進行分析，推算半致死劑量(LD_{50})及 90%致死劑量(LD_{90})。最後以 2.8%第滅寧乳劑 LD_{90} 劑量進行田間無人植保機藥劑防治試驗，並同時評估 3 種不同噴頭(TR8003、LU12003 及 IDKT120025)之防治荔枝椿象效果，藉以擬定無人植保機防治策略。

結果/結論/應用啟示

經 Probit-MSChart program 分析結果顯示，越冬前荔枝椿象 LD_{90} 分別為丁基加保扶 9260.5ppm、亞滅培 2783.8 ppm、賽洛寧 578.6ppm 以及第滅寧 514ppm；越冬後荔枝椿象 LD_{90} 分別為丁基加保扶 17302.3 ppm、亞滅培 680.8 ppm、賽洛寧 199.4ppm 以及第滅寧 19.9ppm。另外以 19.9ppm 第滅寧測試無人植保機裝載不同噴頭之田間防治荔枝椿象試驗，結果顯示 TR8003 防治率最高為 89.3%，LU12003 次之為 75%，IDKT120025 為 72%。供試藥劑依照政府公告之每公頃推薦用藥量，並以常見之 10 公升無人機藥桶進行推算，有效濃度分別為：丁基加保扶 7258ppm、亞滅培 2000ppm、賽洛寧 224ppm 及第滅寧 112ppm。將試驗分析 LD_{90} 濃度與政府公告每公頃推薦用藥量回推之濃度比較，第滅寧、亞滅培及賽洛寧三種藥劑 LD_{90} 防治越冬後荔枝椿象成蟲，濃度均低於政府公告稀釋倍數。另丁基加保扶越冬前後試驗分析 LD_{90} 之稀釋倍數，濃度皆高於政府公告稀釋倍數，因此在進行不同時期的荔枝椿象防治，可依此試驗結果進行藥劑選擇。田間試驗以第滅寧 19.9ppm 搭配噴頭 TR8003 效果較另外兩個噴頭防治率高，未來將建立相對應的無人植保機飛行參數，擬定無人植保機防治荔枝椿象標準作業流程。

關鍵詞（Keywords）：荔枝椿象（*Tessaratoma papillosa* (Drury)）、致死劑量（lethal dose）、越冬（overwintering）、噴頭（nozzle）

PA_09

玉米簇尖蛾(鱗翅目：紋翅蛾科)在台灣的發現以及對倉儲作物的潛在影響

Discovery of *Anatrachyntis rileyi* (Lepidoptera: Cosmopterigidae) in Taiwan and its potential influence on stored products

顏聖紘[1]，王崇羽[1]，葉文彬[2]
Shen-Horn Yen[1], Chung-Yu Wang[1] and Wen-Bin Yeh[2]
[1] 國立中山大學生物科學系 Department of Biological Sciences, National Sun Yat-Sen University
[2] 國立中興大學昆蟲學系 Department of Entomology, National Chung Hsing University
Presenting author's email: shenhornyen@mail.nsysu.edu.tw

背景/研究問題/材料方法

Many lepidopterous species are known as the phytophagous pests of living plants, while there are lepidopterous species of which the larvae do not feed on living plants, but but detritus, humus, decayed wood or dead leaves. Such species are mostly not harmful when they survive in the field. However, when they are introduced to farmland or human environment, they may become pest species that infest stored food products and can be transported via the detritus associated with living plants or packing material. Among all the lepidopterous species infesting stored products, the members of Cosmopterigidae are less attended compared with those of Gelechiidae and Pyralidae, while some species have been reported infesting stored products and become the listed plant quarantine pests. In May, 2021, several individuals of a Cosmopterigidae moth were detected from the pineapples which were about to be exported to China. We then identified it was a *Anatrachyntis* species based on morphological characters, and then used the COI sequence information to reconstruct a Maximum Liklihood and Bayesian tree to infer the taxonomic identity of the species. Eventually, all the COI sequences of Anatrachyntis and Pyroderces plus a species of Labdia were included in the analysis.

結果/結論/應用啟示

The resulting phylogeny and estimate of species divergence show that the species found in the quarantined pineapple fruit is *Anatrachyntis rileyi*, a species described from N. America with uncertain origin. The larva feeds on vegetable waste and has been found in various leguminous pods, coffee beans, milo grain, crassula, and stored products. Since it has been reported infesting rice products since incidentally introduced to Japan, we therefore would urge the authorities to take action to monitor the spread and expansion of this newly introduced pest.

關鍵詞(Keywords)：玉米(corn)、倉儲害蟲(stored product pest)、食碎屑動物(detritivore)、紋翅蛾科（Cosmopterigidae）、外來入侵種（invasive species）

醫學昆蟲學

壁報展示

Posters: Medical Entomology

PM_01

Investigation of *Rickettsia* spp. and *Bartonella* spp. in ectoparasites infesting small mammals in Semarang City, Central Java, Indonesia

Chia Hsuan Chen[1], Martini Martini[2] and Kun HsienTsai[1,3]
[1]Institute of Environmental and Occupational Health Sciences, National Taiwan University, Taipei, Taiwan
[2]Faculty of Public Health, University of Diponegoro, Semarang City, Central Java, Indonesia
[3]Department of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: chia19961109@yahoo.com.tw

背景/研究問題/材料方法

Common small mammals living in human environment include, order Rodentia and order Soricomorpha. Rodents are hosts and reservoirs for several zoonotic diseases, such as plague, hanta virus syndrome, leptospirosis, rickettsial diseases, cat scratch fever, and so on. According to the United Nations, the ratio of human population to rodent population in tropical or subtropical areas is about 1:4, it is a huge population of rodents in Indonesia. In Southeast Asia, *Rickettsia* infection rate is the second most frequently reported infection for non-malarial febrile illnesses among residents, just after dengue, yet there are limited studies in the environment. Zoonotic diseases are worthy of attention under the concept of 'One Health'.

The purpose of this study is to investigate the pathogens of small mammals and ectoparasites in Semarang City, Central Java, Indonesia. During February 2020, 50 live-traps were placed in the four traditional markets (Rasamala, Meteseh, Kedungmundu, Penggaron) and nearby households. Body information and specimen of small mammals were collected in the laboratory of University of Diponegoro (UNDIP).

結果/結論/應用啟示

The results of the survey showed that 107 small mammals of 5 species were captured, *Rattus norvegicus*, *Rattus tanezumi*, *Rattus tiomanicus*, *Bandicota indica*, and *Suncus murinus*. The trapping rate is 26.75% (107/400). Each small mammal was picked heart blood after being anesthesia and kept in Whatman® 903 filter paper. A total of 84 *Xenopsylla cheopis* were collected. To detect pathogens, polymerase chain reaction is necessary to amplify specific genes, citrate synthase gene (*gltA* gene), outer membrane protein B (*ompB* gene), and leptospirosis gene (*secY* gene). Through molecular identification, 3.6% (3/84) fleas positive for *Rickettsia typhi* which were collected from rodents in two markets (Rasamala and Kedungmundu) and one household in Kedungmundu. *Rickettsia typhi* is a pathogen of murine typhus. Besides, 91.67% (77/84) of fleas from 24 rodents were detected *Bartonella* spp., there are 5 clusters of species including, *B. rochalimae*-like (n=5), *B. grahamii* (n=1), *B. tribocorum*-like (n=7), *B. queenslandensis* (n=3), *B. elizabethae* (n=3), and *Bartonella* sp. (n=5). The analysis results of dried blood spot (DBS) samples of small mammals showed 25.71% (27/105) positive sequences for *Bartonella* spp., including *B. rochalimae*-like (n=6), *B. tribocorum*-like (n=11), *B. elizabethae* (n=4), and *Bartonella* sp. (n=6). Totally there were 9 urine in filter

papers, and 2 (22.2%) of them were detected for *Leptospira interrogans*. According to the research results, *Rickettsia*, *Bartonella*, and *Leptospira* were detected in people congregate places and had been recorded of human infections. The results of this investigation provide suggestions for formulating prevention strategies of vector-borne diseases in the future.

關鍵詞（Keywords）：Small mammals, Zoonotic diseases, *Bartonella*, Rickettsiaceae, Leptospirosis

PM_02

花蓮及新北地區伴侶動物外寄生蟲貓蚤攜帶貓蚤立克次體及巴通氏菌之分子檢驗

Molecular detection of *Rickettsia felis* and *Bartonella* spp. in cat fleas (*Ctenocephalides felis*) infesting companion animals from Hualien and New Taipei City

林子玲[1]，曾俊傑[2]，吳文哲[3]，蔡坤憲[1,3,4]
Tzu-Ling Lin[1], Chun-Chieh Tseng[2], Wen-Jer Wu[3] and Kun-Hsien Tsai[1,3,4]
[1] 國立臺灣大學公共衛生學院環境與職業健康科學研究所 Institute of Environmental and Occupational Health Sciences, College of Public Health, National Taiwan University, Taipei, Taiwan
[2] 慈濟大學公共衛生學系 Department and Graduate Institute of Public Health, Tzu Chi University, Hualien, Taiwan
[3] 國立臺灣大學昆蟲學系 Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan
[4] 國立臺灣大學公共衛生學系 Department of Public Health, College of Public Health, National Taiwan University, Taipei, Taiwan
Presenting author's email: r08852009@g.ntu.edu.tw

背景/研究問題/材料方法

Cat fleas (*Ctenocephalides felis*) are small, wingless bloodsucking insects, which are the primary ectoparasites of companion animals, such as cats and dogs. They serve as vectors for *Rickettsia felis* and *Bartonella henselae,* which are two zoonotic pathogens that can cause human diseases. The shared environment of humans and companion animals and cat fleas harboring pathogens may reflect the risk of humans contracting these flea-borne diseases. This study aimed to investigate the haplotype diversity of cat fleas, to determine the prevalence and species of *Rickettsia* spp. and *Bartonella* spp. in cat fleas collected from companion animals in Hualien and New Taipei City. Cat fleas were collected from 10 and 2 animal hospitals in Hualien and New Taipei City, respectively. DNA was extracted from individual fleas. *COI* gene and *gltA* gene were amplified by PCR to identify the species of cat flea and pathogens, respectively.

結果/結論/應用啟示

In Hualien, a total of 155 and 222 cat fleas were collected, in 2015 and from 2019 to 2021, respectively. The sequencing results showed that two *COI* haplotypes of cat flea were in Hualien, which are 100% identical to the existing cat flea *COI* sequences in Taiwan (Accession no.: MG586280 & MT394872). The prevalence of *Rickettsia* in the two periods were 3.9% (6/155) and 3.6% (8/222), respectively. *Rickettsia felis* was the only species found in Hualien. The prevalence of *Bartonella* spp. were 7.1% (11/155) and 5.0% (11/222) in the two periods. Three species of *Bartonella, B. henselae* (n=3), *B. clarridgeiae* (n=9), and *Bartonella* sp. BDB01 (n=1) were detected. In New Taipei City, a total of 116 cat fleas were collected in 2 animal hospitals in 2012. One haplotype of cat flea was in New Taipei City, with 100% identical

to existing sequences in Taiwan (Accession no.: MG586280). *R. felis* and a new record of *Candidatus* Rickettsia senegalensis were detected in New Taipei City. *Bartonella* were detected in 19.0% (22/116) cat fleas, with 5 species, *B. henselae* (n=1), *B. clarridgeiae* (n=4), *B. koehlerae* (n=1), *Bartonella* sp. 1-1C (n=1), and *Bartonella* sp. BDB01 (n=1) being identified. To sum up, the prevalence and species of *R. felis* and *Bartonella* spp. were lower in Hualien than in New Taipei City. Human pathogens, *R. felis* and *B. henselae,* were detected in both Hualien and New Taipei City, indicating that owners of companion animals were at risk for contracting zoonotic diseases. Under the concept of One Health, the health of humans, animals, and the environment was closely related. To decrease the risk of contracting zoonoses, it is important for owners to use ectoparasiticides regularly and to keep the shared environment of animals and humans clean.

關鍵詞（Keywords）：貓蚤（*Ctenocephalides felis*）、貓蚤立克次體（*Rickettsia felis*）、巴通氏菌（*Bartonella* spp.）、伴侶動物（Companion animals）、健康一體（One Health）

PM_03

Development of a scrub typhus diagnostic platform incorporating baculovirus cell-surface display technology

Chih-Chi Liao[1], Chih-Hsuan Tsai[1], Huei-Ru Lo[1], Pey-Ru Lin[2], Chang-Chi Lin[2] and Yu-Chan Chao[1, 3, 4]

廖至騏[1]，蔡智瑄[1]，羅彗如[1]，林珮如[2]，林昌棋[2]，趙裕展[1, 3, 4]

[1]Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan, ROC
[2]Institute of Preventive Medicine, National Defense Medical Center, Taipei, Taiwan, ROC
[3]Department of Entomology, National Chung Hsing University, Taichung, Taiwan, ROC
[4]Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan, ROC

背景/研究問題/材料方法

Scrub typhus (ST), also known as tsutsugamushi disease, was endemic in the Asia-Pacific region (the so-called “tsutsugamushi triangle”), but it has now spread worldwide due to globalization, with one million cases each year. The causative pathogen is *Orientia tsutsugamushi*, a gram-negative and obligate intracellular rickettsial bacterium that is transmitted to warm-blooded animals by bites of *Leptotrombidium* mite larvae (chiggers). Without accurate and timely antibiotic treatment, the fatality can reach 30%. However, clinical diagnosis of ST is problematic because of the broad-spectrum flu-like symptoms, relying instead on observation of skin eschar at the bite site. Consequently, ST can still be easily misdiagnosed as dengue fever, typhus, or malaria. Thus, a rapid and accurate diagnostic method is vital to tackle the ST epidemic. We adopted baculovirus surface-display technology to express three variants of TSA56, the major membrane antigen of *O. tsutsugamushi*, as well as the passenger domain of ScaC (ScaC-PD), on insect Sf21 cell surfaces rather than biosafety level 3 bacteria in an enzyme-linked immunosorbent assay (ELISA).

結果/結論/應用啟示

Our cell-based ELISA comprising the four antigen-displaying cell types interacted with monoclonal antibodies as well as serum samples from ST-positive field-caught rats. The results validated that recombinant TSA56 and ScaC-PD were all properly expressed and displayed on Sf21 cells. This cell-based ELISA presented high accuracy (96.3%), sensitivity (98.6%), and specificity (84.6%) when tested against the ST-positive rat sera. Results of a pilot study using human sera were also highly consistent with the results of immunofluorescence analyses. By adopting this approach, we circumvented complex purification and refolding processes required to generate recombinant *O. tsutsugamushi* antigens and reduced the need for expensive equipment and extensively trained operators. Thus, our system has the potential to become a widely used serological platform for diagnosing ST. (Liao et al., 2021. Frontiers in Immunology accepted.)

關鍵詞（Keywords）：baculovirus surface display, cell-based ELISA, *Orientia tsutsugamushi*, scrub typhus, serological diagnosis

感謝以下贊助單位支持第 42 屆台灣昆蟲學會年會

中西化學工業股份有限公司

美嘉儀器股份有限公司

澄朗興業有限公司

台灣富美實有限公司

頂響能多潔股份有限公司

博視科學教育事業有限公司

臺億環境服務有限公司

台灣肥料股份有限公司

正瀚生技股份有限公司

真善美股份有限公司

亞洲水泥股份有限公司

安農股份有限公司

佳家有限公司

中台興化學工業股份有限公司

嘉泰企業股份有限公司

台灣拜耳股份有限公司

松樹國際有限公司

台北市病媒防治商業同業公會

豐暘開發有限公司

台灣先正達股份有限公司

德城行有限公司

現達國際生物科技有限公司

FMC An Agricultural Sciences Company

台灣富美實有限公司
農業廣告字第 110080 號

富美實擁良好的基礎研發能力，致力於為全球種植者提供創新農業解決方案與應用技術，持續提升農業生產力和作物品質，全力推動綠色農業可持續發展。

殺蟲劑

絲奄奄(剋安勃)(農藥許可證農藥進字02678號)
沃多農(賽安勃)(農藥許可證農藥進字03464號)
吉圃園(因得克)(農藥許可證農藥進字02194號)
富銳(傑他賽滅寧)(農藥許可證農藥進字02141號)
大穀麗(加保扶)(農藥許可證農藥進字01990號)
速洛寧(伽瑪賽洛寧)(農業許可證農藥進字02353號)
好吉馬(馬拉松)(農藥許可證農藥進字01248號)
好吉強(陶斯松)(農藥許可證農藥進字01885號)
好桔青(大滅松)(農藥許可證農藥進字01779號)
金正發(阿納寧)(農藥許可證農藥進字01782號)
金正強(阿巴汀)(農藥許可證農藥進字02452號)

除草劑

草達達(乙基克繁草)(農藥許可證農藥進字02192號)
卡門(可滅蹤)(農藥許可證農藥進字02142號)

殺菌劑

樂富果WP(依普同)(農藥許可證農藥進字03228號)
包利贊(撲克拉錳)(農藥許可證農藥進字01897號)
撲克拉(農藥許可證農藥進字00510號)
福元精SC(依普同)(農藥許可證農藥進字03079號)
福吉安(扶吉胺)(農藥許可證農藥進字02717號)
落菌寧(護汰芬)(農藥許可證農藥進字02193號)
金紅(亞托敏)(農藥許可證農藥進字02823號)
丹克利(得克利)(農藥許可證農藥進字02819號)

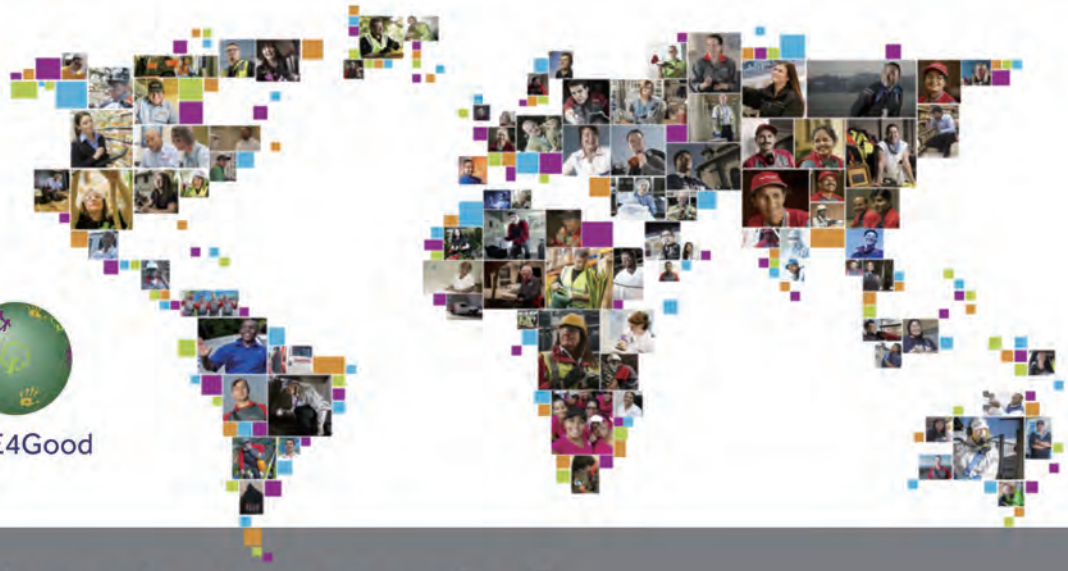
植物營養劑

甘樂Seamaxx TW(肥進(質)字第0303010號)
博嵐Bo-La(肥料登記證肥進(微)字第0303007號)
禾加寶Hi-Phos(肥料登記證肥進(複)字0303009號)
禾盛匯Carnival(肥進(微)字第0303008號)

Rentokil Initial

Protecting People. Enhancing Lives.

DIVERSITY EQUALITY INCLUSION



THE QUEEN'S AWARDS FOR ENTERPRISE: INNOVATION 2020

WINNER BRITAIN'S MOST ADMIRED COMPANIES 2019 Management Today

FTSE4Good

1. A workplace to be proud of
2. Unwavering support to you
3. Fair reward and recognition for your performance
4. Opportunities for all
5. A local - global opportunity

1pco 澄朗

福來朗 HUKUROU

全民都能享受無蟲害的健康環境

All people share a healthy environment without pest.